

85 17 70.8 66 15 US-10-424-599-181984
 86 17 70.8 67 16 US-10-425-115-222248
 87 17 70.8 68 16 US-10-425-115-222248
 88 17 70.8 69 14 US-10-425-115-308662
 89 17 70.8 69 15 US-10-029-386-29425
 90 17 70.8 69 15 US-10-412-699B-1967
 91 17 70.8 69 18 US-10-450-763-41422
 92 17 70.8 70 16 US-10-437-963-172557
 93 17 70.8 71 9 US-09-864-761-45867
 94 17 70.8 71 16 US-10-425-115-204522
 95 17 70.8 71 16 US-10-425-115-269403
 96 17 70.8 72 16 US-10-425-115-286869
 97 17 70.8 73 16 US-10-425-115-236925
 98 17 70.8 74 16 US-10-425-115-200161
 99 17 70.8 75 9 US-09-867-550-510
 100 17 70.8 77 13 US-10-001-843-186
 100 17 70.8 77 16 US-10-437-963-150690

ALIGNMENTS

RESULT 1

US-10-818-036-24
 ; Sequence 24, Application US/10818036
 ; Publication No. US20050222040A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schacter, Bernice Z
 ; APPLICANT: Schacter, Lee P.
 ; APPLICANT: Zeldin, Michael H.
 ; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
 ; FILE REFERENCE: 303544.3000-100
 ; CURRENT APPLICATION NUMBER: US/10/818.036
 ; CURRENT FILING DATE: 2004-04-05
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 24
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-818-036-24

Query Match 70.8%; Score 17; DB 18; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
 | |
 Db 4 FTASW 8

RESULT 2

US-10-818-036-27
 ; Sequence 27, Application US/10818036
 ; Publication No. US20050222040A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schacter, Bernice Z
 ; APPLICANT: Schacter, Lee P.
 ; APPLICANT: Zeldin, Michael H.
 ; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
 ; FILE REFERENCE: 303544.3000-100
 ; CURRENT APPLICATION NUMBER: US/10/818.036
 ; CURRENT FILING DATE: 2004-04-05
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 27
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-818-036-27

Query Match 70.8%; Score 17; DB 18; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.6e+06;

; NAME/KEY: MOD_RES
 ; LOCATION: (8)..(8)
 ; OTHER INFORMATION: AMIDATION
 US-10-818-036-27

Query Match 70.8%; Score 17; DB 18; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
 | |
 Db 4 FTASW 8

RESULT 3

US-10-818-036-28
 ; Sequence 28, Application US/10818036
 ; Publication No. US20050222040A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schacter, Bernice Z
 ; APPLICANT: Schacter, Lee P.
 ; APPLICANT: Zeldin, Michael H.
 ; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
 ; FILE REFERENCE: 303544.3000-100
 ; CURRENT APPLICATION NUMBER: US/10/818.036
 ; CURRENT FILING DATE: 2004-04-05
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 28
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (8)..(8)
 ; OTHER INFORMATION: AMIDATION
 US-10-818-036-28

Query Match 70.8%; Score 17; DB 18; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
 | |
 Db 4 FTASW 8

RESULT 4

US-10-818-036-30
 ; Sequence 30, Application US/10818036
 ; Publication No. US20050222040A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schacter, Bernice Z
 ; APPLICANT: Schacter, Lee P.
 ; APPLICANT: Zeldin, Michael H.
 ; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
 ; FILE REFERENCE: 303544.3000-100
 ; CURRENT APPLICATION NUMBER: US/10/818.036
 ; CURRENT FILING DATE: 2004-04-05
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 30
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)..(1)
 ; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
 US-10-818-036-30

Query Match 70.8%; Score 17; DB 18; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.6e+06;

```
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 FXXXW 6
|
Db 4 FTASW 8

RESULT 5
US-10-072-419-3
; Sequence 3, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Apis mellifera
US-10-072-419-3

Query Match 70.8%; Score 17; DB 14; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 FXXXW 6
|
Db 4 FTSSW 8

RESULT 6
US-10-072-419-8
; Sequence 8, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-072-419-8

Query Match 70.8%; Score 17; DB 14; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 FXXXW 6
|
Db 4 FTSSW 8

RESULT 7
US-10-072-419-8
; Sequence 8, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-072-419-8

Query Match 70.8%; Score 17; DB 14; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 FXXXW 6
|
Db 4 FTSSW 8

RESULT 8
US-10-869-768-3
; Sequence 3, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-818-036-14

Query Match 70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Apis mellifera
US-10-869-768-3

Query Match 70.8%; Score 17; DB 16; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 FXXXW 6
|
Db 4 FTSSW 8

RESULT 8
US-10-869-768-8
; Sequence 8, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-869-768-8

Query Match 70.8%; Score 17; DB 16; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 FXXXW 6
|
Db 4 FTSSW 8

RESULT 9
US-10-818-036-14
; Sequence 14, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-818-036-14

Query Match 70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 FXXXW 6
Db      4 FTASW 8

RESULT 10
US-10-818-036-15
; Sequence 15, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818.036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-818-036-15
Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTASW 8

RESULT 11
US-10-818-036-23
; Sequence 23, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818.036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
US-10-818-036-23
Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTSSW 8

RESULT 12
US-10-818-036-25
; Sequence 25, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818.036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-818-036-25
Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTASW 8

RESULT 13
US-10-818-036-26
; Sequence 26, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818.036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
US-10-818-036-26
Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTASW 8

RESULT 14
US-10-818-036-29
; Sequence 29, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
```


; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818.036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)-(9)
; OTHER INFORMATION: AMIDATION
; US-10-818-036-29

Query Match 70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 4 FTASW 8

RESULT 15
US-09-842-776A-28
; Sequence 28, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CORNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; TITLE OF INVENTION: IN THE STOOL
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842.776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR1) of an
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease
; OTHER INFORMATION: epitope (alternative sequence)
; US-09-842-776A-28

Query Match 70.8%; Score 17; DB 11; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 4 FSTSW 8

RESULT 16
US-10-996-316-139
; Sequence 139, Application US/10996316
; Publication No. US20050123690A1
; GENERAL INFORMATION:
; APPLICANT: Alexion Pharmaceuticals, Inc.
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: McWhirter, John
; APPLICANT: Kretz-Rommel, Anke

Query Match 70.8%; Score 17; DB 14; Length 11;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 4 FTSSW 8

RESULT 17
US-10-072-419-37
; Sequence 37, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072.419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanessa cardui
; US-10-072-419-37

Query Match 70.8%; Score 17; DB 14; Length 11;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 4 FTSSW 8

RESULT 18
US-10-869-768-37
; Sequence 37, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869.768
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072.419
; PRIOR FILING DATE: 2002-02-07

; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC
; TITLE OF INVENTION: LEUKEMIA CELLS AND USES THEREOF
; FILE REFERENCE: 60 CIP IV (1087-43 CIP IV)
; CURRENT APPLICATION NUMBER: US/10/996.316
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/894.672
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/736.188
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/379.151
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254.113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 10
; TYPE: PRT
; ORGANISM: murine
; US-10-996-316-139

Query Match 70.8%; Score 17; DB 18; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 4 FSAAW 8

; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-869-768-37

Query Match 70.8%; Score 17; DB 16; Length 11;
Best Local Similarity 40.0%; Pred. No. 6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FTSSW 8

RESULT 19

US-10-354-240-87
; Sequence 87, Application US/10354240
; Publication No. US20030185847A1
; GENERAL INFORMATION:

; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akino
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SEQ ID NO 103DI
; CURRENT APPLICATION NUMBER: US/10/354,240
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 09/142,524
; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 87
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: CryJ2 peptide, Figure 2, Row 4

US-10-354-240-87

Query Match 70.8%; Score 17; DB 14; Length 15;
Best Local Similarity 40.0%; Pred. No. 8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 9 FTSSW 13

RESULT 20

US-10-354-240-88
; Sequence 88, Application US/10354240
; Publication No. US20030185847A1
; GENERAL INFORMATION:

; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akino
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SEQ ID NO 103DI
; CURRENT APPLICATION NUMBER: US/10/354,240
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 09/142,524

; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: CryJ2 peptide, Figure 2, Row 5

US-10-354-240-88

Query Match 70.8%; Score 17; DB 14; Length 15;
Best Local Similarity 40.0%; Pred. No. 8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FTSSW 8

RESULT 21

US-09-963-339-10
; Sequence 10, Application US/09963339
; Publication No. US20030049700A1
; GENERAL INFORMATION:

; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN
; TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-090001
; CURRENT APPLICATION NUMBER: US/09/963,339
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/235,049
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-963-339-10

Query Match 70.8%; Score 17; DB 10; Length 19;
Best Local Similarity 40.0%; Pred. No. 9.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FSATW 8

RESULT 22

US-10-145-586-59
; Sequence 59, Application US/10145586
; Publication No. US20030138890A1
; GENERAL INFORMATION:

; APPLICANT: Alexandra Gluckemann, Maria
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: M. Galvin, Katherine
; APPLICANT: Weich, Nadine
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
; TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
; FILE REFERENCE: 10448-188001
; CURRENT APPLICATION NUMBER: US/10/145,586
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 59
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-586-59

Query Match      70.8%; Score 17; DB 14; Length 19;
Best Local Similarity 40.0%; Pred. No. 9.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 FXXW 6
      | |
Db      4 FSATW 8

RESULT 23
US-10-931-260-265
; Sequence 265, Application US/10931260
; Publication No. US20050152927A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.;
; Pollock, Joanne;
; Bond, Julian F.;
; Garman, Richard D.;
; Kuo, Mei-Chang;
; Powers, Stephen P.;
; Exley, Mark A.;
; Chen, Xian;
; Shaked, Ze'ev
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; Japanese Cedar Pollen
; NUMBER OF SEQUENCES: 283
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State St
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/931,260
; FILING DATE: 30-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,203
; FILING DATE: 29-Jan-1999
; APPLICATION NUMBER: 08/467,023
; FILING DATE: 1995-JUN-06
; APPLICATION NUMBER: 08/350,225
; FILING DATE: 1994-DEC-06
; APPLICATION NUMBER: 08/226,248
; FILING DATE: 1994-APR-08
; APPLICATION NUMBER: PCT/US93/00139
; FILING DATE: 1993-JAN-15
; APPLICATION NUMBER: 07/938,990
; FILING DATE: 1992-SEP-01
; APPLICATION NUMBER: 07/730,452
; FILING DATE: 1991-JUL-15
; APPLICATION NUMBER: 07/729,134
; FILING DATE: 1991-JUL-12
; APPLICATION NUMBER: 07/975,179
; FILING DATE: 1992-NOV-12
; APPLICATION NUMBER: PCT/US92/05661
; FILING DATE: 1992-JUL-10
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras, Esq.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 265:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-10-931-260-265

Query Match      70.8%; Score 17; DB 18; Length 20;
Best Local Similarity 40.0%; Pred. No. 9.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 FXXW 6
      | |
Db      12 FSTAW 16

RESULT 24
US-10-931-260-264
; Sequence 264, Application US/10931260
; Publication No. US20050152927A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.;
; Pollock, Joanne;
; Bond, Julian F.;
; Garman, Richard D.;
; Kuo, Mei-Chang;
; Powers, Stephen P.;
; Exley, Mark A.;
; Chen, Xian;
; Shaked, Ze'ev
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; Japanese Cedar Pollen
; NUMBER OF SEQUENCES: 283
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State St
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/931,260
; FILING DATE: 30-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,203
; FILING DATE: 29-Jan-1999
; APPLICATION NUMBER: 08/467,023
; FILING DATE: 1995-JUN-06
; APPLICATION NUMBER: 08/350,225
; FILING DATE: 1994-DEC-06
; APPLICATION NUMBER: 08/226,248
; FILING DATE: 1994-APR-08
; APPLICATION NUMBER: PCT/US93/00139
; FILING DATE: 1993-JAN-15
; APPLICATION NUMBER: 07/938,990
; FILING DATE: 1992-SEP-01
; APPLICATION NUMBER: 07/730,452
; FILING DATE: 1991-JUL-15
; APPLICATION NUMBER: 07/729,134
; FILING DATE: 1991-JUL-12
; APPLICATION NUMBER: 07/975,179
; FILING DATE: 1992-NOV-12
; APPLICATION NUMBER: PCT/US92/05661
; FILING DATE: 1992-JUL-10
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras, Esq.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2
```

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; FILING DATE: 1992-NOV-12
; APPLICATION NUMBER: PCT/US92/05661
; FILING DATE: 1992-JUL-10
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandregoutas, Esq.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IM1-028CD2CCPA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 264:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 264:
US-10-931-260-264

Query Match 70.8%; Score 17; DB 18; Length 24;
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 12 FSTAW 16

RESULT 25
US-10-338-777-404
; Sequence 404, Application US/10338777
; Publication No. US20030188343A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Bowen, Benjamin A
; APPLICANT: Haudenschild, Christian D
; APPLICANT: Buckler, Edward S
; TITLE OF INVENTION: Identification of Genes Associated with Growth in Plants
; FILE REFERENCE: 37-0005100S
; CURRENT APPLICATION NUMBER: US/10/338,777
; CURRENT FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 404
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Art. ficial
; FEATURE:
; OTHER INFORMATION: example conservative variation of residues 2-26 of SEQ ID NO:31
US-10-338-777-404

Query Match 70.8%; Score 17; DB 14; Length 25;
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 20 FAASW 24

RESULT 26
US-09-864-761-46828
; Sequence 46828, Application US/09864761
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chun, Wansheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46828
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007739.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.62
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.66
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.61
US-09-864-761-46828

Query Match 70.8%; Score 17; DB 9; Length 27;
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 4 FSATW 8

RESULT 27
US-08-424-550B-428
; Sequence 428, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
```

APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: POREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 428:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-428

Query Match 70.8%; Score 17; DB 8; Length 29;
Best Local Similarity 40.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 12 PASAW 16

RESULT 28
US-10-424-599-160512
; Sequence 160512, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 160512
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_115960C.1.pep
US-10-424-599-160512

Query Match 70.8%; Score 17; DB 15; Length 32;
Best Local Similarity 40.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 18 FTASW 22

RESULT 29
US-10-032-201B-157
; Sequence 157, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-032-201B-157

Query Match 70.8%; Score 17; DB 14; Length 33;
Best Local Similarity 40.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 26 FSATW 30

RESULT 30
US-10-029-386-28347
; Sequence 28347, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G.
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28347
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALL33499.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.45
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.55
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.46
; OTHER INFORMATION: SWISSPROT HIT: Q03368, EVALUE 8.60e+00
US-10-029-386-28347

Query Match 70.8%; Score 17; DB 14; Length 33;
Best Local Similarity 40.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

```

;
; APPLICATION NUMBER: PCT/US93/00139
; FILING DATE: 1993-JAN-15
; APPLICATION NUMBER: 07/938,990
; FILING DATE: 1992-SEP-01
; APPLICATION NUMBER: 07/730,452
; FILING DATE: 1991-JUL-15
; APPLICATION NUMBER: 07/729,134
; FILING DATE: 1991-JUL-12
; APPLICATION NUMBER: 07/975,179
; FILING DATE: 1992-NOV-12
; APPLICATION NUMBER: PCT/US92/05661
; FILING DATE: 1992-JUL-10
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras, Esq.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 137:
; US-10-931-260-137

Query Match 70.8%; Score 17; DB 18; Length 36;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
| |
Db 28 FSATW 32

RESULT 33
US-10-193-795-10
; Sequence 10, Application US/10193795
; Publication No. US20030082202A1
; GENERAL INFORMATION:
; APPLICANT: Flohe, Leopold
; No. US20030082202A1eceleke, Everson
; Kalisz, Henryk
; Montemartini, Marisa
; TITLE OF INVENTION: TRYPADEOXIN, EXPRESSION PLASMID, PROCESS OF
; PRODUCTION, METHOD OF USE, TEST KIT, AND
; PHARMACEUTICAL COMPOSITION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/193,795
; FILING DATE: 12-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,914
; FILING DATE: 11-Jun-1999
; APPLICATION NUMBER: WO PCT/EP97/06983
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:

```

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;
; APPLICATION NUMBER: PCT/US93/00139
; FILING DATE: 1993-JAN-15
; APPLICATION NUMBER: 07/938,990
; FILING DATE: 1992-SEP-01
; APPLICATION NUMBER: 07/730,452
; FILING DATE: 1991-JUL-15
; APPLICATION NUMBER: 07/729,134
; FILING DATE: 1991-JUL-12
; APPLICATION NUMBER: 07/975,179
; FILING DATE: 1992-NOV-12
; APPLICATION NUMBER: PCT/US92/05661
; FILING DATE: 1992-JUL-10
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras, Esq.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 137:
; US-10-931-260-137

Query Match 70.8%; Score 17; DB 15; Length 35;
Best Local Similarity 40.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
| |
Db 22 FSATW 26

RESULT 32
US-10-931-260-137
; Sequence 137, Application US/10931260
; Publication No. US20050152927A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.;
; Pollock, Joanne;
; Bond, Julian F.;
; Garman, Richard D.;
; Kuo, Mei-Chang;
; Powers, Stephen P.;
; Exley, Mark A.;
; Chen, Xian;
; Shaked, Zeev
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; Japanese Cedar Pollen
; NUMBER OF SEQUENCES: 283
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State St
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/931,260
; FILING DATE: 30-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,203
; FILING DATE: 29-Jan-1999
; APPLICATION NUMBER: 08/467,023
; FILING DATE: 1995-JUN-08
; APPLICATION NUMBER: 08/350,225
; FILING DATE: 1994-DEC-06
; APPLICATION NUMBER: 08/226,248
; FILING DATE: 1994-APR-08

```

NAME: Zeller, James P.
REGISTRATION NUMBER: 28.491
REFERENCE/DOCKET NUMBER: 29473/35678
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-193-795-10

Query Match 70.8%; Score 17; DB 14; Length 37;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 11 FSASW 15

RESULT 34
US-10-962-760-10
Sequence 10, Application US/10962760
Publication No. US2005014359A1
GENERAL INFORMATION:
APPLICANT: Nogeceke, Everson
Kalisz, Henryk
Montenarini, Marisa
TITLE OF INVENTION: TRYPTOPAN, EXPRESSION PLASMID, PROCESS OF
PRODUCTION, METHOD OF USE, TEST KIT, AND
PHARMACEUTICAL COMPOSITION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/962,760
FILING DATE: 12-Oct-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP97/06983
FILING DATE: 12-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, James P.
REGISTRATION NUMBER: 28.491
REFERENCE/DOCKET NUMBER: 29473/35678
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-962-760-10

Query Match 70.8%; Score 17; DB 18; Length 37;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 11 FSASW 15

RESULT 35
US-10-818-036-1
Sequence 1, Application US/10818036
Publication No. US20050222040A1
GENERAL INFORMATION:
APPLICANT: Schacter, Bernice Z
APPLICANT: Schacter, Lee P.
APPLICANT: Zeldin, Michael H.
TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
FILE REFERENCE: 303544.3000-100
CURRENT APPLICATION NUMBER: US/10/818,036
CURRENT FILING DATE: 2004-04-05
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 37
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Search sequence
US-10-818-036-1

Query Match 70.8%; Score 17; DB 18; Length 37;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FTASW 36

RESULT 36
US-09-892-877-347
Sequence 347, Application US/09892877
Publication No. US20030077809A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 97 Human secreted proteins
FILE REFERENCE: P2028P1
CURRENT APPLICATION NUMBER: US/09/892,877
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 461
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 347
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-892-877-347

Query Match 70.8%; Score 17; DB 10; Length 38;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 19 FFAAW 23

RESULT 37
US-09-948-783 87
; Sequence 287, Application US/09948783
; Publication No. US20030100051A1
; GENERAL INFORMATION:
; APPLICANT: Rubon et. al.
; TITLE OF INVENTION: 97 Human secreted proteins
; FILE REFERENCE: P2028P2
; CURRENT APPLICATION NUMBER: US/09/948,783
; CURRENT FILING DATE: 2001-03-10
; PRIOR APPLICATION NUMBER: 60/231,846
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: 05/892,877
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/437,658
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/09847
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/085,093
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,094
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,105
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,180
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,927
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,906
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,924
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,928
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,920
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 465
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 287
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-948-783-287

Query Match 70.8%; Score 17; DB 10; Length 38;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 9 AA-W 33

RESULT 38
US-09-057-941-6
; Sequence 6, Application US/09057951
; Patent No. US20020025551A1
; GENERAL INFORMATION:
; APPLICANT: Holzman, Douglas
; TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,951
; FILING DATE: 09-APR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/046001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-057-951-6

Query Match 70.8%; Score 17; DB 9; Length 40;
Best Local Similarity 40.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 6 FSAAW 10

RESULT 39
US-09-864-761-46093
; Sequence 46093, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 46093

LENGTH: 40

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AF233390.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3

US-09-864-761-46093

Query Match

70.8%; Score 17; DB 9; Length 40;

Best Local Similarity 40.0%; Pred. No. 1.5e+04;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

Db 23 FTSSW 27

RESULT 40

US-10-105-150-6

Sequence 6, Application US/10105150

Publication No. US20020119524A1

GENERAL INFORMATION:

APPLICANT: Holtzman, Douglas

TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED

PROTEIN FAMILY AND USES THEREOF

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: PASCSE0 for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/105,150

FILING DATE: 25-Mar-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/057,951

FILING DATE: {unknown}

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 09404/046001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-105-150-6

Query Match 70.8%; Score 17; DB 13; Length 40;
Best Local Similarity 40.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

Db 6 FSAAW 10

Search completed: October 18, 2005, 15:50:34

Job time : 120.706 secs

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GenCore version 5.1.6
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OM protein - protein search using sw model

Run on: October 18, 2005, 15:17:40 ; Search time 123.353 Seconds
(without alignments)
37.362 Million cell updates/sec

Title: US-09-214-371-11

Perfect score: 24

Sequence: 1 XFXXWXXX 9

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_03prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	70.8	9	1 AKH_HELZE	P67787 heliothis z
2	17	70.8	13	2 QXLI2	Q9XLI2 bemisia tab
3	17	70.8	26	2 Q9S880	Q9S880 spinacia ol
4	17	70.8	29	2 Q7R081	Q7R081 plasmodium
5	17	70.8	32	2 Q05602	Q05602 pseudomonas
6	17	70.8	35	2 Q72FN9	Q72FN9 desulfovibr
7	17	70.8	36	2 Q9PV61	Q9PV61 mola mola (
8	17	70.8	38	1 PSAI_PROMA	Q87786 prochlorococ
9	17	70.8	38	2 Q7U4F1	Q7U4F1 synchococcc
10	17	70.8	38	2 Q7V513	Q7V513 prochlorococ
11	17	70.8	38	2 Q9PV63	Q9PV63 pseudopleur
12	17	70.8	40	2 Q9PT24	Q9PT24 oncorhynch
13	17	70.8	40	2 Q9PT28	Q9PT28 salarias sp
14	17	70.8	40	2 Q9PT29	Q9PT29 epinephelus
15	17	70.8	40	2 Q9PU00	Q9PU00 dicentrarch
16	17	70.8	40	2 Q9PU01	Q9PU01 dendrochiru
17	17	70.8	40	2 Q9PU02	Q9PU02 zeus faber
18	17	70.8	40	2 Q9PU03	Q9PU03 sargocentro
19	17	70.8	40	2 Q9PU04	Q9PU04 fundulus he
20	17	70.8	40	2 Q9PU05	Q9PU05 hemiramphus
21	17	70.8	40	2 Q9PU06	Q9PU06 lampris sp.
22	17	70.8	40	2 Q9PV62	Q9PV62 ostracion s
23	17	70.8	40	2 Q9PV64	Q9PV64 channa sp.
24	17	70.8	40	2 Q9PV65	Q9PV65 colisa lali
25	17	70.8	40	2 Q9PV66	Q9PV66 stromateus
26	17	70.8	40	2 Q9PV68	Q9PV68 acanthurus
27	17	70.8	40	2 Q9PV69	Q9PV69 cryptocentr
28	17	70.8	40	2 Q9PV70	Q9PV70 dissostichu
29	17	70.8	40	2 Q9PV71	Q9PV71 mullus sp.
30	17	70.8	40	2 Q9PV72	Q9PV72 lates calca
31	17	70.8	40	2 Q9PV73	Q9PV73 mastacembel

ALIGNMENTS

32	17	70.8	40	2	Q9PV74	Q9PV74 hippocampus
33	17	70.8	40	2	Q9PV75	Q9PV75 poecilia la
34	17	70.8	40	2	Q9PV77	Q9PV77 mugil cepha
35	17	70.8	40	2	Q9PV78	Q9PV78 lophius sp.
36	17	70.8	40	2	Q9PV79	Q9PV79 galaxias ma
37	17	70.8	40	2	Q9PV80	Q9PV80 plecoglossu
38	17	70.8	40	2	Q9PV81	Q9PV81 esox lucius
39	17	70.8	40	2	Q9PV82	Q9PV82 barbus tetr
40	17	70.8	40	2	Q9PV84	Q9PV84 anguilla sp
41	17	70.8	40	2	Q9PV85	Q9PV85 osteoglossu
42	17	70.8	40	2	Q9PV88	Q9PV88 torpedo cal
43	17	70.8	40	2	Q9PV89	Q9PV89 triakis sp.
44	17	70.8	41	2	Q9PU02	Q9PU02 polyporus
45	17	70.8	44	2	Q8XPU4	Q8XPU4 ralstonia s
46	17	70.8	44	2	Q6H9V4	Q6H9V4 phage phi 4
47	17	70.8	49	2	Q8EF00	Q8EF00 shewanella
48	17	70.8	53	2	Q80077	Q80077 staphylococ
49	17	70.8	53	2	Q8SDM7	Q8SDM7 staphylococ
50	17	70.8	53	2	Q8R847	Q8R847 bacterioph
51	17	70.8	53	2	Q9B0G7	Q9B0G7 staphylococ
52	17	70.8	53	2	Q9G031	Q9G031 bacterioph
53	17	70.8	53	2	Q8NVN8	Q8NVN8 staphylococ
54	17	70.8	53	2	Q8NWG8	Q8NWG8 staphylococ
55	17	70.8	53	2	Q931J8	Q931J8 staphylococ
56	17	70.8	53	2	Q99SQ2	Q99SQ2 staphylococ
57	17	70.8	53	2	Q6G7V0	Q6G7V0 staphylococ
58	17	70.8	53	2	Q6GAP3	Q6GAP3 staphylococ
59	17	70.8	53	2	Q6GF65	Q6GF65 staphylococ
60	17	70.8	53	2	Q6GGM4	Q6GGM4 staphylococ
61	17	70.8	54	2	Q645F8	Q645F8 stereochilu
62	17	70.8	54	2	Q8VSJ2	Q8VSJ2 shigella fl
63	17	70.8	54	2	Q6AQ08	Q6AQ08 desulfotale
64	17	70.8	55	2	Q644C2	Q644C2 hydromantes
65	17	70.8	55	2	Q9MBS6	Q9MBS6 staphylococ
66	17	70.8	55	2	Q8FPA2	Q8FPA2 corynebacte
67	17	70.8	57	2	Q8WYF2	Q8WYF2 homo sapien
68	17	70.8	65	1	AKH_MANSE	P67788 manduca sex
69	17	70.8	67	2	Q64109	Q64109 bacterioph
70	17	70.8	67	2	Q34509	Q34509 bacillus su
71	17	70.8	68	2	Q97736	Q97736 human immu
72	17	70.8	68	2	Q6Y2N9	Q6Y2N9 oryza sativ
73	17	70.8	69	2	Q84NA8	Q84NA8 arabidopsis
74	17	70.8	70	2	Q68I24	Q68I24 gasteroste
75	17	70.8	70	2	Q68I27	Q68I27 gasteroste
76	17	70.8	70	2	Q9MJL9	Q9MJL9 scenedesmus
77	17	70.8	70	2	Q69587	Q69587 mycobacteri
78	17	70.8	72	2	Q88601	Q88601 tabacco mos
79	17	70.8	77	1	PUFQ_RHOSH	P15069 rhodobacter
80	17	70.8	78	2	Q678B4	Q678B4 lymphocyacu
81	17	70.8	79	2	Q82YT7	Q82YT7 enterococcu
82	17	70.8	81	2	Q984H4	Q984H4 rhizobium l
83	17	70.8	82	2	Q7EY23	Q7EY23 oryza sativ
84	17	70.8	84	1	Y149_ARCFU	Q30088 archaeoglob
85	17	70.8	84	2	Q60744	Q60744 homo sapien
86	17	70.8	84	2	Q42015	Q42015 arabidopsis
87	17	70.8	85	2	Q6ZLK9	Q6ZLK9 oryza sativ
88	17	70.8	86	2	Q7PP04	Q7PP04 anopheles g
89	17	70.8	87	2	Q8U3P7	Q8U3P7 pyrococcus
90	17	70.8	87	2	Q6YVF4	Q6YVF4 oryza sativ
91	17	70.8	88	1	THI2_DICDI	P29446 dictyosteli
92	17	70.8	88	2	Q8PZ06	Q8PZ06 methanosarc
93	17	70.8	89	2	Q61G64	Q61G64 mycobacteri
94	17	70.8	89	2	Q9B049	Q9B049 mycobacteri
95	17	70.8	89	2	Q7P017	Q7P017 chromobacte
96	17	70.8	92	2	Q9F1H3	Q9F1H3 enterococcu
97	17	70.8	92	2	Q9LCU1	Q9LCU1 thermotoga
98	17	70.8	93	1	CD06_HUMAN	Q99440 homo sapien
99	17	70.8	93	2	Q8TL30	Q8TL30 methanosarc
100	17	70.8	95	2	Q7YX88	Q7YX88 caenorhabdi

```

RESULT 1
AKH_HELZE
ID AKH_HELZE STANDARD; PRT; 9 AA.
AC P67787; P08901;
DT 01-NOV-1988 (Rel. 09, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adipokinetic hormone (Hez-AKH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helioverpa.
OX NCBI_TaxID=7113;
RN [1]
RP SEQUENCE.
RX MEDLINE=86186794; PubMed=3964263;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Holman G.M.,
RA Wagner R.M., Ridgway R.L., Hayes D.K.;
RT "Isolation and primary structure of a peptide from the corpora
RT cardaca of Heliothis zea with adipokinetic activity.";
RL Biochem. Biophys. Res. Commun. 135:622-628(1986).
CC -1- FUNCTION: This hormone, released from cells in the corpora
CC cardaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPH family.
DR PIR; A24244; A24244.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00236; AKH; 1.
KW Amidation; Direct protein sequencing; Flight; Neuropeptide;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 Pyroglutamate carboxylic acid.
FT MOD_RES 9 9 Glycine amide.
SQ SEQUENCE 9 AA; 1026 MW; 403665A5A1A9D1A7 CRC64;

Query Match 70.8%; Score 17; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
DB 4 FTSSW 8

RESULT 2
Q9XLI2
ID Q9XLI2 PRELIMINARY; PRT; 13 AA.
AC Q9XLI2;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Cytochrome oxidase I (Fragment).
OS Bemisia tabaci (Sweetpotato whitefly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleyrodiformes;
OC Aleyrodoidae; Aleyrodidae; Aleyrodinae; Bemisia.
OX NCBI_TaxID=7038;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10583831;
RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,
RA Brown J.K.;
RT "A phylogeographical analysis of the Bemisia tabaci species complex
RT based on mitochondrial DNA markers.";
RL Mol. Ecol. 8:1683-1691(1999).
DR EMBL; AF110703; AAD28415.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;

Query Match 70.8%; Score 17; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
DB 4 FTSSW 8

RESULT 3
Q9S880
ID Q9S880 PRELIMINARY; PRT; 26 AA.
AC Q9S880;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Thioresoxin H2 (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX MEDLINE=91378382; PubMed=1897989;
RA Buchanan B.B.;
RT "Plant thioresoxin h: an animal-like thioresoxin occurring in multiple
RT cell compartments.";
RL Arch. Biochem. Biophys. 287:195-198(1991).
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioresoxin.
DR InterPro; IPR006663; Thioresoxin_dom2.
DR Pfam; PF00085; Thioresoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Redox-active center.
FT NON_TER 1 1
FT NON_TER 26 26
SQ SEQUENCE 26 AA; 2880 MW; A5317FC47DDB8863 CRC64;

Query Match 70.8%; Score 17; DB 2; Length 26;
Best Local Similarity 40.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
DB 6 FTASW 10

RESULT 4
Q7RQ81
ID Q7RQ81 PRELIMINARY; PRT; 29 AA.
AC Q7RQ81;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Names=PY01221;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlson J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,

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RA Florens L., Yates F.R. III, Raine J.D., Sindén R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL: AABL0100318; EAA20511.1; -.
CC KW: Hypothetical protein.
SQ SEQUENCE 29 AA; 3408 MW; F36142D3148EE117 CRC64;

Query Match 70.8%; Score 17; DB 2; Length 29;
Best Local Similarity 40.0%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 11 FSASW 15

RESULT 5
ID O05602 PRELIMINARY; PRT; 32 AA.
AC O05602;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Transposon Tn5041 DNA (fragment).
OS Pseudomonas sp.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KHP41;
RX MEDLINE=97419493; PubMed=9274008;
RA Khlodii G.Y., Yurieva O.V., Gorlenko Z.M., Mindlin S.Z., Bass I.A.,
RA Lomovskaya O.L., Kopteva A.V., Nikiforov V.G.;
RT "Tn5041: a chimeric mercury resistance transposon closely related to
RT the toluene degradative transposon Tn4651."
RL Microbiology 143:2549-2556(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KHP41;
RX Khlodii G.Y., Mindlin S.Z., Gorlenko Z.M., Bass I.A., Kalyaeva E.S.,
RA Nikiforov V.;
RT "Host-dependent transposition of Tn5041."
RL Russ. J. Genet. 36:365-373(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=KHP41;
RX MEDLINE=22315381; PubMed=12427948;
RA Khlodii G., Gorlenko Z., Mindlin S., Hobman J., Nikiforov V.;
RT "Tn5041-like transposons: molecular diversity, evolutionary
RT relationships and distribution of distinct variants in environmental
RT bacteria."
RL Microbiology 148:3569-3582(2002).
DR EMBL; X98999; CAA67458.1; -.
FT NON TER 1 1
FT NON TER 32 32
SQ SEQUENCE 32 AA; 3298 MW; AF42B5EEF917077A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 32;
Best Local Similarity 40.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 11 FSSSW 15

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RESULT 6
Q72FN9
ID Q72FN9 PRELIMINARY; PRT; 35 AA.
AC Q72FN9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=DVU0174;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303);
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.B., Meche B.A., Brinkac L.M.,
RA Dougherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Daviden T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough."
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL; AE017309; AAS94658.1; -.
DR TIGR; DVU0174; -.
KW Complete proteome.
SQ SEQUENCE 35 AA; 3907 MW; CD423DA7D1422A7E CRC64;

Query Match 70.8%; Score 17; DB 2; Length 35;
Best Local Similarity 40.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 15 FATAW 19

RESULT 7
Q9PV61
ID Q9PV61 PRELIMINARY; PRT; 36 AA.
AC Q9PV61;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Dystrophin (fragment).
GN Name=Dyst;
OS Mola mola (ocean sunfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Molidae; Mola.
OX NCBI_TaxID=94237;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137130; AAD54215.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
FT NON TER 1 1
FT NON TER 36 36
SQ SEQUENCE 36 AA; 4181 MW; DE01642A8CAAF18 CRC64;

Query Match 70.8%; Score 17; DB 2; Length 36;
Best Local Similarity 40.0%; Pred. No. 5.9e+03;

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Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXW 6
Db 32 FSSW 36

RESULT 8
PSAI_PROMA
ID PSAL_PROMA STANDARD; PRT; 38 AA.
AC Q87786;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 08-JUL-2004 (Rel. 44, Last annotation update)
DE Photosystem I reaction center subunit VIII.
GN Name=psai; OrderedLocusNames=Pro1678;
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1219;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SARG / COMP 1375 / SS120;
RA van der Staay G.W.M., Moon-van der Staay S.Y., Garczarek L.,
RA Partensky F.;
RT "Characterization of the photosystem I subunits Psai and Psal from two
RT strains of the marine cyanobacterium Prochlorococcus marinus."
RL Photosyn. Res. 57:183-191(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SARG / COMP 1375 / SS120;
RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
RA Dufrene A., Salenouat M., Partensky F., Artiguenave F., Axmann I.M.,
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
RA Wolf Y.I., Hess W.R.;
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT a nearly minimal cyanobacterial genome."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
CC -!- FUNCTION: May help in the organization of the psal subunit.
CC -!- SIMILARITY: Belongs to the psal family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z98594; CAB1178.1; ALT INIT.
DR HAMAP; AE017166; AAQ00722.1; -.
DR HAMAP; MF_00431; atypical; 1.
DR InterPro; IPR001302; PSI_8.
DR Pfam; PF00796; PSI_8; 1.
KW Complete proteome; Photosynthesis; Photosystem I; Transmembrane.
FT TRANSMEM 12 32
SQ SEQUENCE 38 AA; 4081 MW; 19DCDABA650A2F2 CRC64;

Query Match 70.8%; Score 17; DB 1; Length 38;
Best Local Similarity 40.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXW 6
Db 5 FAATW 9

RESULT 9
Q7U4F1
ID Q7U4F1 PRELIMINARY; PRT; 38 AA.
AC Q7U4F1;

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DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Photosystem I subunit VIII (Psai).
GN Name=psai; OrderedLocusNames=SYNW2117;
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarran J.,
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus."
RL Nature 424:1037-1042(2003).
RC EMBL; BX569694; CAE08632.1; -.
KW Complete proteome.
SQ SEQUENCE 38 AA; 3975 MW; 75BEAB4500A52503 CRC64;

Query Match 70.8%; Score 17; DB 2; Length 38;
Best Local Similarity 40.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXW 6
Db 5 FAATW 9

RESULT 10
Q7V513
ID Q7V513 PRELIMINARY; PRT; 38 AA.
AC Q7V513;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Photosystem I subunit VIII (Psai).
GN Name=psai; OrderedLocusNames=PM1767;
OS Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation."
RL Nature 424:1042-1047(2003).
RC EMBL; BX572100; CAE21942.1; -.
KW Complete proteome.
SQ SEQUENCE 38 AA; 4097 MW; 017DCC1CD4C3F4E2 CRC64;

Query Match 70.8%; Score 17; DB 2; Length 38;
Best Local Similarity 40.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXW 6
Db 5 FAATW 9

RESULT 11
Q9PV63
ID Q9PV63 PRELIMINARY; PRT; 38 AA.
AC Q9PV63;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE Dystrophin (Fragment).
GN Name=Dyst;
OS Pseudopleuronectes americanus (Winter flounder) (Pleuronectes americanus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
OX NCBI_TaxID=8265;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267; Venkatesh B., Ning Y., Brenner S.;
RA "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137128; AAD54213.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
FT NON_TER 1
FT NON_TER 38
SQ SEQUENCE 38 AA; 4424 MW; 41C67E01642A8CB0 CRC64;

Query Match 70.8%; Score 17; DB 2; Length 38;
Best Local Similarity 40.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 32 FSSSW 36

RESULT 12
Q9PT24
ID Q9PT24 PRELIMINARY; PRT; 40 AA.
AC Q9PT24
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Pleuronectidae; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267; Venkatesh B., Ning Y., Brenner S.;
RA "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137093; AAD54187.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4551 MW; B485AA19BDB4B17 CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 32 FSSSW 36

RESULT 13
Q9PT28
ID Q9PT28 PRELIMINARY; PRT; 40 AA.

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AC Q9PT28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Salarias sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Blennioidei; Blenniidae; Salarias.
OX NCBI_TaxID=94312;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267; Venkatesh B., Ning Y., Brenner S.;
RA "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137121; AAD54206.1; -.
DR EMBL; AF137120; AAD54206.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 32 FSSSW 36

RESULT 14
Q9PT29
ID Q9PT29 PRELIMINARY; PRT; 40 AA.
AC Q9PT29
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Epinephelus coioides (Orange-spotted grouper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae; Serranidae; Epinephelinae; Epinephelus.
OX NCBI_TaxID=94232;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267; Venkatesh B., Ning Y., Brenner S.;
RA "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137117; AAD54203.1; -.
DR EMBL; AF137116; AAD54203.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6

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Db          32 FSSSW 36
RESULT 15
Q9PU00
ID Q9PU00 PRELIMINARY; PRT; 40 AA.
AC Q9PU00;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Dicotylarchus labrax (European sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Dicentrarchus.
OX NCBI_TaxID=13489;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137115; AAD54202.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXWW 6
Db 32 FSSSW 36

RESULT 16
Q9PU01
ID Q9PU01 PRELIMINARY; PRT; 40 AA.
AC Q9PU01;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Dendrochirus zebra (Zebra turkeyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Scorpaenoidae; Scorpaenidae; Pteroinae; Dendrochirus.
OX NCBI_TaxID=94308;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137112; AAD54200.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXWW 6
Db 32 FSSSW 36

RESULT 17
Q9PU02
ID Q9PU02 PRELIMINARY; PRT; 40 AA.
AC Q9PU02;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Zeus faber (John Dory).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Zeiformes; Zeidae; Zeus.
OX NCBI_TaxID=64108;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137108; AAD55460.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4645 MW; BA7D49A676A3642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXWW 6
Db 32 FSSSW 36

RESULT 18
Q9PU03
ID Q9PU03 PRELIMINARY; PRT; 40 AA.
AC Q9PU03;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Sargocentron sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Beryciformes; Holocentridae;
OC Sargocentron.
OX NCBI_TaxID=94226;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137106; AAD54196.1; -.

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SQ SEQUENCE 40 AA; 4638 MW; B49D49A67E0167E5 CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXWW 6
Db 32 FSSSW 36

RESULT 17
Q9PU02
ID Q9PU02 PRELIMINARY; PRT; 40 AA.
AC Q9PU02;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Zeus faber (John Dory).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Zeiformes; Zeidae; Zeus.
OX NCBI_TaxID=64108;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137108; AAD55460.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4645 MW; BA7D49A676A3642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXWW 6
Db 32 FSSSW 36

RESULT 18
Q9PU03
ID Q9PU03 PRELIMINARY; PRT; 40 AA.
AC Q9PU03;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Sargocentron sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Beryciformes; Holocentridae;
OC Sargocentron.
OX NCBI_TaxID=94226;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137106; AAD54196.1; -.

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DR EMBL; AF137105; AAD54196.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4579 MW; B49C92D67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 32 FSSW 36

RESULT 19
Q9PU04 ID Q9PU04 PRELIMINARY; PRT; 40 AA.
AC Q9PU04;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137103; AAD54194.1; -.
DR EMBL; AF137102; AAD54194.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 32 FSSW 36

RESULT 20
Q9PU05 ID Q9PU05 PRELIMINARY; PRT; 40 AA.
AC Q9PU05;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Hemiramphus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Hemiramphidae; Hemiramphus.
OX NCBI_TaxID=94223;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=93398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137101; AAD54193.1; -.
DR EMBL; AF137100; AAD54193.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 32 FSSW 36

RESULT 21
Q9PU06 ID Q9PU06 PRELIMINARY; PRT; 40 AA.
AC Q9PU06;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Lampiris sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Lampridiformes; Lampridae; Lampiris.
OX NCBI_TaxID=94303;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137096; AAD54189.1; -.
DR EMBL; AF137095; AAD54189.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 32 FSSW 36

RESULT 22
Q9PV62 ID Q9PV62 PRELIMINARY; PRT; 40 AA.
AC Q9PV62;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Ostracion sp. IMCB-2002.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Ostraciidae; Ostreacion; unclassified Ostreacion.
OX NCBI_TaxID=188530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4582 MW; B49D4BCBE01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FSSW 36

RESULT 23
Q9PV64
ID Q9PV64 PRELIMINARY; PRT; 40 AA.
AC Q9PV64;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Channa sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Channidae;
OC Channidae; Channa.
OX NCBI_TaxID=94222;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FSSW 36

RESULT 24
Q9PV65
ID Q9PV65 PRELIMINARY; PRT; 40 AA.
AC Q9PV65;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Colisa lalia (dwarf gourami).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Anabantoidae; Belontiidae; Colisa.
OX NCBI_TaxID=50373;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137126; AAD54211.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FSSW 36

RESULT 25
Q9PV66
ID Q9PV66 PRELIMINARY; PRT; 40 AA.
AC Q9PV66;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Stromateus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Stromateoidae; Stromateidae; Stromateus.
OX NCBI_TaxID=94245;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137125; AAD54210.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FSSW 36

RESULT 26
Q9PV67
ID Q9PV67 PRELIMINARY; PRT; 40 AA.
AC Q9PV67;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Stromateus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Stromateoidae; Stromateidae; Stromateus.
OX NCBI_TaxID=94245;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137125; AAD54210.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FSSW 36

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RESULT 26
Q9PV68      PRELIMINARY;      PRT;      40 AA.
AC Q9PV68;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Acanthurus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Acanthuroidei; Acanthuridae; Acanthurus.
OX NCBI_TaxID=94220;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137123; AAD54208.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4592 MW; B48FFE566BDB542A CRC64;

Query Match      70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXXX 6
Db      32 FSSSW 36

RESULT 27
Q9PV69      PRELIMINARY;      PRT;      40 AA.
AC Q9PV69;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Cryptocentrus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidel;
OC Gobiidae; Cryptocentrus.
OX NCBI_TaxID=94314;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137122; AAD54207.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
DR PROSITE; PS50021; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4611 MW; B49D49A67E01756E CRC64;

Query Match      70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXXX 6
Db      32 FSSSW 36

RESULT 28
Q9PV70      PRELIMINARY;      PRT;      40 AA.
AC Q9PV70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Dissostichus mawsoni (Antarctic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidel; Nototheniidae; Dissostichus.
OX NCBI_TaxID=36200;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137119; AAD54205.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match      70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXXX 6
Db      32 FSSSW 36

RESULT 29
Q9PV71      PRELIMINARY;      PRT;      40 AA.
AC Q9PV71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Mullus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidel;
OC Mullidae; Mullus.
OX NCBI_TaxID=94224;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137118; AAD54204.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40

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SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;
Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXXW 6
Db 32 FSSSW 36

RESULT 30
Q9PV72 ID Q9PV72 PRELIMINARY; PRT; 40 AA.
AC Q9PV72;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Latex calcarifer (Barramundi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Centropomidae; Lates.
OC NCBI_TaxID=8187;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137113; AAD54201.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;
Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXXW 6
Db 32 FSSSW 36

RESULT 31
Q9PV73 ID Q9PV73 PRELIMINARY; PRT; 40 AA.
AC Q9PV73;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Mastacembelus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Synbranchiiformes;
OC Mastacembelidae; Mastacembelus.
OC NCBI_TaxID=94235;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137110; AAD54199.1; -.
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;
Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXXW 6
Db 32 FSSSW 36

RESULT 32
Q9PV74 ID Q9PV74 PRELIMINARY; PRT; 40 AA.
AC Q9PV74;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Hippocampus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
OC Syngnathidae; Hippocampus.
OC NCBI_TaxID=72047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137109; AAD54198.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
DR PROSITE; PS50021; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4541 MW; B49D487D0E01642A CRC64;
Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXXW 6
Db 32 FSSSW 36

RESULT 33
Q9PV75 ID Q9PV75 PRELIMINARY; PRT; 40 AA.
AC Q9PV75;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Poecilia latipinna.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Poecilia.
OC NCBI_TaxID=48699;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137104; AAD54195.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FSSW 36

RESULT 34
Q9PV77
ID Q9PV77 PRELIMINARY; PRT; 40 AA.
AC Q9PV77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Mugil cephalus (Flathead mullet) (Mugil japonicus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Mugilomorpha; Mugilidae;
OC Mugil
OX NCBI_TaxID=48193;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137098; AAD54191.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FSSW 36

RESULT 35
Q9PV78
ID Q9PV78 PRELIMINARY; PRT; 40 AA.
AC Q9PV78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Lophius sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

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OC Acanthomorpha; Paracanthopterygii; Lophiiformes; Lophiidae; Lophius.
OX NCBI_TaxID=30791;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137097; AAD54190.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FSSW 36

RESULT 36
Q9PV79
ID Q9PV79 PRELIMINARY; PRT; 40 AA.
AC Q9PV79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Galaxias maculatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Galaxiidae; Galaxias.
OX NCBI_TaxID=61620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137094; AAD54188.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4613 MW; BA7C92D67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FSSW 36

RESULT 37
Q9PV80
ID Q9PV80 PRELIMINARY; PRT; 40 AA.
AC Q9PV80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;

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OS Plecoglossus altivelis
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Osmeridae; Plecoglossus.
OX NCBI_TaxID=61084;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137092; AAD54186.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4512 MW; B4931BF59BDB542A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FSSW 36

RESULT 38
Q9PV81 ID Q9PV81 PRELIMINARY; PRT; 40 AA.
AC Q9PV81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN NamesDyst;
OS Eox lucius (Northern pike).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Esociformes;
OC Esocidae; Eox.
OX NCBI_TaxID=8010;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137091; AAD54185.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4542 MW; 09155AAL93794B14 CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FSSW 36

RESULT 39
Q9PV82 ID Q9PV82 PRELIMINARY; PRT; 40 AA.
AC Q9PV82;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN NamesDyst;
OS Barbus tetrazona.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Barbus.
OX NCBI_TaxID=94221;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137090; AAD54184.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4573 MW; 459B37C198C3E736 CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FSSW 36

RESULT 40
Q9PV84 ID Q9PV84 PRELIMINARY; PRT; 40 AA.
AC Q9PV84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN NamesDyst;
OS Anguilla sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=62126;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137088; AAD54182.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
DR PROSITE; PSS0021; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4574 MW; 557846B6BDB5437 CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 32 FSSW 36

Search completed: October 18, 2005, 15:30:10
Job time : 124.353 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:18:31 ; Search time 25.9412 Seconds
(without alignments)
33.381 Million cell updates/sec

Title: us-09-214-371-11

Perfect score: 24

Sequence: 1 FXFXXXWXXX 9

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79.*

1: Pirl.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	70.8	9	2 A24244	adipokinetic hormo
2	17	70.8	53	2 T00172	hypothetical prote
3	17	70.8	53	2 D89989	hypothetical prote
4	17	70.8	63	2 T29202	hypothetical prote
5	17	70.8	65	1 A32613	adipokinetic hormo
6	17	70.8	67	2 T12860	hypothetical prote
7	17	70.8	70	2 A86942	hypothetical prote
8	17	70.8	72	2 S15137	thioredoxin h2 - s
9	17	70.8	77	2 S18581	pufQ protein - Rho
10	17	70.8	77	2 T50736	pufQ protein [impo
11	17	70.8	84	2 E62868	hypothetical prote
12	17	70.8	88	2 B46264	thioredoxin 2 - sl
13	17	70.8	98	2 F47624	ig heavy chain V-I
14	17	70.8	99	2 S37444	gene E2 protein -
15	17	70.8	99	2 S37447	gene E2 protein -
16	17	70.8	99	2 S37441	gene E2 protein -
17	17	70.8	99	2 S37448	gene E2 protein -
18	17	70.8	99	2 S37442	gene E2 protein -
19	17	70.8	102	2 G71043	hypothetical prote
20	17	70.8	102	2 B56956	GTP-binding protei
21	17	70.8	104	1 A28086	thioredoxin - rabb
22	17	70.8	105	1 A30006	thioredoxin - chic
23	17	70.8	105	1 JH0568	thioredoxin [valid
24	17	70.8	105	1 J50667	thioredoxin - rhes
25	17	70.8	105	1 S04107	thioredoxin - mous
26	17	70.8	105	1 S04352	thioredoxin - rat
27	17	70.8	107	2 T33843	hypothetical prote
28	17	70.8	108	2 AH2101	thioredoxin [impor
29	17	70.8	112	2 PH0980	ig heavy chain V r

30	17	70.8	112	2 AF2549	hypothetical prote
31	17	70.8	113	1 S57775	thioredoxin h, cyt
32	17	70.8	114	1 JQ2242	thioredoxin h - Ar
33	17	70.8	115	1 G3HJUN	ig heavy chain V-I
34	17	70.8	115	1 PL0238	ig heavy chain V r
35	17	70.8	115	2 G72642	probable surface p
36	17	70.8	116	2 T10739	thioredoxin - comm
37	17	70.8	117	2 PL0237	ig heavy chain V r
38	17	70.8	117	2 PL0234	ig heavy chain V r
39	17	70.8	117	2 PL0235	ig heavy chain V r
40	17	70.8	118	1 S34812	thioredoxin h2 - c
41	17	70.8	118	2 S58118	thioredoxin (clone
42	17	70.8	118	2 S58120	thioredoxin (clone
43	17	70.8	118	2 T10170	thioredoxin - east
44	17	70.8	118	2 PL0231	ig heavy chain V r
45	17	70.8	118	2 F82424	diacylglycerol kin
46	17	70.8	119	2 T08142	thioredoxin h homo
47	17	70.8	119	2 D86330	F6F9.21 protein -
48	17	70.8	119	2 T50867	thioredoxin-like p
49	17	70.8	119	2 A24672	ig heavy chain pre
50	17	70.8	119	2 B72526	hypothetical prote
51	17	70.8	122	2 T04090	probable thioredox
52	17	70.8	123	2 S34009	ig heavy chain V r
53	17	70.8	125	2 T50866	probable thioredox
54	17	70.8	125	2 S58119	thioredoxin (clone
55	17	70.8	126	1 S16590	thioredoxin h1 - c
56	17	70.8	131	2 T50862	thioredoxin-like p
57	17	70.8	131	2 T50863	thioredoxin-like p
58	17	70.8	131	2 T50864	thioredoxin-like p
59	17	70.8	131	2 T50865	thioredoxin-like p
60	17	70.8	133	2 S58123	thioredoxin (clone
61	17	70.8	136	2 A10124	probable prepinin
62	17	70.8	138	2 S03526	ig heavy chain pre
63	17	70.8	141	2 T17760	hypothetical prote
64	17	70.8	141	2 S50690	hypothetical prote
65	17	70.8	141	2 C95330	probable nucleotid
66	17	70.8	142	2 T47190	ig heavy chain var
67	17	70.8	144	2 A36324	growth arrest-spec
68	17	70.8	146	2 A11809	hypothetical prote
69	17	70.8	147	2 F87432	hypothetical prote
70	17	70.8	149	2 T23939	hypothetical prote
71	17	70.8	150	2 D69100	probable protein d
72	17	70.8	152	2 F72702	hypothetical prote
73	17	70.8	156	2 T48047	hypothetical prote
74	17	70.8	158	2 S74730	hypothetical prote
75	17	70.8	160	2 A53293	flm3-region hypoth
76	17	70.8	160	2 S76328	hypothetical prote
77	17	70.8	161	2 AC0966	probable PTS syste
78	17	70.8	174	2 S73301	hypothetical prote
79	17	70.8	174	2 T02276	hypothetical prote
80	17	70.8	174	2 T29491	hypothetical prote
81	17	70.8	180	2 G70028	conserved hypothet
82	17	70.8	180	2 T51724	phosphotransferase
83	17	70.8	182	2 T17625	hypothetical prote
84	17	70.8	182	2 S53822	fucoxanthin chloro
85	17	70.8	183	2 T38917	hypothetical prote
86	17	70.8	189	2 T51064	hypothetical prote
87	17	70.8	191	2 S76398	hypothetical prote
88	17	70.8	194	2 T00482	probable thioredox
89	17	70.8	201	2 AC3593	probable integral
90	17	70.8	204	2 B82410	conserved hypothet
91	17	70.8	205	2 S75300	hypothetical prote
92	17	70.8	206	2 E83515	conserved hypothet
93	17	70.8	207	2 AC0006	probable membrane
94	17	70.8	207	2 T46415	hypothetical prote
95	17	70.8	208	1 D71802	hypothetical prote
96	17	70.8	208	1 G64715	conserved hypothet
97	17	70.8	211	2 S53824	fucoxanthin chloro
98	17	70.8	212	2 B47698	hemagglutinin hag2
99	17	70.8	216	2 S53821	fucoxanthin chloro
100	17	70.8	217	2 C70629	probable mutT3 pro

ALIGNMENTS

RESULT 1

A24244
adipokinet hormone - bollworm
N/Alternate names: Hez-BKH
C/Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C/Date: 31-Mar-1998 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C/Accession: A24244
R/Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
Biochem. Biophys. Res. Commun. 135, 622-628, 1986
A/Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helio
A/Reference number: A24244; MUID:86186794; PMID:3964263
A/Accession: A24244
A/Molecule type: protein
A/Residues: 1-9 <JAP>
A/Cross-references: UNIPROT:P08901
C/Superfamily: adipokinet hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 70.8%; Score 17; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
| |
Db 4 FTSSW 8

RESULT 2

T00172
hypothetical protein 38 - Staphylococcus aureus phage phi PVL
C/Species: Staphylococcus aureus phage phi PVL
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T00172
R/Kaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Y.
Bionci. Biotechnol. Biochem. 61, 1960-1962, 1997
A/Title: Panton-Valentine leukocidin genes in a phage-like particle isolated from mitomy
A/Reference number: 214119; MUID:98067870; PMID:9404084
A/Accession: T00172
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-53 <KAN>
A/Cross-references: UNIPROT:O80077; EMBL:AB009866; NID:d1204727; PIDN:BAA31912.1; PID:d1

Query Match 70.8%; Score 17; DB 2; Length 53;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
| |
Db 28 FTTAW 32

RESULT 3

D89989
hypothetical protein SAS063 [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: D89989
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mitutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: D89989
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-53 <KUR>

A/Cross-references: UNIPROT:Q99SQ2; GB:BA000018; PID:g13701784; PIDN:BAB43077.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: SAS063

Query Match 70.8%; Score 17; DB 2; Length 53;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
| |
Db 28 FTTAW 32

RESULT 4

T29202
hypothetical protein F28F9.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T29202
R/Nelson, J.; Wohldmann, P.
A/Description: The sequence of C. elegans cosmid F28F9.
A/Reference number: Z20587
A/Accession: T29202
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-63 <NEL>
A/Cross-references: UNIPROT:Q94194; EMBL:U70850; PIDN:AAB09124.1; GSPDB:GN00022; CESP:F28
A/Experimental source: strain Bristol N2; clone F28F9
C/Genetics:
A/Gene: CESP:F28F9.3
A/Map position: 4
A/Introns: 38/1

Query Match 70.8%; Score 17; DB 2; Length 63;
Best Local Similarity 40.0%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
| |
Db 30 FATAW 34

RESULT 5

A32613
adipokinet hormone precursor - tobacco hornworm
C/Species: Manduca sexta (tobacco hornworm)
C/Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C/Accession: A32613
R/Bradfield, J.Y.; Keeley, L.L.
J. Biol. Chem. 264, 12791-12793, 1989
A/Title: Adipokinet hormone gene sequence from Manduca sexta.
A/Reference number: A32613; MUID:89327232; PMID:2753887
A/Accession: A32613
A/Molecule type: DNA
A/Residues: 1-65 <BRA>
A/Cross-references: UNIPROT:P08901; GB:J04972; NID:g159478; PIDN:AAA29299.1; PID:g159479

C/Genetics:
A/Superfamily: adipokinet hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-28/Product: adipokinet hormone #status predicted <MAT>
F/20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F/28/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gly

Query Match 70.8%; Score 17; DB 1; Length 65;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
| |

Db 23 FTSSW 27

RESULT 6

T12860

hypothetical protein yopZ - Bacillus subtilis phage SPBc2

C:Species: Bacillus subtilis phage SPBc2

C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: T12860; H69918

R:Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.

A:Submitted to the EMBL Data Library, August 1997

A:Description: The complete nucleotide sequence of the Bacillus subtilis SPBc2 prophage

A:Reference number: 217583

A:Accession: T12860

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-67 <LAZ>

A:Cross-references: UNIPROT:O64109; EMBL:AF020713; NID:G3025478; PID:G3025574; PIDN:AAC1

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet

C:Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A:Erlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, E.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: H69918

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-67 <KUN>

A:Cross-references: GB:Z99114; GB:Z99115; GB:AL009126; NID:G2634478; PIDN:CAB13989.1; PI

A:Experimental source: strain 168

C:Genetics:

A:Gene: yopZ

Query Match 70.8%; Score 17; DB 2; Length 67;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 49 FASSW 53

RESULT 7

A86942

hypothetical protein [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: A86942

R:Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: A86942

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-70 <STO>

A:Cross-references: UNIPROT:O69587; GB:AL450380; NID:G13092599; PIDN:CAC29773.1; GSPDB:C

C:Genetics:

A:Gene: ML0265

Query Match 70.8%; Score 17; DB 2; Length 70;
Best Local Similarity 40.0%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 14 FTTSW 18

RESULT 8

S15137

thioredoxin h2 - spinach (fragments)

C:Species: Spinacia oleracea (spinach)

C:Date: 25-Feb-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: S15137

R:Marcus, F.; Chamberlain, S.H.; Chu, C.; Maslarsz, F.R.; Shin, S.; Yee, B.C.; Buchanan,

Arch. Biochem. Biophys. 287, 195-198, 1991

A:Title: Plant thioredoxin h: an animal-like thioredoxin occurring in multiple cell comp

A:Reference number: S15137; MUID:91378382; PMID:1897989

A:Accession: S15137

A:Molecule type: protein

A:Residues: 1-72 <MAR>

A:Cross-references: UNIPROT:Q9S881

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

Query Match 70.8%; Score 17; DB 2; Length 72;
Best Local Similarity 40.0%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 6 FTASW 10

RESULT 9

S18581

pufQ protein - Rhodobacter sphaeroides

C:Species: Rhodobacter sphaeroides

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: S18581; S32854

R:Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.

Mol. Microbiol. 5, 2649-2661, 1991

A:Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon reg

A:Reference number: S18580; MUID:92140030; PMID:1779756

A:Accession: S18581

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-77 <HUN>

A:Cross-references: UNIPROT:P16069; EMBL:X68795; NID:G49170; PID:G49175

C:Genetics:

A:Gene: pufQ

C:Superfamily: pufQ protein

Query Match 70.8%; Score 17; DB 2; Length 77;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 60 FASAW 64

RESULT 10

T50756

pufQ protein [imported] - Rhodobacter sphaeroides

C:Species: Rhodobacter sphaeroides

C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004

C:Accession: T50756

R:Choudhary, M.; Kaplan, S.

Nucleic Acids Res. 28, 862-867, 2000

A:Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2

A:Reference number: Z25222; MUID:20115911; PMID:10648776

A;Accession: T50756
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-77 <CHO>
A;Cross-references: UNIPROT:P16069; EMBL:AF195122; PIDN:AAF24300.1
A;Experimental source: strain 2.4.1
C;Genetics:
C;Gene: pufQ
C;Superfamily: pufQ protein

Query Match 70.8%; Score 17; DB 2; Length 77;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 60 FASAW 64

RESULT 11

E69268
hypothetical protein AF0149 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: E69268
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69268
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-84 <KLE>
A;Cross-references: UNIPROT:O30088; GB:AE001096; GB:AE000782; NID:g2689419; PIDN:AAB9108

Query Match 70.8%; Score 17; DB 2; Length 84;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 42 FASAW 46

RESULT 12

B46264
thioredoxin 2 - slime mold (Dictyostelium discoideum) (fragment)
C;Species: Dictyostelium discoideum
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Aug-2004
C;Accession: B46264
R;Wetterauer, B.; Jacquot, J.P.; Veron, M.
J. Biol. Chem. 267, 9895-9904, 1992
A;Title: Thioredoxins from Dictyostelium discoideum are a developmentally regulated mult
A;Reference number: A46264; MUID:92250653; PMID:1577820
A;Accession: B46264
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-88 <WE>
A;Cross-references: UNIPROT:P29446; GB:M91382; NID:g167930; PIDN:AAA33259.1; PID:g167931
C;Superfamily: Thioredoxin; thioredoxin homology
F;8-88/Domain: thioredoxin homology <THR>

Query Match 70.8%; Score 17; DB 2; Length 88;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 26 FASAW 30

RESULT 13

F47624
IG heavy chain V-I region - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: F47624
R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990
A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation
A;Reference number: A47624; MUID:90237760; PMID:2110243
A;Accession: F47624
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-98 <HAL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 17; DB 2; Length 98;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 29 FSSTW 33

RESULT 14

S37444
gene E2 protein - human papillomavirus type 5 (fragment)
C;Species: human papillomavirus type 5
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37444
R;Deau, A.C.
submitted to the EMBL Data Library, August 1993
A;Reference number: S37440
A;Accession: S37444
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <DEA>
A;Cross-references: UNIPROT:Q81977; EMBL:X74648
C;Superfamily: papillomavirus E2 protein

Query Match 70.8%; Score 17; DB 2; Length 99;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 46 FSTTW 50

RESULT 15

S37447
gene E2 protein - human papillomavirus type 5 (fragment)
C;Species: human papillomavirus type 5
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37447
R;Deau, A.C.
submitted to the EMBL Data Library, August 1993
A;Reference number: S37440
A;Accession: S37447
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <DEA>
A;Cross-references: UNIPROT:Q81979; EMBL:X74651; NID:g404204; PIDN:CAA52715.1; PID:g404204
C;Superfamily: papillomavirus E2 protein

Query Match 70.8%; Score 17; DB 2; Length 99;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
46 FSTTW 50

Db

RESULT 16
S37441
gene E2 protein - human papillomavirus type 5 (fragment)
C:Species: human papillomavirus type 5
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S37441
R:Deau, A.C.
submitted to the EMBL Data Library, August 1993
A:Reference number: S37440
A:Accession: S37441
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <DEA>
A:Cross-references: UNIPROT:Q81973; EMBL:X74645; NID:G404161; PIDN:CAA52709.1; PID:G4041
C:Superfamily: papillomavirus E2 protein

Query Match 70.8%; Score 17; DB 2; Length 99;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
46 FSTTW 50

Db

RESULT 17
S37448
gene E2 protein - human papillomavirus type 5 (fragment)
C:Species: human papillomavirus type 5
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S37448
R:Deau, A.C.
submitted to the EMBL Data Library, August 1993
A:Reference number: S37440
A:Accession: S37448
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <DEA>
A:Cross-references: UNIPROT:Q81981; EMBL:X74652
C:Superfamily: papillomavirus E2 protein

Query Match 70.8%; Score 17; DB 2; Length 99;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
46 FSTTW 50

Db

RESULT 18
S37442
gene E2 protein - human papillomavirus type 5 (fragment)
C:Species: human papillomavirus type 5
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S37442
R:Deau, A.C.
submitted to the EMBL Data Library, August 1993
A:Reference number: S37440
A:Accession: S37442
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <DEA>
A:Cross-references: UNIPROT:Q81975; EMBL:X74646
C:Superfamily: papillomavirus E2 protein

Query Match 70.8%; Score 17; DB 2; Length 99;

Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
46 FSTTW 50

Db

RESULT 19
G71043
hypothetical protein PH1639 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: G71043
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yanamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: G71043
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-102 <KAW>
A:Cross-references: UNIPROT:O59305; GB:AP000006; NID:G3236133; PIDN:BAA30751.1; PID:G325
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1639

Query Match 70.8%; Score 17; DB 2; Length 102;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
34 FASW 38

Db

RESULT 20
B56956
GTP-binding protein-associated protein (clone c) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: B56956
R:Janoueix-Lerosey, I.; Jollivet, F.; Camonis, J.; Marche, P.N.; Goud, B.
J. Biol. Chem. 270, 14801-14808, 1995
A:Title: Two-hybrid system screen with the small GTP-binding protein Rab6. Identification
A:Reference number: A56956; MUID:95301579; PMID:7782346
A:Accession: B56956
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <JAN>
A:Cross-references: UNIPROT:Q62145; GB:L40934; NID:G722666; PIDN:AAA78788.1; PID:G722667

Query Match 70.8%; Score 17; DB 2; Length 102;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
61 FASW 65

Db

RESULT 21
A28086
thioredoxin - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Jun-1989 #sequence_revision 26-May-1994 #text_change 16-Aug-2004
C:Accession: A28086
R:Johnson, R.S.; Mathews, W.R.; Biemann, K.; Hopper, S.
J. Biol. Chem. 263, 9589-9597, 1988
A:Title: Amino acid sequence of thioredoxin isolated from rabbit bone marrow determined
A:Reference number: A28086; MUID:88257078; PMID:3164311

A;Accession: A28086
A;Molecule type: protein

A;Residues: 1-104 <JOH>
A;Cross-references: UNIPROT:P08628

C;Superfamily: Thioresdoxin; thioresdoxin homology

C;Keywords: redox-active disulfide

F;8-91/Domain: thioresdoxin homology <THR>

F;31-34/Disulfide bonds: redox-active #status predicted

Query Match 70.8%; Score 17; DB 1; Length 104;

Best Local Similarity 40.0%; Pred. No. 2.1e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXX 6

Db 26 FSATW 30

RESULT 22

A30006

thioresdoxin - chicken

C;Species: Gallus gallus (chicken)

C;Date: 31-Mar-1989 #sequence_revision 26-May-1994 #text_change 16-Aug-2004

A;Accession: A30006

R;Jones, S.W.; Luk, K.C.

J. Biol. Chem. 263, 9607-9611, 1988

A;Title: Isolation of a chicken thioresdoxin cDNA clone: thioresdoxin mRNA is differential

A;Reference number: A30006; MUID:88257080; PMID:2838473

A;Accession: A30006

A;Molecule type: mRNA

A;Residues: 1-105 <JON>

C;Cross-references: UNIPROT:P08629; GB:J03882; NID:G212765; PIDN:AAA49092.1; PID:G212766

C;Superfamily: Thioresdoxin; thioresdoxin homology

C;Keywords: redox-active disulfide

F;9-92/Domain: thioresdoxin homology <THR>

F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 70.8%; Score 17; DB 1; Length 105;

Best Local Similarity 40.0%; Pred. No. 2.1e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXX 6

Db 27 FSATW 31

RESULT 23

JH0568

thioresdoxin [validated] - human

N;Alternate names: APL-derived factor (ADF); eosinophil cytotoxicity-enhancing factor; t

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 26-May-1994 #text_change 16-Aug-2004

A;Accession: JH0568; S04106; S44375; A31993; PT0079; A60749; A38922; S53453; A60870

R;Tonissen, K.F.; Wells, J.R.E.

Gene 102, 221-228, 1991

A;Title: Isolation and characterization of human thioresdoxin-encoding genes.

A;Reference number: JH0568; MUID:91340156; PMID:1874447

A;Accession: JH0568

A;Molecule type: DNA

A;Residues: 1-105 <TON>

C;Cross-references: UNIPROT:P10599; EMBL:X54539; NID:G37455; PIDN:CAA38410.1; PID:G82572

R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,

EMBO J. 8, 757-764, 1989

A;Title: APL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to thioresdoxin

A;Reference number: S04106; MUID:89251607; PMID:2785919

A;Accession: S04106

A;Molecule type: mRNA

A;Residues: 1-105 <TAGI>

A;Cross-references: GB:X77584; NID:G453963; PIDN:CAA54687.1; PID:G453964

A;Note: this sequence has been revised in reference S44375

R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,

EMBO J. 13, 2244, 1994

A;Reference number: S44375; MUID:94244626; PMID:8187776

A;Contents: erratum
A;Accession: S44375

A;Molecule type: mRNA

A;Residues: 1-105 <TAG2>

A;Cross-references: EMBL:X77584; NID:G453963; PIDN:CAA54687.1; PID:G453964

R;Wollman, E.E.; d'Aurion, L.; Rimsky, L.; Shaw, A.; Jacquot, J.P.; Wingfield, P.; Graber,

J. Biol. Chem. 263, 15506-15512, 1988

A;Title: Cloning and expression of a cDNA for human thioresdoxin.

A;Reference number: A31993; MUID:89008454; PMID:3170595

A;Accession: A31993

A;Molecule type: mRNA

A;Residues: 1-38; 'N', 40-73; 'T', 75-105 <WOL>

A;Cross-references: GB:J04026; NID:G339648; PIDN:AAA74596.1; PID:G339649

R;Martin, H.; Dean, M.

Biochem. Biophys. Res. Commun. 175, 123-128, 1991

A;Title: Identification of a thioresdoxin-related protein associated with plasma membranes

A;Reference number: PT0079; MUID:91151337; PMID:1998498

A;Accession: PT0079

A;Molecule type: protein

A;Residues: 2-13; 'X', 15 <MAR>

R;Silberstein, D.S.; Ali, M.H.; Baker, S.L.; David, J.R.

J. Immunol. 143, 979-983, 1989

A;Title: Human eosinophil cytotoxicity-enhancing factor. Purification, physical characteri

A;Reference number: A60749; MUID:89309777; PMID:2745979

A;Accession: A60749

A;Molecule type: protein

A;Residues: 2-12; 'K', 14-15; 'XX', 18-19; 'X', 21-22 <SIL>

A;Note: the abstract is inconsistent with figure 4 in having one undetermined residue aft

R;Rimsky, L.; Wakasugi, H.; Ferrara, P.; Robin, P.; Capdevielle, J.; Tursz, T.; Fradelizi,

J. Immunol. 136, 3304-3310, 1986

A;Title: Purification to homogeneity and NH-2-terminal amino acid sequence of a novel int

A;Reference number: A38922; MUID:86169684; PMID:3485686

A;Accession: A38922

A;Molecule type: protein

A;Residues: 2-16 <WAK>

R;Dean, M.F.; Martin, H.; Sansom, P.A.

Biochem. J. 304, 861-867, 1994

A;Title: Characterization of a thioresdoxin-related surface protein.

A;Reference number: S53453; MUID:95118305; PMID:7818492

A;Accession: S53453

A;Molecule type: protein

A;Residues: 1-21;38-57 <DEA>

A;Note: described to be a surface-associated thioresdoxin

R;Wakasugi, H.; Rimsky, L.; Mahe, Y.; Kamel, A.M.; Fradelizi, D.; Tursz, T.; Bertoglio, L.

Proc. Natl. Acad. Sci. U.S.A. 84, 804-808, 1987

A;Title: Epstein-Barr virus-containing B-cell line produces an interleukin 1 that it uses

A;Reference number: A60870; MUID:87118252; PMID:3027706

A;Contents: annotation

R;Weichsel, A.; Gasdaska, J.R.; Powis, G.; Montfort, W.R.

submitted to the Brookhaven Protein Data Bank, February 1996

A;Reference number: A65533; PDB:1ERT

A;Contents: annotation; X-ray crystallography, 1.7 angstroms, reduced form, residues 1-10

R;Weichsel, A.; Gasdaska, J.R.; Powis, G.; Montfort, W.R.

submitted to the Brookhaven Protein Data Bank, February 1996

A;Reference number: A65534; PDB:1ERU

A;Contents: annotation; X-ray crystallography, 2.1 angstroms, oxidized form, residues 1-

R;Forman-kay, J.D.; Clore, G.M.; Gronenborn, A.M.

submitted to the Brookhaven Protein Data Bank, December 1990

A;Reference number: A50924; PDB:4TRX

A;Contents: annotation; conformation by (1)H-NMR, residues 1-73; 'T', 75-105

R;Forman-kay, J.D.; Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.

Biochemistry 30, 2685-2698, 1991

A;Title: High-resolution three-dimensional structure of reduced recombinant human thiores

A;Reference number: A38953; MUID:91159399; PMID:2001356

A;Contents: annotation; conformation by (1)H- and (15)N-NMR

C;Comment: This small ubiquitous protein functions in many intracellular biological path.

C;Genetics:

A;Gene: GDB:TXN

A;Cross-references: GDB:120475; OMIM:187700

A;Map position: 9q31-9q31

A;Introns: 8/3; 43/3; 63/3; 85/3

C;Superfamily: Thioresdoxin; thioresdoxin homology

C;Keywords: redox-active disulfide

F;2-105/Product: thioredoxin #status experimental <MAT>
F;9-92/Domain: thioredoxin homology <THR>
F;32-35/Disulfide bonds: redox-active #status experimental

Query Match 70.8%; Score 17; DB 1; Length 105;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 27 FSATW 31

RESULT 24

JS0667
thioredoxin - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 30-Jun-1992 #sequence_revision 26-May-1994 #text_change 16-Aug-2004
C;Accession: JS0667
R;An, G.; Wu, R.

Biochem. Biophys. Res. Commun. 183, 170-175, 1992
A;Title: Thioredoxin gene expression is transcriptionally up-regulated by retinol in monocytes
A;Reference number: JS0667; MUID:92181438; PMID:1543487
A;Accession: JS0667
A;Molecule type: mRNA
A;Residues: 1-105 <ANG>
A;Cross-references: UNIPROT:P29451; GB:M84643; NID:G342338; PIDN:AAA36921.1; PID:G342339
C;Superfamily: Thioredoxin; thioredoxin homology
C;Keywords: redox-active disulfide
F;9-92/Domain: thioredoxin homology <THR>
F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 70.8%; Score 17; DB 1; Length 105;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 27 FSATW 31

RESULT 25

S04107
thioredoxin - mouse
N;Alternate names: ATL-derived factor (ADF)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 16-Aug-2004
C;Accession: JC4068; S44376; S04107
R;Matsui, M.; Taniguchi, Y.; Hirota, K.; Taketo, M.; Yodoi, J.
Gene 152, 165-171, 1995
A;Title: Structure of the mouse thioredoxin-encoding gene and its processed pseudogene.
A;Reference number: JC4068; MUID:95137382; PMID:7835695
A;Accession: JC4068
A;Molecule type: DNA

A;Residues: 1-105 <MAT>
A;Cross-references: UNIPROT:P10639; DDBJ:D21855; NID:G517128
R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai, E.
EMBO J. 13, 2244, 1994
A;Reference number: S44375; MUID:94244626; PMID:8187776
A;Contents: erratum
A;Accession: S44376
A;Molecule type: mRNA

A;Residues: 1-105 <TAG1>
A;Cross-references: EMBL:X77585; NID:G453971; PIDN:CAA54688.1; PID:G453972
R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai, E.
EMBO J. 8, 757-764, 1989
A;Title: ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to thioredoxin
A;Reference number: S04106; MUID:89251607; PMID:2785919
A;Accession: S04107
A;Molecule type: mRNA
A;Residues: 1-93, 'N' 94-96, 'ALT', 100-104, 'S' <TAG2>
A;Cross-references: GB:X77585

C;Comment: This small ubiquitous protein functions in many intracellular biological path

C;Genetics:

A;Gene: MGI:Txn
A;Cross-references: MGI:36258
A;Map position: 4:24.6
A;Introns: 29/2; 44/1; 84/2
C;Superfamily: Thioredoxin; thioredoxin homology
C;Keywords: redox-active disulfide
F;9-92/Domain: thioredoxin homology <THR>
F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 70.8%; Score 17; DB 1; Length 105;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 27 FSATW 31

RESULT 26

S04352
thioredoxin - rat
N;Alternate names: thioredoxin-related surface protein SASP
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1990 #sequence_revision 26-May-1994 #text_change 16-Aug-2004
C;Accession: S04352; S66372
R;Tonissen, K.F.; Robins, A.J.; Wells, J.R.E.
Nucleic Acids Res. 17, 3973, 1989
A;Title: Nucleotide sequence of a cDNA encoding rat thioredoxin.
A;Reference number: S04352; MUID:89282399; PMID:2734107
A;Accession: S04352
A;Molecule type: mRNA
A;Residues: 1-105 <TON>
A;Cross-references: UNIPROT:P11232; EMBL:X14878; NID:G57385; PIDN:CAA33019.1; PID:G57386
R;Dean, M.F.; Martin, H.; Sansom, P.A.
Biochem. J. 304, 861-867, 1994
A;Title: Characterization of a thioredoxin-related surface protein.

A;Reference number: S53453; MUID:95118305; PMID:7818492
A;Accession: S66372
A;Molecule type: protein

A;Residues: 2-21 <DEA>
A;Note: 12-Lys, 15-Gly, 16-Leu, 17-Gln, and 18-Leu were also found
A;Note: described to be a surface-associated thioredoxin
C;Superfamily: Thioredoxin; thioredoxin homology
C;Keywords: redox-active disulfide
F;2-105/Product: thioredoxin #status experimental <MAT>
F;9-92/Domain: thioredoxin homology <THR>
F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 70.8%; Score 17; DB 1; Length 105;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 27 FSATW 31

RESULT 27

T33843
hypothetical protein Y44E3A.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33843
R;Woessner, J.; Graves, T.; Keppler, D.
submitted to the EMBL Data Library, November 1998
A;Description: The sequence of C. elegans cosmid Y44E3A.
A;Reference number: Z21422
A;Accession: T33843
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-107 <WOB>
A;Cross-references: UNIPROT:Q9TXH8; EMBL:AF106589; PIDN:AAC78230.1; GSPDB:GN00019; CESP:

A:Experimental source: strain Bristol N2; clone Y44E3A

C:Genetics:

A:Gene: CBSP:Y44E3A.3

A:Map position: 1

A:Introns: 31/2

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 70.8%; Score 17; DB 2; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXWX 6

Db 27 FTASW 31

RESULT 28

AH2101

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 16-Aug-2004

C:Accession: AH2101

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AH2101

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-108 <KUR>

A:Cross-references: UNIPROT:Q8VUH9; GB:BA000019; PIDN:BAB74066.1; PID:gl7131459; GSPDB:G

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all2367

C:Superfamily: Thioredoxin; thioredoxin homology

Query Match 70.8%; Score 17; DB 2; Length 108;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXWX 6

Db 28 FTATW 32

RESULT 29

PH0980

Ig heavy chain V region (clone 17b.13) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH0980

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH0980

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-112 <TIL>

A:Experimental source: B cell, strain [N2B x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 17; DB 2; Length 112;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXWX 6

Db 29 FSSSW 33

RESULT 30

AF2549

hypothetical protein all7681 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120bel

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AF2549

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AF2549

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-112 <KUR>

A:Cross-references: UNIPROT:Q8ZS31; GB:AP003602; PIDN:BAH77324.1; PID:gl7134766; GSPDB:G

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all7681

A:Genome: plasmid

Query Match 70.8%; Score 17; DB 2; Length 112;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXWX 6

Db 87 FASAW 91

RESULT 31

SS7775

thioredoxin h, cytosolic [validated] - Chlamydomonas reinhardtii

C:Species: Chlamydomonas reinhardtii

C:Date: 27-Oct-1995 #sequence_revision 21-Jan-1997 #text_change 16-Aug-2004

C:Accession: SS7775; SS7799; SS4868; S16090; SS4870

R;Stein, M.; Jacquot, J.P.; Jeannette, E.; Decottignies, P.; Hodges, M.; Lancelin, J.M.;

Plant Mol. Biol. 28, 487-503, 1995

A:Title: Chlamydomonas reinhardtii thioredoxins: structure of the genes coding for the c

on and biochemical properties.

A:Reference number: SS7774; MUID:95359406; PMID:7632918

A:Accession: SS7775

A:Molecule type: DNA

A:Residues: 1-113 <STE>

A:Cross-references: UNIPROT:P80028; EMBL:X80887; NID:g840742; PIDN:CAA56850.1; PID:g84074

A:Accession: SS7799

A:Molecule type: protein

A:Residues: 2-15 <STW>

R;Stein, M.; Hodges, M.; Jeanette, E.; Lancelin, J.M.; Jacquot, J.P.

submitted to the EMBL Data Library, April 1994

A:Description: Chlamydomonas reinhardtii thioredoxins I : cDNA and amino acid deduced se

A:Reference number: SS4844

A:Accession: SS4868

A:Molecule type: mRNA

A:Residues: 1-113 <STF>

A:Cross-references: EMBL:X78822; NID:g840740; PIDN:CAA55399.1; PID:g840741

R;Decottignies, P.; Schmitter, J.M.; Dutka, S.; Jacquot, J.P.; Miginiac-Maslow, M.

Eur. J. Biochem. 198, 505-512, 1991

A:Title: Characterization and primary structure of a second thioredoxin from the green a

A:Reference number: S16090; MUID:91249849; PMID:2040309

A:Accession: S16090

A:Molecule type: protein

A:Residues: 2-112 <MIG>

R;Mittard, V.; Blackledge, M.J.; Stein, M.; Jacquot, J.P.; Marion, D.; Lancelin, J.M.

submitted to the Brookhaven Protein Data Bank, May 1996

A:Reference number: R66748; PDB:1TOF

A:Contents: annotation; conformation by (1)H, (13)C, (15)N-NMR, residues 2-113

R;Mittard, V.; Morelle, N.; Brutscher, B.; Simorre, J.P.; Marion, D.; Stein, M.; Jacquot

Eur. J. Biochem. 229, 473-485, 1995

A:Title: (1)H, (13)C, (15)N-NMR resonance assignments of oxidized thioredoxin h from the

R spectroscopy and computer-assisted backbone assignment.
 A;Reference number: A58618; MUID:95262711; PMID:7744070
 A;Contents: annotation; conformation by (1)H, (13)C, (15)N-NMR
 C;Genetics:
 A;Introns: 27/3; 35/3; 69/3
 C;Superfamily: Thioresdoxin; thioresdoxin homology
 C;Keywords: redox-active disulfide
 F;2-113/Product: thioresdoxin h #status experimental <MAT>
 F;15-98/Domain: thioresdoxin homology <THR>
 F;37-40/Disulfide bonds: redox-active #status experimental

Query Match 70.8%; Score 17; DB 1; Length 113;
 Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
 |
 Db 32 FTATW 36

RESULT 32

JQ2242
 thioresdoxin h - Arabidopsis thaliana
 N;Alternate names: protein F24M12.70
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 19-May-1994 #sequence revision 26-May-1994 #text_change 16-Aug-2004
 C;Accession: JQ2242; T45734; S23905
 R;Rivera-Madrid, R.; Marinho, P.; Brugidou, C.; Chartier, Y.; Meyer, Y.
 Plant Physiol. 102, 327-328, 1993
 A;Title: Nucleotide sequence of a cDNA clone encoding an Arabidopsis thaliana thioresdoxin
 A;Reference number: JQ2242; MUID:94151431; PMID:8108503
 A;Accession: JQ2242
 A;Molecule type: mRNA
 A;Residues: 1-114 <RV>
 A;Cross-references: UNIPROT:P29448; EMBL:Z14084; NID:G16551; PIDN:CAA78462.1; PID:G16552
 R;Vitale, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Lemcke,
 submitted to the Protein Sequence Database, December 1999
 A;Reference number: 223012
 A;Accession: T45734
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-114 <VIT>
 A;Cross-references: EMBL:AL132980
 A;Experimental source: cultivar Columbia; BAC clone F24M12
 C;Genetics:
 A;Gene: F24M12.70

A;Map position: 3
 A;Introns: 30/3; 71/3
 C;Superfamily: Thioresdoxin; thioresdoxin homology
 C;Keywords: redox-active disulfide
 F;18-100/Domain: thioresdoxin homology <THR>
 F;40-43/Disulfide bonds: redox-active #status predicted

Query Match 70.8%; Score 17; DB 1; Length 114;
 Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
 |
 Db 35 FTASW 39

RESULT 33

G3HUJN
 Ig heavy chain V-III region (Jon) - human (tentative sequence)
 C;Species: Homo sapiens (man)
 C;Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text_change 09-Jul-2004
 C;Accession: A02063
 R;Capra, J.D.; Kehoe, J.M.
 Proc. Natl. Acad. Sci. U.S.A. 71, 845-848, 1974
 A;Title: Variable region sequences of five human immunoglobulin heavy chains of the V-HI
 A;Reference number: A93794; MUID:74142702; PMID:4522793
 A;Accession: A02063

A;Molecule type: protein
 A;Residues: 1-115 <CAP>
 A;Cross-references: UNIPROT:P01780
 C;Comment: This chain was isolated from an IgG3 myeloma protein.
 C;Genetics:
 A;Gene: GDB:IGHV@
 A;Cross-references: GDB:128528; OMIM:147070
 A;Map position: 14q32.33-14q32.33
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>
 F;22-96/Disulfide bonds: #status predicted

Query Match 70.8%; Score 17; DB 1; Length 115;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
 |
 Db 29 FSTAW 33

RESULT 34

PL0238
 Ig heavy chain V region (anti-DNA, 6NVH and 6QVH) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C;Accession: PL0238
 R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990
 A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A;Reference number: PL0231; MUID:90111618; PMID:2104919
 A;Accession: PL0238
 A;Molecule type: mRNA
 A;Residues: 1-115 <SHL>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;1-30/Region: framework 1
 F;15-98/Domain: immunoglobulin homology <IMM>
 F;31-35/Region: complementarity-determining 1
 F;36-49/Region: framework 2
 F;50-66/Region: complementarity-determining 2
 F;67-98/Region: framework 3
 F;99-107/Region: complementarity-determining 3
 F;108-115/Region: framework 4

Query Match 70.8%; Score 17; DB 2; Length 115;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
 |
 Db 29 FSSSW 33

RESULT 35

G72642
 Probable surface protein-1 APE0575 - Aeropyrum pernix (strain K1)
 C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: G72642
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: G72642
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-115 <KAW>
 A;Cross-references: UNIPROT:Q9YEK3; DDBJ:AP000060; NID:G5104188; PIDN:BAA79543.1; PID:d1
 A;Experimental source: strain K1
 C;Genetics:

Query Match 70.8%; Score 17; DB 2; Length 115;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
 |
 Db 29 FSSSW 33

A;Gene: APE0575

Query Match 70.8%; Score 17; DB 2; Length 115;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
 DB 2 FSAW 6

RESULT 36

T10739
 Thioresoxin - common buckwheat
 C;Species: Fegopyrum esculentum (common buckwheat)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T10739
 R;Fujino, K.
 submitted to the EMBL Data Library, September 1996
 A;Reference number: Z17109
 A;Accession: T10739
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-116 <FUJ>
 A;Cross-references: UNIPROT:Q96419; EMBL:D87984
 A;Experimental source: cv. Kitayuki
 C;Function:
 A;Description: participates, by the reversible oxidation of an active center disulfide
 C;Superfamily: thioresoxin; thioresoxin homology
 C;Keywords: redox-active disulfide
 F;17-99/Domain: thioresoxin homology <TXN>

Query Match 70.8%; Score 17; DB 2; Length 116;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
 DB 34 FTASW 38

RESULT 37

PL0237
 IG heavy chain V region (anti-DNA, 1A11VH) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C;Accession: PL0237
 R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
 J. Exp. Med. 171, 265-297, 1990
 A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A;Reference number: PL0231; MUID:90111618; PMID:2104919
 A;Accession: PL0237
 A;Molecule type: mRNA
 A;Residues: 1-117 <SHL>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-30/Region: framework 1
 F;15-98/Domain: immunoglobulin homology <IMM>
 F;31-35/Region: complementarity-determining 1
 F;36-49/Region: framework 2
 F;50-66/Region: complementarity-determining 2
 F;67-98/Region: framework 3
 F;99-109/Region: complementarity-determining 3
 F;110-117/Region: framework 4

Query Match 70.8%; Score 17; DB 2; Length 117;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
 DB 29 FSSW 33

RESULT 38

PL0234
 IG heavy chain V region (anti-DNA, 3H9VH) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C;Accession: PL0234
 R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
 J. Exp. Med. 171, 265-297, 1990
 A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A;Reference number: PL0231; MUID:90111618; PMID:2104919
 A;Accession: PL0234
 A;Molecule type: mRNA
 A;Residues: 1-117 <SHL>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-30/Region: framework 1
 F;15-98/Domain: immunoglobulin homology <IMM>
 F;31-35/Region: complementarity-determining 1
 F;36-49/Region: framework 2
 F;50-66/Region: complementarity-determining 2
 F;67-98/Region: framework 3
 F;99-109/Region: complementarity-determining 3
 F;110-117/Region: framework 4

Query Match 70.8%; Score 17; DB 2; Length 117;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
 DB 29 FSSW 33

RESULT 39

PL0235
 IG heavy chain V region (anti-DNA, 2F2VH and 4H8VH) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C;Accession: PL0235
 R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
 J. Exp. Med. 171, 265-297, 1990
 A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A;Reference number: PL0231; MUID:90111618; PMID:2104919
 A;Accession: PL0235
 A;Molecule type: mRNA
 A;Residues: 1-117 <SHL>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-30/Region: framework 1
 F;15-98/Domain: immunoglobulin homology <IMM>
 F;31-35/Region: complementarity-determining 1
 F;36-49/Region: framework 2
 F;50-66/Region: complementarity-determining 2
 F;67-98/Region: framework 3
 F;99-109/Region: complementarity-determining 3
 F;110-117/Region: framework 4

Query Match 70.8%; Score 17; DB 2; Length 117;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
 DB 29 FSSW 33

RESULT 40

S34812
 Thioresoxin h2 - common tobacco
 C;Species: Nicotiana tabacum (common tobacco)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Aug-2004
 C;Accession: S34812

R;Brugidou, C.; Marty, I.; Chartier, Y.; Meyer, Y.
Mol. Gen. Genet. 238, 285-293, 1993
A:Title: The Nicotiana tabacum genome encodes two cytoplasmic thioredoxin genes which are
A:Reference number: S34812; MUID:93241165; PMID:8479434
A:Accession: S34812
A:Molecule type: DNA
A:Residues: 1-118 <BRU>
A:Cross-references: UNIPROT:Q07090; EMBL:Z11803; NID:G297518; PIDN:CAA77847.1; PID:G2975
C:Genetics:
A:Introns: 29/3; 70/3
C:Superfamily: Thioredoxin; thioredoxin homology
F:17-99/Domain: thioredoxin homology <THR>

Query Match 70.8%; Score 17; DB 1; Length 118;
Best Local Similarity 40.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
|
Db 34 FTASW 38

Search completed: October 18, 2005, 15:31:04
Job time : 26.9412 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:31:13 ; Search time 122.824 Seconds
(without alignments)
28.340 Million cell updates/sec

Title: US-09-214-371-11

Perfect score: 24

Sequence: 1 XFXXXXXXX 9

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 716780

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	70.8	9	ADC07129	Honeybee
2	17	70.8	9	ADC07134	Painted 1
3	17	70.8	10	AB10010	H. pylori
4	17	70.8	10	AB86090	H. pylori
5	17	70.8	10	AB86058	H. pylori
6	17	70.8	11	ADC07163	Painted 1
7	17	70.8	13	AAE05735	Complen
8	17	70.8	13	ABG75574	CDR3 pept
9	17	70.8	14	AAW98088	Human pep
10	17	70.8	15	AAW97874	Japan ced
11	17	70.8	15	AAW97875	Japan ced
12	17	70.8	15	AAW57758	Residues
13	17	70.8	19	AAE23038	Human thi
14	17	70.8	20	AAW42165	T-cell ep
15	17	70.8	20	AAW42165	Complen
16	16	66.7	5	ADR68284	Androgen
17	16	66.7	6	AAW76953	Fusion im
18	16	66.7	6	ABR46309	Staphyloc
19	16	66.7	6	ABR46270	Staphyloc
20	16	66.7	6	ABR46702	Staphyloc
21	16	66.7	6	ABR47093	Staphyloc
22	16	66.7	6	ABR45149	Staphyloc
23	16	66.7	6	ABR45486	Staphyloc
24	16	66.7	6	ABR45878	Staphyloc
25	16	66.7	6	ABR46661	Staphyloc

26	16	66.7	6	ABR47053	Staphyloc
27	16	66.7	6	ABR45190	Staphyloc
28	16	66.7	6	ABR45877	Staphyloc
29	16	66.7	6	ABR46310	Staphyloc
30	16	66.7	6	ABR47094	Staphyloc
31	16	66.7	6	ABR46701	Staphyloc
32	16	66.7	6	ABR47054	Staphyloc
33	16	66.7	6	ABR45525	Staphyloc
34	16	66.7	6	ABR45918	Staphyloc
35	16	66.7	6	ABR45189	Staphyloc
36	16	66.7	6	ABR45485	Staphyloc
37	16	66.7	6	ABR45150	Staphyloc
38	16	66.7	6	ABR45526	Staphyloc
39	16	66.7	6	ABR46269	Staphyloc
40	16	66.7	6	ABR46662	Staphyloc
41	16	66.7	6	ABR45917	Staphyloc
42	16	66.7	6	ADL17086	Phage-dis
43	16	66.7	7	ABP53945	VEGFR-3 b
44	16	66.7	7	ADB47984	Novel hum
45	16	66.7	7	ADJ55539	Novel hum
46	16	66.7	8	AAV18082	Histamine
47	16	66.7	8	ABR53957	Beta-secr
48	16	66.7	8	ABR54100	Beta-secr
49	16	66.7	8	ABR54133	Beta-secr
50	16	66.7	8	ABR54102	Beta-secr
51	16	66.7	8	ABR54137	Beta-secr
52	16	66.7	8	ABR54108	Beta-secr
53	16	66.7	8	ABR54106	Beta-secr
54	16	66.7	8	ABR54135	Beta-secr
55	16	66.7	8	ABR53955	Beta-secr
56	16	66.7	8	ABR54129	Beta-secr
57	16	66.7	8	ABR54139	Beta-secr
58	16	66.7	8	ABR54104	Beta-secr
59	16	66.7	8	ABR54131	Beta-secr
60	16	66.7	8	ABR53953	Beta-secr
61	16	66.7	8	ABR54127	Beta-secr
62	16	66.7	8	ABR54141	Beta-secr
63	16	66.7	8	ADC07151	Libanaseid
64	16	66.7	8	ADC07141	Phymateus
65	16	66.7	8	ADC07150	Crickert A
66	16	66.7	8	ADC07130	Desert lo
67	16	66.7	8	ADC07137	Migratory
68	16	66.7	8	ADC07156	Onitis AK
69	16	66.7	8	ADR69591	Novel hyb
70	16	66.7	8	ADL27410	Amino aci
71	16	66.7	9	AAV48085	Immunogen
72	16	66.7	9	AAE01057	Human sec
73	16	66.7	9	ABP53956	VEGFR-3 b
74	16	66.7	9	ABP47522	N. mening
75	16	66.7	9	ABG97262	Human leu
76	16	66.7	9	AAE31347	Human tyr
77	16	66.7	9	ADH41183	Human tar
78	16	66.7	9	ADH41163	Human tar
79	16	66.7	9	ADK09130	Human pap
80	16	66.7	9	ADK09595	Human pap
81	16	66.7	9	ADN65877	HLA bindi
82	16	66.7	9	ADQ71598	Cancer re
83	16	66.7	9	ADQ72073	Cancer re
84	16	66.7	9	ADQ68606	Cancer re
85	16	66.7	9	ADQ72380	Cancer re
86	16	66.7	9	ADQ69652	Cancer re
87	16	66.7	9	ADQ72453	Cancer re
88	16	66.7	9	ADQ69664	Cancer re
89	16	66.7	9	ADQ71463	Cancer re
90	16	66.7	9	ADQ72148	Cancer re
91	16	66.7	9	ADQ72299	Cancer re
92	16	66.7	9	ADQ69952	Cancer re
93	16	66.7	9	ADQ70871	Cancer re
94	16	66.7	9	ADQ72479	Cancer re
95	16	66.7	9	ADQ70635	Cancer re
96	16	66.7	9	ADQ68180	Cancer re
97	16	66.7	9	ADQ70322	Cancer re
98	16	66.7	9	ADQ72207	Cancer re

99	16	66.7	10	8	ADP26276	Agp26276 Plasmodiu	172	16	66.7	13	4	AAB73644	Aab73644 Pan-DR bi
100	16	66.7	10	1	AAP50792	Aap50792 Sequence	173	16	66.7	13	4	AAB20154	Aab20154 PADRE pep
101	16	66.7	10	1	AAP82754	Aap82754 Sequence	174	16	66.7	13	5	AAB80293	Aab80293 Pan DR ep
102	16	66.7	10	3	AAB26399	Aab26399 Human CAS	175	16	66.7	13	5	ABG31776	Abg31776 Pan DR ep
103	16	66.7	10	4	AAB26393	Aab26393 Human CAS	176	16	66.7	13	5	AAE26369	Aae26369 PADRE pep
104	16	66.7	10	4	AAB87239	Aab87239 Breast-ca	177	16	66.7	13	6	ABP72696	Abp72696 T cell ep
105	16	66.7	10	4	ABBS2440	Abbs2440 Human API	178	16	66.7	13	6	AAO30456	Aao30456 Pan DR ep
106	16	66.7	10	4	AAB35295	Aab35295 Murine PS	179	16	66.7	13	6	AAO30463	Aao30463 Pan DR ep
107	16	66.7	10	5	ABG93457	Abg93457 Alcr amin	180	16	66.7	13	7	ABR82484	Abr82484 Universal
108	16	66.7	10	5	AAB72831	Aab72831 Anti-NG2	181	16	66.7	13	7	ADC81611	Adc81611 Universal
109	16	66.7	10	5	ABG78903	Abg78903 Multiple	182	16	66.7	13	8	ADM06893	Adm06893 Pan DR bi
110	16	66.7	10	6	ABR01558	Abro1558 Human ant	183	16	66.7	13	8	ADP73620	Adp73620 PADRE T c
111	16	66.7	10	6	ABR58766	AbR58766 Alzheimer	184	16	66.7	13	8	ADP48563	Adp48563 Pan DR ep
112	16	66.7	10	6	AAO31089	Aao31089 Human D5-	185	16	66.7	13	8	ADP79777	Adp79777 HLA epitope
113	16	66.7	10	7	ADB79048	Adb79048 Human ant	186	16	66.7	14	2	AAR72636	Aar72636 Cladospor
114	16	66.7	10	7	ADC07160	Adc07160 Corn earw	187	16	66.7	14	4	AAM98495	Aam98495 Human pep
115	16	66.7	10	7	ADC07162	Adc07162 Tentredo	188	16	66.7	14	4	AAM98808	Aam98808 Human pep
116	16	66.7	10	8	ADE85702	AdE85702 Human Eph	189	16	66.7	14	5	AAM49498	Aam49498 Ophiostom
117	16	66.7	10	8	ADH17813	Adh17813 AbM softw	190	16	66.7	14	8	ADS54226	AdS54226 Anti-huma
118	16	66.7	10	8	ADK09671	Adk09671 Human pap	191	16	66.7	15	2	AAR51379	Aar51379 Antigenic
119	16	66.7	10	8	ADK09188	Adk09188 Human pap	192	16	66.7	15	2	AAW07992	Aaw07992 gpi20 pep
120	16	66.7	10	8	ADN31802	Adn31802 Human Alz	193	16	66.7	15	2	AAW76978	Aaw76978 Fusion im
121	16	66.7	10	8	ADM78084	Adm78084 Human SJB	194	16	66.7	15	3	AAW29726	Aaw29726 Gangliosid
122	16	66.7	10	8	ADP47006	Adp47006 Murine he	195	16	66.7	15	3	AAW83247	Aay83247 CVB5RFP fa
123	16	66.7	10	8	ADP47009	Adp47009 Murine he	196	16	66.7	15	3	AAB13300	Aab13300 Caenorhab
124	16	66.7	10	8	ADQ72837	Adq72837 Cancer re	197	16	66.7	15	3	AAB29164	Aab29164 Peptide #
125	16	66.7	10	8	ADQ73638	Adq73638 Cancer re	198	16	66.7	15	4	AAB57714	Aab57714 D.melanog
126	16	66.7	10	8	ADQ69470	Adq69470 Cancer re	199	16	66.7	15	5	AAM47919	Aam47919 Human cla
127	16	66.7	10	8	ADQ72592	Adq72592 Cancer re	200	16	66.7	15	5	AAO20307	Aao20307 Human ple
128	16	66.7	10	8	ADQ73094	Adq73094 Cancer re	201	16	66.7	15	5	AAO20896	Aao20896 N-termina
129	16	66.7	10	8	ADQ69764	Adq69764 Cancer re	202	16	66.7	15	5	AAM47805	Aam47805 Miniature
130	16	66.7	10	8	ADQ73285	Adq73285 Cancer re	203	16	66.7	15	5	ABW77835	Abw77835 Peptide u
131	16	66.7	10	8	ADQ73425	Adq73425 Cancer re	204	16	66.7	15	6	ABR44352	Abr44352 N-termina
132	16	66.7	10	8	ADQ72862	Adq72862 Cancer re	205	16	66.7	15	6	ABP58627	Abp58627 Human end
133	16	66.7	10	8	ADQ73694	Adq73694 Cancer re	206	16	66.7	15	7	ADF12276	Adf12276 Drosophil
134	16	66.7	10	8	ADQ70508	Adq70508 Cancer re	207	16	66.7	15	8	ADQ74628	Adq74628 Cancer re
135	16	66.7	10	8	ADQ68354	Adq68354 Cancer re	208	16	66.7	15	8	ADQ74366	Adq74366 Cancer re
136	16	66.7	10	8	ADQ73492	Adq73492 Cancer re	209	16	66.7	15	8	ADQ73948	Adq73948 Cancer re
137	16	66.7	10	8	ADQ73555	Adq73555 Cancer re	210	16	66.7	15	8	ADQ74000	Adq74000 Cancer re
138	16	66.7	10	8	ADQ69105	Adq69105 Cancer re	211	16	66.7	15	8	ADQ74469	Adq74469 Cancer re
139	16	66.7	10	8	ADQ68777	Adq68777 Cancer re	212	16	66.7	15	8	ADQ74001	Adq74001 Cancer re
140	16	66.7	10	8	ADP47172	Adp47172 Human pho	213	16	66.7	15	8	ADQ74122	Adq74122 Cancer re
141	16	66.7	10	8	ADP47157	Adp47157 Human pho	214	16	66.7	15	8	ADQ74177	Adq74177 Cancer re
142	16	66.7	10	8	ADP47192	Adp47192 Human pho	215	16	66.7	15	8	ADQ74313	Adq74313 Cancer re
143	16	66.7	10	8	ADP47139	Adp47139 Human pho	216	16	66.7	15	8	ADQ74213	Adq74213 Cancer re
144	16	66.7	10	8	ADP47175	Adp47175 Human pho	217	16	66.7	15	8	ADR68288	Adr68288 Androgen
145	16	66.7	10	8	ADR03387	Adr03387 Humanised	218	16	66.7	16	7	ADC22804	Adc22804 Human RAT
146	16	66.7	10	8	ADR03386	Adr03386 Humanised	219	16	66.7	16	7	AAW73469	Aaw73469 Human sec
147	16	66.7	10	8	ADR03383	Adr03383 Humanised	220	16	66.7	16	7	AAE39001	Aae39001 Human G p
148	16	66.7	10	8	ADRI9445	Adri9445 TRPI deri	221	16	66.7	16	7	ADH14277	Adh14277 Mutated e
149	16	66.7	10	8	ADR89805	Adr89805 Anti-CD70	222	16	66.7	17	2	AAW05080	Aaw05080 Generic e
150	16	66.7	11	5	ABP47662	Abp47662 N. mening	223	16	66.7	17	2	AAW07949	Aaw07949 gpi20 pep
151	16	66.7	11	6	AAE31825	Aae31825 Androgen	224	16	66.7	17	2	AAW60595	Aaw60595 Cladospor
152	16	66.7	11	6	AAE31805	Aae31805 Androgen	225	16	66.7	17	2	AAW60595	Aay22119 Human uri
153	16	66.7	11	8	ADGI5913	Adgi5913 Synthetic	226	16	66.7	17	3	AAV97262	Aay97262 Calycin c
154	16	66.7	11	8	ADGI5912	Adgi5912 Synthetic	227	16	66.7	17	3	ABG70457	Abg70457 CDR3 regi
155	16	66.7	11	8	ADGI5911	Adgi5911 Synthetic	228	16	66.7	17	5	AAU82493	Aau82493 Liama CDR
156	16	66.7	11	8	ADQ82020	Adq82020 Camelidae	229	16	66.7	17	5	ABW1385	Abw1385 Yeast eno
157	16	66.7	12	2	AAW32654	Aaw32654 Human pla	230	16	66.7	17	6	ABO27485	Abo27485 Anti-Rh(D
158	16	66.7	12	2	AAW71784	Aaw71784 Mimotope	231	16	66.7	17	6	ABO27486	Abo27486 Anti-Rh(D
159	16	66.7	12	4	AAW60021	Aaw60021 Internali	232	16	66.7	17	7	ADC22805	Adc22805 Human G p
160	16	66.7	12	5	AAE29104	Aae29104 Human DBH	233	16	66.7	17	7	ADD71551	Add71551 Human uri
161	16	66.7	12	5	AAE29118	Aae29118 Human DBH	234	16	66.7	17	7	ADH14278	Adh14278 Mutated e
162	16	66.7	12	6	AAE30883	Aae30883 p300-bind	235	16	66.7	17	8	ABO57902	Abo57902 Human gen
163	16	66.7	12	7	ADA88856	Ada88856 Internali	236	16	66.7	17	8	ABO56359	Abo56359 Human gen
164	16	66.7	12	7	ADC28198	Adc28198 Synthetic	237	16	66.7	18	2	AAW18153	Aaw18153 Cationic,
165	16	66.7	12	8	ADL23639	Adl23639 RAD51C pr	238	16	66.7	18	3	AAB13301	Aab13301 Caenorhab
166	16	66.7	13	2	AAW70250	Aaw70250 Pan DR-bi	239	16	66.7	18	3	AAB13299	Aab13299 Caenorhab
167	16	66.7	13	2	AAW22121	Aaw22121 Padre (pa	240	16	66.7	18	5	AAU91088	Aau91088 Human sec
168	16	66.7	13	2	AAW64575	Aaw64575 Human Pac	241	16	66.7	18	5	AAU91081	Aau91081 Human sec
169	16	66.7	13	3	AAV52558	Aay52558 Universal	242	16	66.7	18	5	ABG65209	Abg65209 Human alb
170	16	66.7	13	3	AAW36289	Aaw36289 Promiscuo	243	16	66.7	18	5	ABG65210	Abg65210 Human alb
171	16	66.7	13	4	AAW99710	Aaw99710 Pan-DR-bi	244	16	66.7	18	8	ADL18453	Adl18453 Antimicro

245	16	66.7	18	8	ADL78477	Adl78477 Albumin f	318	15	62.5	6	6	ABR46423	Staphyloc
246	16	66.7	18	3	ADL78476	Adl78476 Albumin f	319	15	62.5	6	6	ABR46659	Staphyloc
247	16	66.7	19	3	AAB52193	Human ant	320	15	62.5	6	6	ABR46719	Staphyloc
248	16	66.7	19	4	AAM21012	Peptide #	321	15	62.5	6	6	ABR46759	Staphyloc
249	16	66.7	19	4	ABB43110	Peptide #	322	15	62.5	6	6	ABR45182	Staphyloc
250	16	66.7	19	4	AAM36940	Peptide #	323	15	62.5	6	6	ABR45517	Staphyloc
251	16	66.7	19	4	ABB26248	Protein #	324	15	62.5	6	6	ABR45518	Staphyloc
252	16	66.7	19	4	AAM76834	Human bon	325	15	62.5	6	6	ABR46301	Staphyloc
253	16	66.7	19	4	AAM64011	Human bra	326	15	62.5	6	6	ABR46379	Staphyloc
254	16	66.7	19	4	ABG58507	Human liv	327	15	62.5	6	6	ABR46439	Staphyloc
255	16	66.7	19	5	ABG45977	Human pep	328	15	62.5	6	6	ABR46475	Staphyloc
256	16	66.7	19	8	ADR68829	Androgen	329	15	62.5	6	6	ABR46495	Staphyloc
257	16	66.7	20	2	AAR63841	HIV-1 gp1	330	15	62.5	6	6	ABR46531	Staphyloc
258	16	66.7	20	2	AAW08045	HIV pepti	331	15	62.5	6	6	ABR46694	Staphyloc
259	16	66.7	20	2	AAW08044	HIV pepti	332	15	62.5	6	6	ABR45501	Staphyloc
260	16	66.7	20	2	AAR88352	Adenomato	333	15	62.5	6	6	ABR45510	Staphyloc
261	16	66.7	20	2	AAO2155	Peptide u	334	15	62.5	6	6	ABR45901	Staphyloc
262	16	66.7	20	3	AYY07999	Murine an	335	15	62.5	6	6	ABR45915	Staphyloc
263	16	66.7	20	3	AAB10376	HBV core	336	15	62.5	6	6	ABR46268	Staphyloc
264	16	66.7	20	4	ABB50791	Human sec	337	15	62.5	6	6	ABR45894	Staphyloc
265	16	66.7	20	5	AAE20323	Human B7-	338	15	62.5	6	6	ABR46308	Staphyloc
266	16	66.7	20	5	ABP30920	OE8 antib	339	15	62.5	6	6	ABR46435	Staphyloc
267	16	66.7	20	5	ABP30919	OE8 antib	340	15	62.5	6	6	ABR46535	Staphyloc
268	16	66.7	20	6	ABO45048	Novel hum	341	15	62.5	6	6	ABR46678	Staphyloc
269	16	66.7	20	7	ABO26528	Protein a	342	15	62.5	6	6	ABR45166	Staphyloc
270	16	66.7	20	7	ADA08565	Human OE8	343	15	62.5	6	6	ABR45181	Staphyloc
271	16	66.7	20	7	ADA08564	Human OE8	344	15	62.5	6	6	ABR46293	Staphyloc
272	16	66.7	20	7	ADC99562	Cancer-re	345	15	62.5	6	6	ABR46647	Staphyloc
273	16	66.7	20	7	ABW01365	Human HEA	346	15	62.5	6	6	ABR46693	Staphyloc
274	16	66.7	20	7	ADF08907	Secreted	347	15	62.5	6	6	ABR46699	Staphyloc
275	16	66.7	20	7	ADF08908	Secreted	348	15	62.5	6	6	ABR47077	Staphyloc
276	16	66.7	20	7	ADP09113	Secreted	349	15	62.5	6	6	ABR47092	Staphyloc
277	16	66.7	20	7	ADP09114	Secreted	350	15	62.5	6	6	ABR45147	Staphyloc
278	16	66.7	20	7	ADG46195	O8E antib	351	15	62.5	6	6	ABR45187	Staphyloc
279	16	66.7	20	7	ADG46194	O8E antib	352	15	62.5	6	6	ABR45484	Staphyloc
280	16	66.7	20	8	ADR05597	Novel ssd	353	15	62.5	6	6	ABR45509	Staphyloc
281	15	62.5	5	2	AAW17807	Cyclic pe	354	15	62.5	6	6	ABR46267	Staphyloc
282	15	62.5	5	2	AAW17812	Cyclic pe	355	15	62.5	6	6	ABR45909	Staphyloc
283	15	62.5	5	2	AAW17806	Cyclic pe	356	15	62.5	6	6	ABR46383	Staphyloc
284	15	62.5	5	2	AAW33038	Carbohydr	357	15	62.5	6	6	ABR46715	Staphyloc
285	15	62.5	5	3	ABM07280	Motif bln	358	15	62.5	6	6	ABR46755	Staphyloc
286	15	62.5	5	3	ABP67371	Human CD6	359	15	62.5	6	6	ABR47070	Staphyloc
287	15	62.5	5	6	ABU87123	Carbohydr	360	15	62.5	6	6	ABR47085	Staphyloc
288	15	62.5	5	8	ADR68292	Androgen	361	15	62.5	6	6	ABR45502	Staphyloc
289	15	62.5	5	8	ADR68294	Androgen	362	15	62.5	6	6	ABR45876	Staphyloc
290	15	62.5	6	1	AAP50709	Hexapepti	363	15	62.5	6	6	ABR46294	Staphyloc
291	15	62.5	6	2	AAR54182	CHA255 11	364	15	62.5	6	6	ABR46419	Staphyloc
292	15	62.5	6	2	AAR89913	p53/MDM2	365	15	62.5	6	6	ABR46660	Staphyloc
293	15	62.5	6	2	AAW13606	p53 minim	366	15	62.5	6	6	ABR47078	Staphyloc
294	15	62.5	6	2	AAW13606	p53 prote	367	15	62.5	6	6	ABR45165	Staphyloc
295	15	62.5	6	2	AAW04677	Peptide #	368	15	62.5	6	6	ABR45165	Staphyloc
296	15	62.5	6	3	ABM17074	Mdm/hdm a	369	15	62.5	6	6	ABR45483	Staphyloc
297	15	62.5	6	5	ABP73169	Mdm/hdm a	370	15	62.5	6	6	ABR45524	Staphyloc
298	15	62.5	6	5	ABP73161	Human CD6	371	15	62.5	6	6	ABR45910	Staphyloc
299	15	62.5	6	6	ABR46285	Staphyloc	372	15	62.5	6	6	ABR46685	Staphyloc
300	15	62.5	6	6	ABR46643	Staphyloc	373	15	62.5	6	6	ABR46685	Staphyloc
301	15	62.5	6	6	ABR45148	Staphyloc	374	15	62.5	6	6	ABR47091	Staphyloc
302	15	62.5	6	6	ABR46479	Staphyloc	375	15	62.5	6	6	ABR45916	Staphyloc
303	15	62.5	6	6	ABR47051	Staphyloc	376	15	62.5	6	6	ABR46302	Staphyloc
304	15	62.5	6	6	ABR47069	Staphyloc	377	15	62.5	6	6	ABR46603	Staphyloc
305	15	62.5	6	6	ABR45893	Staphyloc	378	15	62.5	6	6	ABR46677	Staphyloc
306	15	62.5	6	6	ABR46491	Staphyloc	379	15	62.5	6	6	ABG73432	Human p53
307	15	62.5	6	6	ABR46607	Staphyloc	380	15	62.5	6	6	ABG73433	Human p53
308	15	62.5	6	6	ABR46700	Staphyloc	381	15	62.5	6	7	ABR82526	Human apy
309	15	62.5	6	6	ABR45188	Staphyloc	382	15	62.5	6	7	ADJ73323	Mdm/hdm a
310	15	62.5	6	6	ABR45173	Staphyloc	383	15	62.5	6	8	ADJ52957	CH1 delet
311	15	62.5	6	6	ABR45523	Staphyloc	384	15	62.5	6	8	ADJ51918	CH1 delet
312	15	62.5	6	6	ABR45875	Staphyloc	385	15	62.5	7	1	AAP93327	Sequence
313	15	62.5	6	6	ABR45902	Staphyloc	386	15	62.5	7	2	AAR32880	Tryptic p
314	15	62.5	6	6	ABR46286	Staphyloc	387	15	62.5	7	2	AAR89921	Antibody
315	15	62.5	6	6	ABR46307	Staphyloc	388	15	62.5	7	2	AAR89925	p53 bindi
316	15	62.5	6	6	ABR47086	Staphyloc	389	15	62.5	7	2	AAW34151	Angiopoie
317	15	62.5	6	6	ABR45174	Staphyloc	390	15	62.5	7	2	AAW94141	FG loop s

391	15	62.5	7	3	AA92380	Heptapept	Aay82380	464	15	62.5	8	6	ABR54070	Beta-secr
392	15	62.5	7	3	AA57789	TRAM-inte	Aay57789	465	15	62.5	8	6	ABR54078	Beta-secr
393	15	62.5	7	3	AA23205	Hsp47-bin	Aab23205	466	15	62.5	8	6	ABR54080	Beta-secr
394	15	62.5	7	3	AA01512	Peptide w	Aab01512	467	15	62.5	8	6	ABR53951	Beta-secr
395	15	62.5	7	4	AAAB73050	Lutelinisi	Aab73050	468	15	62.5	8	6	ABR54049	Beta-secr
396	15	62.5	7	4	AAAM47040	H11 bindi	Aam47040	469	15	62.5	8	6	ABR53996	Beta-secr
397	15	62.5	7	4	AAAM46975	H11 bindi	Aam46975	470	15	62.5	8	6	ABR54000	Beta-secr
398	15	62.5	7	4	AAAM46990	H11 bindi	Aam46990	471	15	62.5	8	6	ABR54047	Beta-secr
399	15	62.5	7	4	AAAM46970	H11 bindi	Aam46970	472	15	62.5	8	6	ABR54025	Beta-secr
400	15	62.5	7	5	AB934392	Ubiquitin	Abp934392	473	15	62.5	8	6	ABR53994	Beta-secr
401	15	62.5	7	5	ABP67352	Human CD6	Abp67352	474	15	62.5	8	6	ABR54023	Beta-secr
402	15	62.5	7	5	ABP67752	Human CD6	Abp67752	475	15	62.5	8	6	ABR54017	Beta-secr
403	15	62.5	7	5	ABG77724	Targettin	Abg77724	476	15	62.5	8	6	ABR54011	Beta-secr
404	15	62.5	7	7	ADL17146	Phage-dis	Adl17146	477	15	62.5	8	6	ABP71906	R erythr
405	15	62.5	7	7	ADL17080	Phage-dis	Adl17080	478	15	62.5	8	7	ADP20439	Human sec
406	15	62.5	7	7	ADL17130	Phage-dis	Adl17130	479	15	62.5	8	7	ADC07142	Golden-wi
407	15	62.5	7	7	ADL17176	Phage-dis	Adl17176	480	15	62.5	8	7	ADC07143	Emperor d
408	15	62.5	7	7	ADL17077	Phage-dis	Adl17077	481	15	62.5	8	7	ADF10743	Human sec
409	15	62.5	7	7	ADL17227	Phage-dis	Adl17227	482	15	62.5	8	7	ADL17302	DENSIN-18
410	15	62.5	7	8	ADH08433	IGF produ	Adh08433	483	15	62.5	8	8	ADK01990	Hepatitis
411	15	62.5	7	8	ADI32411	FG loop p	Adi32411	484	15	62.5	8	8	ADK01958	Human pap
412	15	62.5	7	8	ADR68302	Androgen	Aar68302	485	15	62.5	8	8	ADQ28799	Human cel
413	15	62.5	8	2	AAAR61038	Dynorphin	Aar61038	486	15	62.5	8	8	ADQ28800	Human cel
414	15	62.5	8	2	AAAW94606	Human ins	Aaw94606	487	15	62.5	8	8	ADR69714	Novel hyb
415	15	62.5	8	2	AAAY21268	Human sem	Aay21268	488	15	62.5	8	8	ADSO0534	Human Apo
416	15	62.5	8	2	AAAW37209	Human onc	Aaw37209	489	15	62.5	8	8	ADSO0532	Human Apo
417	15	62.5	8	2	AAAW37186	Human onc	Aaw37186	490	15	62.5	8	8	ADSO0533	Human Apo
418	15	62.5	8	2	AAAW37176	Human onc	Aaw37176	491	15	62.5	8	8	ADSO0535	Human Apo
419	15	62.5	8	2	AAAW37185	Human onc	Aaw37185	492	15	62.5	8	8	ADSO0533	Human Apo
420	15	62.5	8	2	AAAW37206	Human MDM	Aaw37206	493	15	62.5	8	8	ADR99992	Human apo
421	15	62.5	8	2	AAAW37177	Human onc	Aaw37177	494	15	62.5	8	8	ADR99994	Human apo
422	15	62.5	8	2	AAAW37207	Human MDM	Aaw37207	495	15	62.5	8	8	ADR99993	Human apo
423	15	62.5	8	2	AAAY25556	Human MHC	Aay25556	496	15	62.5	8	8	ADSO4213	Human apo
424	15	62.5	8	3	AAAY85386	IL-2 deri	Aay85386	497	15	62.5	8	8	ADSO4215	Human apo
425	15	62.5	8	3	AAAY85387	IL-2 deri	Aay85387	498	15	62.5	8	8	ADSO4216	Human apo
426	15	62.5	8	3	AAAY85388	IL-2 deri	Aay85388	499	15	62.5	8	8	ADSO4214	Human apo
427	15	62.5	8	3	AAAB09130	Hepatitis	Aab09130	500	15	62.5	9	2	AAAR53342	Chimeric
428	15	62.5	8	4	AAAB22220	Glycine m	Aab22220	501	15	62.5	9	2	AAAW00686	Peptide c
429	15	62.5	8	5	ABP67745	Human CD6	Abp67745	502	15	62.5	9	2	AAAW45692	HBV env 3
430	15	62.5	8	5	ABP67344	Human CD6	Abp67344	503	15	62.5	9	2	AAAW39724	Human car
431	15	62.5	8	6	ABP99660	Human sec	Abp99660	504	15	62.5	9	2	AAAW43849	Specific
432	15	62.5	8	6	ABP98083	Amino aci	Abp98083	505	15	62.5	9	2	AAAW43845	Specific
433	15	62.5	8	6	ABP98084	Amino aci	Abp98084	506	15	62.5	9	2	AAAW81310	Human iNO
434	15	62.5	8	6	ABP98081	Amino aci	Abp98081	507	15	62.5	9	2	AAW81250	Human iNO
435	15	62.5	8	6	ABP98082	Amino aci	Abp98082	508	15	62.5	9	2	AAW72493	Dengue vi
436	15	62.5	8	6	ABR01140	Human gen	Abro1140	509	15	62.5	9	2	AAW46351	Amino aci
437	15	62.5	8	6	ADA98274	Human sec	Ada98274	510	15	62.5	9	2	AAW46349	Amino aci
438	15	62.5	8	6	ABP68159	Bacillus	Abp68159	511	15	62.5	9	2	AAW46348	Amino aci
439	15	62.5	8	6	ABP68163	Bacillus	Abp68163	512	15	62.5	9	2	AAW46350	Amino aci
440	15	62.5	8	6	ABP68181	Bacillus	Abp68181	513	15	62.5	9	2	AAW37199	Human onc
441	15	62.5	8	6	ABP68158	Bacillus	Abp68158	514	15	62.5	9	2	AAAY46725	Immunogen
442	15	62.5	8	6	ABP68166	Bacillus	Abp68166	515	15	62.5	9	2	AAAY25555	Human MHC
443	15	62.5	8	6	ABP68160	Bacillus	Abp68160	516	15	62.5	9	2	AAAY27259	Human tum
444	15	62.5	8	6	ABR54027	Beta-secr	AbR54027	517	15	62.5	9	3	AAAY84757	Antigenic
445	15	62.5	8	6	ABR54059	Beta-secr	AbR54059	518	15	62.5	9	3	AAAY84765	Antigenic
446	15	62.5	8	6	ABR53990	Beta-secr	AbR53990	519	15	62.5	9	3	AAAY84756	Antigenic
447	15	62.5	8	6	ABR54021	Beta-secr	AbR54021	520	15	62.5	9	3	AAAY84758	Antigenic
448	15	62.5	8	6	ABR54074	Beta-secr	AbR54074	521	15	62.5	9	3	AAAY84759	Antigenic
449	15	62.5	8	6	ABR53998	Beta-secr	AbR53998	522	15	62.5	9	3	AAAY71328	Rat neu1
450	15	62.5	8	6	ABR54015	Beta-secr	AbR54015	523	15	62.5	9	3	AAAB23806	Phage dis
451	15	62.5	8	6	ABR53986	Beta-secr	AbR53986	524	15	62.5	9	3	AAAB34807	Human sec
452	15	62.5	8	6	ABR54072	Beta-secr	AbR54072	525	15	62.5	9	3	AAAB01629	Chimaeric
453	15	62.5	8	6	ABR54045	Beta-secr	AbR54045	526	15	62.5	9	4	ABM46945	Human SAR
454	15	62.5	8	6	ABR54068	Beta-secr	AbR54068	527	15	62.5	9	4	ABM00050	Savinas a
455	15	62.5	8	6	ABR53988	Beta-secr	AbR53988	528	15	62.5	9	4	ABM00058	Savinas a
456	15	62.5	8	6	ABR54053	Beta-secr	AbR54053	529	15	62.5	9	4	ABM00059	Savinas a
457	15	62.5	8	6	ABR54055	Beta-secr	AbR54055	530	15	62.5	9	4	AAAB75691	HLA Class
458	15	62.5	8	6	ABR54057	Beta-secr	AbR54057	531	15	62.5	9	4	AAAG63257	Complem
459	15	62.5	8	6	ABR54076	Beta-secr	AbR54076	532	15	62.5	9	4	AAAM24637	Human MHC
460	15	62.5	8	6	ABR54082	Beta-secr	AbR54082	533	15	62.5	9	5	ABG79074	Human CEA
461	15	62.5	8	6	ABR54051	Beta-secr	AbR54051	534	15	62.5	9	5	ABG35129	Pancreati
462	15	62.5	8	6	ABR53992	Beta-secr	AbR53992	535	15	62.5	9	5	ABP47446	N. mening
463	15	62.5	8	6	ABR54019	Beta-secr	AbR54019	536	15	62.5	9	5	ABG97340	Human leu

537	15	62.5	9	5	ABG97341	Abg97341 Human leu	610	15	62.5	9	6	ABJ61113	ABJ61113	ABJ61113 184P1E2-r
538	15	62.5	9	5	AAO18872	AAO18872 Human CEA	611	15	62.5	9	6	ABJ61402	ABJ61402	ABJ61402 184P1E2-r
539	15	62.5	9	5	ABP67738	ABP67738 Human CD6	612	15	62.5	9	6	ABJ58361	ABJ58361	ABJ58361 184P1E2-r
540	15	62.5	9	5	ABP67337	ABP67337 Human CD6	613	15	62.5	9	6	ABJ60622	ABJ60622	ABJ60622 184P1E2-r
541	15	62.5	9	5	ABJ11741	ABJ11741 Human 125	614	15	62.5	9	6	ABJ63441	ABJ63441	ABJ63441 184P1E2-r
542	15	62.5	9	5	ABJ12589	ABJ12589 Human 125	615	15	62.5	9	6	ABJ63923	ABJ63923	ABJ63923 184P1E2-r
543	15	62.5	9	5	ABJ12352	ABJ12352 Human 125	616	15	62.5	9	6	ABJ63965	ABJ63965	ABJ63965 184P1E2-r
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545	15	62.5	9	5	ABJ11833	ABJ11833 Human 125	618	15	62.5	9	6	ABJ58971	ABJ58971	ABJ58971 184P1E2-r
546	15	62.5	9	5	ABJ12880	ABJ12880 Human 125	619	15	62.5	9	6	ABJ60509	ABJ60509	ABJ60509 184P1E2-r
547	15	62.5	9	5	ABJ113175	ABJ113175 Human 125	620	15	62.5	9	6	ABJ62494	ABJ62494	ABJ62494 184P1E2-r
548	15	62.5	9	5	ABJ112444	ABJ112444 Human 125	621	15	62.5	9	6	ABJ64062	ABJ64062	ABJ64062 184P1E2-r
549	15	62.5	9	5	ABJ112211	ABJ112211 Human 125	622	15	62.5	9	6	ABJ64839	ABJ64839	ABJ64839 184P1E2-r
550	15	62.5	9	5	ABJ09544	ABJ09544 Hepatitis	623	15	62.5	9	6	ABJ65025	ABJ65025	ABJ65025 184P1E2-r
551	15	62.5	9	5	ABG60517	ABG60517 Selective	624	15	62.5	9	6	ABJ57376	ABJ57376	ABJ57376 184P1E2-r
552	15	62.5	9	5	AAE31317	AAE31317 Human p53	625	15	62.5	9	6	ABJ63110	ABJ63110	ABJ63110 184P1E2-r
553	15	62.5	9	5	AAE31316	AAE31316 Human p53	626	15	62.5	9	6	ABJ63111	ABJ63111	ABJ63111 184P1E2-r
554	15	62.5	9	5	AAE31395	AAE31395 Human p53	627	15	62.5	9	6	ABJ62218	ABJ62218	ABJ62218 184P1E2-r
555	15	62.5	9	5	AAU09701	AAU09701 Anti-mela	628	15	62.5	9	6	ABO27023	ABO27023	ABO27023 Yellow fe
556	15	62.5	9	5	AAU96014	AAU96014 Carcino e	629	15	62.5	9	6	ABO27024	ABO27024	ABO27024 West nile
557	15	62.5	9	6	ABJ20021	ABJ20021 MHC bindi	630	15	62.5	9	6	ABO27025	ABO27025	ABO27025 Murray va
558	15	62.5	9	6	ABR56915	ABR56915 Pancreati	631	15	62.5	9	6	ABO27026	ABO27026	ABO27026 Kunjin vi
559	15	62.5	9	6	ABR24615	ABR24615 Human can	632	15	62.5	9	7	ADA07879	ADA07879	ADA07879 Viral pro
560	15	62.5	9	6	ABR24590	ABR24590 Human can	633	15	62.5	9	7	ADA07878	ADA07878	ADA07878 Viral pro
561	15	62.5	9	6	ABR25041	ABR25041 Human can	634	15	62.5	9	7	ADA07881	ADA07881	ADA07881 Viral pro
562	15	62.5	9	6	ABR25394	ABR25394 Human can	635	15	62.5	9	7	ADA07880	ADA07880	ADA07880 Viral pro
563	15	62.5	9	6	ABR24408	ABR24408 Human can	636	15	62.5	9	7	ADD26353	ADD26353	ADD26353 Staphyloc
564	15	62.5	9	6	ABR24647	ABR24647 Human can	637	15	62.5	9	7	ADD94560	ADD94560	ADD94560 Human SIM
565	15	62.5	9	6	ABR20240	ABR20240 Human can	638	15	62.5	9	7	ADD94768	ADD94768	ADD94768 Human SIM
566	15	62.5	9	6	ABR25665	ABR25665 Human can	639	15	62.5	9	7	ADD94574	ADD94574	ADD94574 Human SIM
567	15	62.5	9	6	ABR25205	ABR25205 Human can	640	15	62.5	9	7	ADG38574	ADG38574	ADG38574 Human car
568	15	62.5	9	6	ABR24809	ABR24809 Human can	641	15	62.5	9	7	ADG38572	ADG38572	ADG38572 Human car
569	15	62.5	9	6	ABR25596	ABR25596 Human can	642	15	62.5	9	7	AAO24240	AAO24240	AAO24240 MHC bindi
570	15	62.5	9	6	ABR23040	ABR23040 Human can	643	15	62.5	9	7	AAO24239	AAO24239	AAO24239 MHC bindi
571	15	62.5	9	6	ABR21629	ABR21629 Human can	644	15	62.5	9	7	ADI03011	ADI03011	ADI03011 Human mon
572	15	62.5	9	6	ABJ58972	ABJ58972 184P1E2-r	645	15	62.5	9	7	ADL17217	ADL17217	ADL17217 Phage-dis
573	15	62.5	9	6	ABJ59510	ABJ59510 184P1E2-r	646	15	62.5	9	7	ADL17251	ADL17251	ADL17251 Phage-dis
574	15	62.5	9	6	ABJ63247	ABJ63247 184P1E2-r	647	15	62.5	9	7	ADL17455	ADL17455	ADL17455 Human SNT
575	15	62.5	9	6	ABJ65204	ABJ65204 184P1E2-r	648	15	62.5	9	7	ADL17228	ADL17228	ADL17228 Phage-dis
576	15	62.5	9	6	ABJ61887	ABJ61887 184P1E2-r	649	15	62.5	9	7	ADK65171	ADK65171	ADK65171 Human VEG
577	15	62.5	9	6	ABJ63999	ABJ63999 184P1E2-r	650	15	62.5	9	7	ADK65120	ADK65120	ADK65120 Human VEG
578	15	62.5	9	6	ABJ64840	ABJ64840 184P1E2-r	651	15	62.5	9	8	ADG89640	ADG89640	ADG89640 Class I H
579	15	62.5	9	6	ABJ605010	ABJ605010 184P1E2-r	652	15	62.5	9	8	ADK39506	ADK39506	ADK39506 Hepatitis
580	15	62.5	9	6	ABJ62064	ABJ62064 184P1E2-r	653	15	62.5	9	8	ADK10586	ADK10586	ADK10586 Human pap
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583	15	62.5	9	6	ABJ58585	ABJ58585 184P1E2-r	656	15	62.5	9	8	ADK10587	ADK10587	ADK10587 Human pap
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585	15	62.5	9	6	ABJ59965	ABJ59965 184P1E2-r	658	15	62.5	9	8	ADK10585	ADK10585	ADK10585 Human pap
586	15	62.5	9	6	ABJ61159	ABJ61159 184P1E2-r	659	15	62.5	9	8	ADK05911	ADK05911	ADK05911 Hepatitis
587	15	62.5	9	6	ABJ64098	ABJ64098 184P1E2-r	660	15	62.5	9	8	ADK10584	ADK10584	ADK10584 Human pap
588	15	62.5	9	6	ABJ64452	ABJ64452 184P1E2-r	661	15	62.5	9	8	ADM12337	ADM12337	ADM12337 MHC class
589	15	62.5	9	6	ABJ60738	ABJ60738 184P1E2-r	662	15	62.5	9	8	ADL19695	ADL19695	ADL19695 125P5C8 p
590	15	62.5	9	6	ABJ65172	ABJ65172 184P1E2-r	663	15	62.5	9	8	ADL19077	ADL19077	ADL19077 125P5C8 p
591	15	62.5	9	6	ABJ59130	ABJ59130 184P1E2-r	664	15	62.5	9	8	ADL18847	ADL18847	ADL18847 125P5C8 p
592	15	62.5	9	6	ABJ59833	ABJ59833 184P1E2-r	665	15	62.5	9	8	ADL19603	ADL19603	ADL19603 125P5C8 p
593	15	62.5	9	6	ABJ59945	ABJ59945 184P1E2-r	666	15	62.5	9	8	ADL19840	ADL19840	ADL19840 125P5C8 p
594	15	62.5	9	6	ABJ60623	ABJ60623 184P1E2-r	667	15	62.5	9	8	ADL18985	ADL18985	ADL18985 125P5C8 p
595	15	62.5	9	6	ABJ63529	ABJ63529 184P1E2-r	668	15	62.5	9	8	ADL20131	ADL20131	ADL20131 125P5C8 p
596	15	62.5	9	6	ABJ65631	ABJ65631 184P1E2-r	669	15	62.5	9	8	ADL20425	ADL20425	ADL20425 125P5C8 p
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608	15	62.5	9	6	ABJ62994	ABJ62994 184P1E2-r	681	15	62.5	10	2	AAW62010	AAW62010	AAW62010 Heavy cha
609	15	62.5	9	6	ABJ61053	ABJ61053 184P1E2-r	682	15	62.5	10	2	AAW37198	AAW37198	AAW37198 Human onc

683 15 62.5 10 2 AAY25554 Human MHC
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ABJ68164 184P1E2-r
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ADD94160 Mouse HUI
ADD94632 Human SIM
ADFI0400 Serum alb
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ADL17226 Phage-dis
ADL17327 Human scr
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ADL17219 Phage-dis
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ADP47005 Murine he
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ADR03385 Humanised
ADQ90923 Pancreat i

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830	15	62.5	10	8	ADP79877	Adp79877 Human HLA	903	15	62.5	12	6	AAE30893	Aae30893 MDM2-bind
831	15	62.5	10	8	ADP80344	Adp80344 Human HLA	904	15	62.5	12	6	AAE30886	Aae30886 MDM2-bind
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833	15	62.5	10	8	ADR70840	Adr70840 Synthetic	906	15	62.5	12	6	ABR00856	AbR00856 Bioactive
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836	15	62.5	11	2	AAW05784	Aaw05784 Presenili	909	15	62.5	12	7	ADP78490	Adp78490 Peptide 3
837	15	62.5	11	2	AAW11231	Aaw11231 Peptide A	910	15	62.5	12	7	ADL10310	Adl10310 Human mon
838	15	62.5	11	2	AAW12288	Aaw12288 Mycobacte	911	15	62.5	12	7	ADL17289	Adl17289 DENIN-18
839	15	62.5	11	2	AAW62114	Aaw62114 Human MDM	912	15	62.5	12	7	ADJ73326	Adj73326 Mdm/hdm a
840	15	62.5	11	2	RAY25553	Ray25553 Human MHC	913	15	62.5	12	7	ADJ73330	Adj73330 Mdm/hdm a
841	15	62.5	11	4	AAU27152	Aau27152 Human Leu	914	15	62.5	12	7	ADJ73339	Adj73339 Mdm/hdm a
842	15	62.5	11	4	AAU26842	Aau26842 Human Leu	915	15	62.5	12	7	ADJ73324	Adj73324 Mdm/hdm a
843	15	62.5	11	5	ABP47586	Abp47586 N. mening	916	15	62.5	12	7	ADJ73336	Adj73336 Mdm/hdm a
844	15	62.5	11	5	ABP67727	Abp67727 Human CD6	917	15	62.5	12	7	ADJ73327	Adj73327 Mdm/hdm a
845	15	62.5	11	5	ABP67326	Abp67326 Human CD6	918	15	62.5	12	7	ADJ73337	Adj73337 Mdm/hdm a
846	15	62.5	11	5	AAU93631	Aau93631 Granulocy	919	15	62.5	12	7	ADJ73338	Adj73338 Mdm/hdm a
847	15	62.5	11	5	AAW52269	Aaw52269 Miniature	920	15	62.5	12	7	ADJ73325	Adj73325 Mdm/hdm a
848	15	62.5	11	5	ABG67493	Abg67493 Human ADP	921	15	62.5	12	8	ADI34264	Adi34264 Wild type
849	15	62.5	11	6	ABR59507	AbR59507 S. aureus	922	15	62.5	12	8	ADJ52964	Adj52964 CH1 delet
850	15	62.5	11	6	ADA23607	Ada23607 Alzheimer	923	15	62.5	12	8	ADJ52960	Adj52960 CH1 delet
851	15	62.5	11	8	ADG15910	Adg15910 Synthetic	924	15	62.5	12	8	ADJ52959	Adj52959 CH1 delet
852	15	62.5	11	8	ADG15914	Adg15914 Synthetic	925	15	62.5	12	8	ADJ52971	Adj52971 CH1 delet
853	15	62.5	11	8	ADJ25786	Adj25786 MDM2 bind	926	15	62.5	12	8	ADJ52972	Adj52972 CH1 delet
854	15	62.5	11	8	ADJ25912	Adj25912 MDM2 bind	927	15	62.5	12	8	ADJ52970	Adj52970 CH1 delet
855	15	62.5	11	8	ADN64806	Adn64806 HLA bindi	928	15	62.5	12	8	ADJ52958	Adj52958 CH1 delet
856	15	62.5	11	8	ADR20392	Adr20392 Tryptic d	929	15	62.5	12	8	ADJ52961	Adj52961 CH1 delet
857	15	62.5	11	8	ADP80368	Adp80368 Human HLA	930	15	62.5	12	8	ADJ52973	Adj52973 CH1 delet
858	15	62.5	12	1	AP93573	Ap93573 Extracell	931	15	62.5	12	8	ADJ51921	Adj51921 CH1 delet
859	15	62.5	12	2	AA77621	Aa77621 Ascorbate	932	15	62.5	12	8	ADJ51922	Adj51922 CH1 delet
860	15	62.5	12	2	AA83344	Aa83344 Kb-bindin	933	15	62.5	12	8	ADJ51920	Adj51920 CH1 delet
861	15	62.5	12	2	AAW29957	Aaw29957 Cysteine	934	15	62.5	12	8	ADJ51932	Adj51932 CH1 delet
862	15	62.5	12	2	AAW18715	Aaw18715 C-src exo	935	15	62.5	12	8	ADJ51931	Adj51931 CH1 delet
863	15	62.5	12	2	AAW81309	Aaw81309 Human iNO	936	15	62.5	12	8	ADJ51919	Adj51919 CH1 delet
864	15	62.5	12	2	AAW81249	Aaw81249 Human iNO	937	15	62.5	12	8	ADJ51934	Adj51934 CH1 delet
865	15	62.5	12	2	AAW37190	Aaw37190 Human onc	938	15	62.5	12	8	ADJ51933	Adj51933 CH1 delet
866	15	62.5	12	2	AAW37184	Aaw37184 Human onc	939	15	62.5	12	8	ADJ57768	Adj57768 Surface g
867	15	62.5	12	2	AAW37195	Aaw37195 Human onc	940	15	62.5	12	8	ADJ57296	Adj57296 Provasopr
868	15	62.5	12	2	AAW37171	Aaw37171 Human onc	941	15	62.5	12	8	ADN65746	Adn65746 HLA bindi
869	15	62.5	12	2	AAW37182	Aaw37182 Human onc	942	15	62.5	12	8	ADR42787	Adr42787 Modulator
870	15	62.5	12	2	AAW37181	Aaw37181 Human p53	943	15	62.5	12	8	ADR42787	Adr42787 Modulator
871	15	62.5	12	2	AAW37188	Aaw37188 Human onc	944	15	62.5	13	2	AAW49316	Aaw49316 Beta2m po
872	15	62.5	12	2	AAW37189	Aaw37189 Human onc	945	15	62.5	13	2	AAW59205	Aaw59205 Seq ID 10
873	15	62.5	12	2	AAW37222	Aaw37222 MDM2 bind	946	15	62.5	13	2	AAW40094	Aaw40094 Seq ID 10
874	15	62.5	12	2	AAW37222	Aaw37222 MDM2 bind	947	15	62.5	13	2	AAW67036	Aaw67036 Polioviru
875	15	62.5	12	3	AAV66808	Aav66808 T cell an	948	15	62.5	13	2	AAV25551	Aav25551 Human MHC
876	15	62.5	12	3	AB17076	Ab17076 Mdm/hdm a	949	15	62.5	13	3	AAV57799	Aav57799 TRAM-inte
877	15	62.5	12	3	AB17087	Ab17087 Mdm/hdm a	950	15	62.5	13	4	AA20427	Aa20427 Anti-FIX/
878	15	62.5	12	3	AB17089	Ab17089 Mdm/hdm a	951	15	62.5	13	4	AA20390	Aa20390 Anti-FIX/
879	15	62.5	12	3	AB17081	Ab17081 Mdm/hdm a	952	15	62.5	13	4	AA20390	Aa20390 Anti-FIX/
880	15	62.5	12	3	AB17078	Ab17078 Mdm/hdm a	953	15	62.5	13	4	AA20390	Aa20390 Anti-FIX/
881	15	62.5	12	3	AB17090	Ab17090 Mdm/hdm a	954	15	62.5	13	4	AA20390	Aa20390 Anti-FIX/
882	15	62.5	12	3	AB17088	Ab17088 Mdm/hdm a	955	15	62.5	13	4	AA20390	Aa20390 Anti-FIX/
883	15	62.5	12	3	AB17075	Ab17075 Mdm/hdm a	956	15	62.5	13	5	ABP67720	Abp67720 Human CD6
884	15	62.5	12	3	AB17077	Ab17077 Mdm/hdm a	957	15	62.5	13	5	ABP67720	Abp67720 Human CD6
885	15	62.5	12	3	AAV93809	Aav93809 Reactive	958	15	62.5	13	5	ABP59059	Abp59059 Peptide #
886	15	62.5	12	3	AAV93867	Aav93867 Reactive	959	15	62.5	13	5	ADG67226	Adg67226 Human 5G1
887	15	62.5	12	4	AA886005	Aa886005 DCM-asso	960	15	62.5	13	5	ADG66202	Adg66202 Human pro
888	15	62.5	12	5	ABG78401	Abg78401 Memapsin	961	15	62.5	13	5	ADG66200	Adg66200 Human pro
889	15	62.5	12	5	ABG73170	Abg73170 Mdm/hdm a	962	15	62.5	13	5	ADG67227	Adg67227 Human 5G1
890	15	62.5	12	5	ABG73170	Abg73170 Mdm/hdm a	963	15	62.5	13	5	ADG66203	Adg66203 Human pro
891	15	62.5	12	5	ABG73172	Abg73172 Mdm/hdm a	964	15	62.5	13	5	ADG67228	Adg67228 Human 5G1
892	15	62.5	12	5	ABG73185	Abg73185 Mdm/hdm a	965	15	62.5	13	5	ADG66201	Adg66201 Human pro
893	15	62.5	12	5	ABG73184	Abg73184 Mdm/hdm a	966	15	62.5	13	5	ADG67229	Adg67229 Human 5G1
894	15	62.5	12	5	ABG73176	Abg73176 Mdm/hdm a	967	15	62.5	13	6	ABP76124	Abp76124 Human GEN
895	15	62.5	12	5	ABG73183	Abg73183 Mdm/hdm a	968	15	62.5	13	6	ABP76126	Abp76126 Human GEN
896	15	62.5	12	5	ABG73173	Abg73173 Mdm/hdm a	969	15	62.5	13	6	ABP76127	Abp76127 Human GEN
897	15	62.5	12	5	ABG73171	Abg73171 Mdm/hdm a	970	15	62.5	13	6	ABP76125	Abp76125 Human GEN
898	15	62.5	12	5	ABG73182	Abg73182 Mdm/hdm a	971	15	62.5	13	7	AAO30274	Aao30274 Trichoder
899	15	62.5	12	5	ABP67723	Abp67723 Human CD6	972	15	62.5	13	7	ADP56957	Adp56957 Interfaci
900	15	62.5	12	5	ABP67322	Abp67322 Human CD6	973	15	62.5	13	7	ADP56957	Adp56957 Interfaci
901	15	62.5	12	5	ABG60547	Abg60547 Selective	974	15	62.5	13	7	ADP56957	Adp56957 Interfaci

975 15 62.5 13 7 ADF75890 Antimicro
 976 15 62.5 13 7 ADI57984 Anti-TNF-
 977 15 62.5 13 7 ADI57985 Anti-TNF-
 978 15 62.5 13 7 ADI57983 Anti-TNF-
 979 15 62.5 13 7 ADI57986 Anti-TNF-
 980 15 62.5 13 8 ADH94540 Lecithin
 981 15 62.5 13 8 ADO57860 Human for
 982 15 62.5 13 8 ADO24819 Polioviru
 983 15 62.5 13 8 ADR05553 Novel ssd
 984 15 62.5 14 2 AAW09477 Thrombopo
 985 15 62.5 14 2 AAW36764 Thrombopo
 986 15 62.5 14 2 AAW36628 Thrombopo
 987 15 62.5 14 2 AAW33471 P2 predom
 988 15 62.5 14 2 AAW37197 Human onc
 989 15 62.5 14 2 AAY25550 Human MHC
 990 15 62.5 14 2 AAY42867 Vpr-bind
 991 15 62.5 14 3 AAB17012 TPO-mimet
 992 15 62.5 14 3 AAB13866 L2/HNK1 C
 993 15 62.5 14 4 AAB20428 Anti-FIX/
 994 15 62.5 14 4 AAM98166 Human pep
 995 15 62.5 14 4 AAM98390 Human pep
 996 15 62.5 14 4 AAM00740 Human pro
 997 15 62.5 14 4 AAM00739 Human pro
 998 15 62.5 14 4 AAU25847 Human thr
 999 15 62.5 14 4 AAG98212 Human SNP
 1000 15 62.5 14 4 AAB86012 DCM-assoc

ALIGNMENTS

RESULT 1
 ADC07129
 ID ADC07129 standard; peptide; 9 AA.
 XX
 AC ADC07129;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Honeybee AKH peptide.
 XX
 KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;
 KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;
 KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;
 KW obesity; type II diabetes; cholelithiasis; hypertension;
 KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;
 KW renal failure; liver; chronic pain; sleep apnea; stroke;
 KW urinary incontinence; honeybee.
 XX
 OS Synthetic.
 OS Apis mellifera.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label= OTHER
 FT /note= "OTHER = Pyroglutamic acid"
 FT Misc-difference 9 /note= "Preferably C-terminal amide"
 FT
 FT WO2003066080-A1.
 XX
 PN 14-AUG-2003.
 XX
 PD 07-FEB-2003; 2003WO-US003800.
 XX
 PF 07-FEB-2002; 2002US-00072419.
 XX
 PR 07-FEB-2002; 2002US-00072419.
 XX
 PA (BLMB-) BLM GROUP.
 XX
 PI Schacter BZ, Schacter LP;
 XX
 DR WPI; 2003-712542/67.
 XX
 PT Pharmaceutical composition useful for promoting weight loss, comprises an
 insect adipokinetic hormone, having a pyroglutamate residue at its amino

PT Pharmaceutical composition useful for promoting weight loss, comprises an
 insect adipokinetic hormone, having a pyroglutamate residue at its amino
 terminus.
 PT
 XX Claim 29; Page 20; 82pp; English.
 PS
 CC The invention relates to a novel method of promoting lipid mobilisation
 in a human which comprises administering an insect adipokinetic hormone
 (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,
 CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,
 CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The
 CC method of the invention may be useful for treating obesity, type II
 CC diabetes, cholelithiasis, hypertension, coronary heart disease, renal
 CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal
 CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary
 CC incontinence. The current sequence is that of the honeybee AKH peptide of
 the invention.
 CC
 SQ Sequence 9 AA;
 Query Match 70.8%; Score 17; DB 7; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXW 6
 Db 4 FTSSW 8
 RESULT 2
 ADC07134
 ID ADC07134 standard; peptide; 9 AA.
 XX
 AC ADC07134;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Painted lady AKH peptide.
 XX
 KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;
 KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;
 KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;
 KW obesity; type II diabetes; cholelithiasis; hypertension;
 KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;
 KW renal failure; liver; chronic pain; sleep apnea; stroke;
 KW urinary incontinence; painted lady.
 XX
 OS Synthetic.
 OS Vanessa cardui.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label= OTHER
 FT /note= "OTHER = Pyroglutamic acid"
 FT Misc-difference 9 /note= "Preferably C-terminal amide"
 FT
 FT WO2003066080-A1.
 XX
 PN 14-AUG-2003.
 XX
 PD 07-FEB-2003; 2003WO-US003800.
 XX
 PF 07-FEB-2002; 2002US-00072419.
 XX
 PR (BLMB-) BLM GROUP.
 XX
 PA Schacter BZ, Schacter LP;
 XX
 PI WPI; 2003-712542/67.
 XX
 DR Pharmaceutical composition useful for promoting weight loss, comprises an
 insect adipokinetic hormone, having a pyroglutamate residue at its amino

PT terminus.
 PS Claim 29; Page 20; 82pp; English.
 CC The invention relates to a novel method of promoting lipid mobilisation
 CC in a human which comprises administering an insect adipokinetic hormone
 CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,
 CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,
 CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The
 CC method of the invention may be useful for treating obesity, type II
 CC diabetes, cholelithiasis, hypertension, coronary heart disease, renal
 CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal
 CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary
 CC incontinence. The current sequence is that of the painted lady AKH
 CC peptide of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 70.8%; Score 17; DB 7; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 FXXXW 6
 Db 4 FTSSW 8
 RESULT 3
 AAB10010
 ID AAB10010 standard; protein; 10 AA.
 XX
 AC AAB10010;
 XX
 DT 01-NOV-2000 (first entry)
 XX
 DE H. pylori beta-urease-binding antibody heavy chain CDR1 protein #2.
 XX
 KW Acid-resistant microorganism; detection; faecal; intestine; infection;
 KW monoclonal antibody; heavy chain; complementarity determining region;
 KW CDR; beta-urease.
 XX
 OS Unidentified.
 XX
 PN WO200026671-A1.
 XX
 PD 11-MAY-2000.
 XX
 PF 29-OCT-1999; 99WO-EP008212.
 XX
 PR 29-OCT-1998; 98EP-00120517.
 PR 06-NOV-1998; 98EP-00120687.
 XX
 PA (CONN-) CONNEX GMBH.
 XX
 PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
 PI Ringels A;
 XX
 DR WPI: 2000-365747/31.
 DR N-PSDB; AAA40166.
 XX
 PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
 PT pylori, comprises reacting a fecal sample with two binding reagents for
 PT antigens that survive intestinal passage.
 PS
 PS Claim 26; Page 22; 84pp; German.
 XX
 CC This invention describes a novel method for the detection of a mammalian
 CC infection by an acid-resistant microorganism (A) by treating a faecal
 CC sample with at least two different monoclonal antibodies (Mab) (or their
 CC fragments or derivatives) or aptamers (collectively (I)) and detecting
 CC formation of a complex (C) between (I) and the corresponding antigen of
 CC (A). The first and second (I) bind to epitopes of different antigens
 CC (Ag). These epitopes are present, after passage through the intestines,
 CC
 CC in at least some mammals, and have either: (i) their native structure; or
 CC (ii) a structure against which an antibody is produced by an animal
 CC infected or immunized with (A), or its extract, lysate, derived protein
 CC or fragment, or with a synthetic peptide. Practically all mammals display
 CC at least one of the specified epitopes. The method is used to detect
 CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
 CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M.
 CC tuberculosis, C. jejuni and C. pylori. (I) may also be used
 CC therapeutically. The method is direct and non-invasive, and provides an
 CC inexpensive and easily standardizable diagnosis, despite possible
 CC degradation of antigens during passage through the intestines. This
 CC sequence represents a fragment of a H. pylori beta-urease-binding
 CC antibody heavy chain complementarity determining region CDR1 which is
 CC used to illustrate the method of the invention
 XX
 SQ Sequence 10 AA;
 Query Match 70.8%; Score 17; DB 3; Length 10;
 Best Local Similarity 40.0%; Pred. No. 3.4e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 FXXXW 6
 Db 4 FTSSW 8
 RESULT 4
 AAB86090
 ID AAB86090 standard; peptide; 10 AA.
 XX
 AC AAB86090;
 XX
 DT 17-JUL-2001 (first entry)
 XX
 DE H. pylori beta-urease derived antibody light chain CDR1 #1.
 XX
 KW Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
 KW acid-resistant microorganism; complementarity determining region; CDR;
 KW feces; heavy chain; light chain.
 XX
 OS Unidentified.
 XX
 PN WO200127612-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 12-OCT-2000; 2000WO-EP010057.
 XX
 PR 12-OCT-1999; 99EP-00120351.
 PR 16-MAR-2000; 2000EP-00105592.
 PR 31-MAR-2000; 2000EP-00107028.
 PR 10-MAY-2000; 2000EP-00110110.
 XX
 PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
 XX
 PI Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;
 PI WPI: 2001-282086/29.
 DR N-PSDB; AAF88117.
 XX
 PT Detecting infections by acid-resistant microorganisms, particularly for
 PT diagnosing Helicobacter pylori, comprises immunochromatographic detection
 PT of antigen in feces.
 PS
 PS Claim 27; Page 27; 90pp; German.
 XX
 CC This invention describes a novel method for detecting infection by an
 CC acid-resistant microorganism (A), in a mammal, using
 CC immunochromatography. The method is used to diagnose infection by an acid
 CC -resistant microorganism (A), in a mammal, such as Helicobacter,
 CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
 CC H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,
 CC inexpensive and non-invasive, and may indicate the stage of infection. A

CC test strip used in the method may include a filter to eliminate particles
 CC present in the sample and only a single receptor provides a reasonably
 CC secure diagnosis, with specificity and selectivity improved by detecting
 CC several epitopes (of catalase) or different antigens (catalase and beta-
 CC urease). The method can be automated. This sequence represents a
 CC complementarity determining region (CDR) from an antibody raised against
 CC the H. pylori catalase or beta-urease antigen which is used to illustrate
 CC the method of the invention
 XX
 SQ Sequence 10 AA;

Query Match 70.8%; Score 17; DB 4; Length 10;
 Best Local Similarity 40.0%; Pred. No. 3.4e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXHW 6
 |
 4 FSTSW 8

RESULT 5
 AAB86058
 ID AAB86058 standard; peptide; 10 AA.

AC AAB86058;

XX 17-JUL-2001 (first entry)

DE H. pylori beta-urease derived antibody light chain CDR1 #1.

XX Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;
 KW infection; acid-resistant microorganism; fecal; antibody; diagnosis;
 KW antibacterial; complementarity determining region.

XX Unidentified.

XX W0200127613-A2.

XX 19-APR-2001.

XX 12-OCT-2000; 2000WO-EP010058.

XX 12-OCT-1999; 99EP-00120351.

PR 16-MAR-2000; 2000EP-00105592.

PR 31-MAR-2000; 2000EP-00107028.

PR 10-MAY-2000; 2000EP-00110110.

XX (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

PI Reiter C, Cullmann G, Heppner P, Ringels A, Mueller H, Haindl E;

XX WPI; 2001-282087/29.

DR N-PSDB; AAF88060.

XX Detecting infections by acid-resistant microorganisms, particularly for
 PT diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
 FT sample.

XX Claim 23; Page 17; 89pp; German.

XX This invention describes a novel method for detecting, in a mammal,
 CC infection by an acid-resistant microorganism (A) which comprises reacting
 CC a fecal sample with: (i) a receptor (R) such that a complex is formed
 CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part
 CC complex is formed with Ag, and the formation of a complex detected. R are
 CC specific for an Ag which, after passage through the intestines, at least
 CC in some mammals, retains a native (or corresponding) structure against
 CC which the mammal produces antibodies (when immunized or infected with
 CC (A), or its extracts, lysates or derived proteins (or fragments) or
 CC synthetic peptides). The products of the invention have antibacterial
 CC activity. The method is used to diagnose infection by Helicobacter,
 CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
 CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the

CC progress of treatment. Receptors, particularly antibodies, directed
 CC against Ag can be used therapeutically for treatment of infections. The
 CC method requires only one R to provide a reasonably secure diagnosis.
 CC (although use of two R improves sensitivity), so is relatively
 CC inexpensive and more easily standardized. Also it is direct, non-
 CC invasive, suitable for automation and may indicate the stage of an
 CC infection. This sequence represents a complementarity determining region
 CC (CDR) from an antibody generated against a Helicobacter pylori antigen
 CC (catalase or beta-urease) which is used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 10 AA;

Query Match 70.8%; Score 17; DB 4; Length 10;
 Best Local Similarity 40.0%; Pred. No. 3.4e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXHW 6
 |
 4 FSTSW 8

RESULT 6

ADC07163

ID ADC07163 standard; peptide; 11 AA.

XX ADC07163;

XX 18-DEC-2003 (first entry)

DT Painted lady AKH peptide 2.

XX lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;
 KW antidiabetic; hypotensive; cardiant; antiarthritic; cyostatic;
 KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;
 KW obesity; type II diabetes; cholelithiasis; hypertension;
 KW coronary heart disease; atherosclerosis; glycogenosis; arthritis; cancer;
 KW renal failure; liver; chronic pain; sleep apnea; stroke;
 KW urinary incontinence; painted lady.

XX Synthetic.

OS Vanessa cardui.

XX Key Location/Qualifiers

PH Modified-site 1

FT /label= OTHER

FT /note= "OTHER = Pyroglutamic acid"

FT Misc-difference 11

FT /note= "Preferably C-terminal amide"

XX W02003066080-A1.

XX 14-AUG-2003.

XX 07-FEB-2003; 2003WO-US003800.

XX 07-FEB-2002; 2002US-00072419.

XX (BLMB-) BLM GROUP.

XX Schacter BZ, Schacter LP;

XX WPI; 2003-712542/67.

XX Pharmaceutical composition useful for promoting weight loss, comprises an
 PT insect adipokinetic hormone, having a pyroglutamate residue at its amino
 FT terminus.

XX Claim 29; Page 20; 82pp; English.

XX The invention relates to a novel method of promoting lipid mobilisation
 CC in a human which comprises administering an insect adipokinetic hormone
 CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,

CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,
 CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The
 CC method of the invention may be useful for treating obesity, type II
 CC diabetes, cholelithiasis, hypertension, coronary heart disease,
 CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal
 CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary
 CC incontinence. The current sequence is that of the painted lady AKH
 CC peptide 2 of the invention.
 XX
 SQ Sequence 11 AA;
 Query Match 70.8%; Score 17; DB 7; Length 11;
 Best Local Similarity 40.0%; Pred. No. 3.6e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 FXXXW 6
 Db 4 FTSSW 8
 RESULT 7
 AAE05735
 ID AAE05735 standard; peptide; 13 AA.
 AC AAE05735;
 XX
 XX 24-SEP-2001 (first entry)
 XX
 XX Complementarity-determining region 3 (CDR3) of MoPhabs #7.
 XX CDR3; complementarity-determining region 3; monoclonal phage antibody;
 KW MoPhabs; antigen.
 KW
 XX Synthetic.
 OS
 XX US6265150-B1.
 PN
 XX 24-JUL-2001.
 PD
 XX 26-MAY-1998; 98US-00085072.
 XX
 XX 07-JUN-1995; 95US-00483633.
 PR 18-SEP-1997; 97US-00932892.
 PR
 XX (BECT) BECTON DICKINSON & CO.
 PA (CRUC-) CRUCCELL HOLLAND BV.
 PA
 XX Terstappen LW, Logtenberg T;
 PI
 XX WPI; 2001-463929/50.
 DR
 XX Obtaining a phage particle, useful for obtaining human antibodies against
 PT known and novel surface antigens, by incubating a phage library with
 PT target cells to allow binding of the antibody fragment to the antigen.
 PT
 XX Example 6; Col 6; 6pp; English.
 PS
 XX The invention relates to a method of obtaining a phage particle which has
 CC an antibody fragment directed against an antigen associated with the
 CC surface of target cells in a heterogeneous cell population. The method
 CC involves incubating a library of phage particles with the target cells to
 CC allow binding of the antibody fragment expressed on the surface of the
 CC phage particles to the antigen associated with the target cells. The
 CC method is useful for obtaining human antibodies against known and novel
 CC surface antigens in their native configuration, expressed on
 CC phenotypically defined subpopulations of cells. The present sequence is
 CC complementarity-determining region 3 (CDR3) of monoclonal phage
 CC antibodies (MoPhabs) used in the exemplification of the invention
 XX
 SQ Sequence 13 AA;
 Query Match 70.8%; Score 17; DB 4; Length 13;
 Best Local Similarity 40.0%; Pred. No. 4.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 FXXXW 6
 Db 6 FASSW 10
 RESULT 8
 ABG75574
 ID ABG75574 standard; peptide; 13 AA.
 XX
 AC ABG75574;
 XX
 XX 22-APR-2003 (first entry)
 XX
 XX CDR3 peptide sequence, #7, used in phage antibody construction.
 XX
 XX Phage; antibody; antigen; target cell; phage particle;
 KW cell-type specific phage antibody library; phage antibody; Phab;
 KW monoclonal phage antibody; MoPhab; blood cell; foetal bone marrow cell;
 KW complementarity determining region 3; CDR3; human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX US2002132228-A1.
 PN
 XX 19-SEP-2002.
 PD
 XX 24-MAY-2001; 2001US-00865048.
 XX
 XX 07-JUN-1995; 95US-00483633.
 PR 18-SEP-1997; 97US-00932892.
 PR 26-MAY-1998; 98US-00085072.
 PR
 XX (TERS/) TERSTAPPEN L W M M.
 PA (LOGT/) LOGTENBERG T.
 PA
 XX Terstappen LMMM, Logtenberg T;
 PI
 XX WPI; 2003-174076/17.
 DR
 XX Obtaining phage having antibody specific for cell surface antigen of
 PT target cells in heterogeneous cell population, by incubating phage
 PT antibody library with target cells, and separating phage particles bound
 PT target cells.
 PT
 XX Example 6; Page 4; 5pp; English.
 PS
 XX The invention discloses a method for obtaining a phage comprising an
 CC antibody, or its fragment, directed against antigens associated with a
 CC target cells surface in a heterogeneous cell population. The method
 CC comprises providing a library of antibodies, or their fragments,
 CC expressed on the surface of phage particles, incubating the phage,
 CC antibody library with the target cells, separating the target cells and
 CC phage particles associated with them from the phage particles not
 CC associated with the target cells and then recovering the phage particles.
 CC Also disclosed is a cell-type specific phage antibody library and an
 CC antibody, or antibody fragment, obtained using the method. The method is
 CC useful for obtaining a selection of phage antibodies (Phabs) and
 CC monoclonal phage antibodies (MoPhabs). The method is also useful for
 CC detecting known and novel structures on various populations of blood and
 CC foetal bone marrow cells. The sequence presented is an example of the
 CC partly randomised human complementarity determining region 3 (CDR3) used
 CC in the construction of the antibodies
 XX
 SQ Sequence 13 AA;
 Query Match 70.8%; Score 17; DB 6; Length 13;
 Best Local Similarity 40.0%; Pred. No. 4.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 FXXXW 6

```

Db      | 6 PASSW 10
|
RESULT 9
AAM98088
ID AAM98088 standard; peptide; 14 AA.
AC
XX
AC AAM98088;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human peptide #1363 encoded by a SNP oligonucleotide.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX
OS Homo sapiens.
XX
PN HQ200147944-A2.
XX
PD 05-JUL-2001.
XX
XX 28-DEC-2000; 2000MO-US035498.
XX
PF 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
PA
XX Shimketa RA, Leach M;
PI
XX WPI; 2001-465210/50.
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Disclosure; Page 3967; 4143pp; English.
XX
XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogene, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms
XX
SQ Sequence 14 AA;
Query Match 70.8%; Score 17; DB 4; Length 14;
Best Local Similarity 40.0%; Pred. No. 4.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXW 6
|
Db 6 FASTW 10
|
RESULT 10
AAR97874
ID AAR97874 standard; peptide; 15 AA.
XX
AC AAR97874;
XX
DT 16-AUG-1996 (first entry)
XX
DE Japan cedar pollen mature allergen Cry j II amino acids 16-30.
XX
KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
KW Sugi pollinosis; diagnosis; treatment.
XX
OS Cryptomeria japonica.
XX
PN JP08047392-A.
XX
PD 20-FEB-1996.
XX
PF 07-NOV-1994; 94JP-00297840.
XX
PR 05-NOV-1993; 93JP-00276773.
PR 26-MAY-1994; 94JP-00134868.
XX
XX (MEIP ) MEIJI MILK PROD CO LTD.
XX
XX WPI; 1996-166249/17.
XX
XX Japan cedar pollen allergen Cry j II epitope - comprises at least part of
PT specified 460 aminoacid protein.
XX
PS Claim 8; Fig 3; 17pp; Japanese.
XX
XX AAR97871-R97960 are overlapping peptides used for the epitope mapping of
CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
CC peptides of it are useful in the diagnosis, prevention and treatment of
CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant
CC regions of the allergen were identified using the overlapping peptides of
CC the full epitope derived from a Cry j II antigen-specific T cell line.
CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460
CC amino acid allergen are the most allergenic of the 90 peptides tested
XX
SQ Sequence 15 AA;
Query Match 70.8%; Score 17; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXW 6
|
Db 9 FSTAW 13
|
RESULT 11
AAR97875
ID AAR97875 standard; peptide; 15 AA.
XX
AC AAR97875;
XX
DT 16-AUG-1996 (first entry)
XX
DE Japan cedar pollen mature allergen Cry j II amino acids 21-35.
XX
KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
KW Sugi pollinosis; diagnosis; treatment.
XX
OS Cryptomeria japonica.
XX
PN JP08047392-A.
XX
PD 20-FEB-1996.
XX

```


PF 07-NOV-1994; 94JP-00297840.
 XX
 PR 05-NOV-1993; 93JP-00276773.
 PR 26-MAY-1994; 94JP-00134868.
 XX
 PA (MEIP) MEIJI MILK PROD CO LTD.
 XX
 DR WPI; 1996-166249/17.
 XX
 PT Japan cedar pollen allergen Cry j II epitope - comprises at least part of
 PT specified 460 aminoacid protein.
 XX
 PS Claim 8; Fig 3; 17pp; Japanese.
 XX
 CC AAR97871-R97960 are overlapping peptides used for the epitope mapping of
 CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
 CC peptides of it are useful in the diagnosis, prevention and treatment of
 CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant
 CC regions of the allergen were identified using the overlapping peptides of
 CC the full epitope derived from a Cry j II antigen-specific T cell line.
 CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460
 CC amino acid allergen are the most allergenic of the 90 peptides tested
 XX
 SQ Sequence 15 AA;
 CC
 Query Match 70.8%; Score 17; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXW 6
 DB 4 FSTW 8
 RESULT 12
 AAW57758
 ID AAW57758 standard; peptide; 15 AA.
 XX
 AC AAW57758;
 XX
 DT 17-SEP-1998 (first entry)
 XX
 DE Residues 16-30 of Cry j 2.
 XX
 CC Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;
 KW HLA class II molecule.
 XX
 OS Cryptomeria japonica.
 XX
 PN WO9820902-A1.
 XX
 PD 22-MAY-1998.
 XX
 PP 12-NOV-1997; 97WO-JP004129.
 XX
 PR 13-NOV-1996; 96JP-00302053.
 XX
 PA (MEIP) MEIJI MILK PROD CO LTD.
 XX
 PI Sone T, Kume A, Dairiki K, Kino K;
 XX
 DR WPI; 1998-297617/26.
 XX
 PT Peptides derived from Japanese cedar pollen antigens are
 PT immunotherapeutic agents - useful for allergy treatment and typing HLA
 PT class II molecules in allergy sufferers.
 XX
 PS Claim 12; Page 29; 50pp; Japanese.
 XX
 CC This sequence represents residues 16-30 of the Cry j 2 protein, and is a
 CC peptide of the invention. The peptides are derived from Japanese cedar
 CC pollen antigens, and are used as immunotherapeutic agents in the
 CC treatment of allergy. The peptides can be used for identification and

CC typing of the particular HLA class II molecules in an allergy sufferer,
 CC and also for peptide immunotherapy of an allergy. Using these peptides
 CC the immunotherapy can be targeted more specifically to the requirements
 CC of the individual patient, allowing more effective treatment of an
 CC allergy, including those patients for whom treatment with a conventional
 CC immunotherapeutic agent is ineffective
 XX
 SQ Sequence 15 AA;
 CC
 Query Match 70.8%; Score 17; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXW 6
 DB 9 FSTW 13
 RESULT 13
 AAE23038
 ID AAE23038 standard; peptide; 19 AA.
 XX
 AC AAE23038;
 XX
 DT 21-AUG-2002 (first entry)
 XX
 DE Human thioresdoxin, 47916 peptide.
 XX
 KW Human; thioresdoxin; 22108; 47916; haematopoietic disorder; leukaemia;
 KW cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;
 KW cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;
 KW brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;
 KW cytostatic; carcinoma; cardiac; neuroprotective; antiinflammatory;
 KW gene therapy; nootropic.
 XX
 OS Homo sapiens.
 XX
 PN WO200226803-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 25-SEP-2001; 2001WO-US029967.
 XX
 PR 25-SEP-2000; 2000US-0235049P.
 XX
 PA (MILL-) MILLENIUM PHARM INC.
 XX
 PI Bandaru R, Kapeller-Libermann R;
 XX
 DR WPI; 2002-416475/44.
 XX
 PT New human thioresdoxin nucleic acid and polypeptide molecules, designated
 PT 22108 and 47916, useful for diagnosing, preventing or treating cancer
 PT (e.g. carcinoma), cardiovascular diseases (e.g. heart failure) or brain
 PT disorders.
 XX
 PS Disclosure; Page 11; 124pp; English.
 XX
 CC The invention relates to human thioresdoxin nucleic acid and polypeptide
 CC molecules, designated 22108 and 47916. The compound that modulates the
 CC activity or expression of 22108 and 47916 nucleic acid is useful for
 CC treating or preventing a disorder characterised by aberrant activity of
 CC 22108 and 47916-expressing cell, specifically for reducing or inhibiting
 CC the aberrant activity of the 22108 and 47916-expressing cancer cell. The
 CC 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,
 CC preventing or treating cancer in a subject (e.g. carcinoma, sarcoma,
 CC metastatic or haematopoietic disorders (e.g. leukaemia), or cancers of the
 CC lung, breast, thyroid, head neck, prostate or genito-urinary tract),
 CC cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart
 CC failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's
 CC diseases). The thioresdoxin DNA is also useful in gene therapy. The
 CC present sequence is human thioresdoxin, 47916 peptide
 XX

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SQ Sequence 19 AA;
  Query Match      70.8%; Score 17; DB 5; Length 19;
  Best Local Similarity 40.0%; Pred. No. 5.6e+03;
  Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXX 6
  | | |
Db 4 FSATW 8

RESULT 14
AAW42165
ID AAW42165 standard; peptide; 20 AA.
XX
AC AAW42165;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-JUN-1998 (first entry)
XX
DE T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.
XX
KW Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;
KW diagnosis; allergy; spring tree pollen disease; pollinosis.
XX
OS Chamaecyparis obtusa.
XX
PN WO9747648-A1.
XX
PD 18-DEC-1997.
XX
PF 12-JUN-1997; 97WO-JP002031.
XX
PR 14-JUN-1996; 96JP-00153527.
XX
PA (MEIP ) MEIJI MILK PROD CO LTD.
XX
PI Kino K, Dairiri K;
XX
DR WPI; 1998-052242/05.
XX
T-cell epitope peptide portion of Japanese cypress pollen antigens Chao1
and Chao2 - used for diagnosis and treatment of spring tree pollen
disease.
XX
PS Claim 2; Page 36; 71pp; Japanese.
XX
The present sequence represents a T-cell epitope peptide from Japanese
cypress pollen antigen Chao2. The present invention describes peptides
which correspond to the T-cell epitope sites on Japanese cypress pollen
antigens Chao1 and Chao2. The peptides can be used as a reagent for the
diagnosis of allergy to Japanese cypress pollen, and as an antigen in the
treatment and prevention of spring tree pollen disease in which the
pollinosis involves reactivity to Japanese cypress pollen. (Updated on 25
-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
field.)
XX
SQ Sequence 20 AA;
  Query Match      70.8%; Score 17; DB 2; Length 20;
  Best Local Similarity 40.0%; Pred. No. 5.8e+03;
  Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXX 6
  | | |
Db 8 FATTW 12

RESULT 15
AAG62999
ID AAG62999 standard; peptide; 20 AA.
XX
  
```

```

AC AAG62999;
XX
DT 01-OCT-2001 (first entry)
XX
DE Complementarity determining region 3 (CDR3) of VH chain of clone G101.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB004501.
XX
PR 13-DEC-1999; 99US-0170599P.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases.
XX
PS Claim 1; Page 76; 109pp; English.
XX
AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
of VL and VH chains of antibodies of the invention. The specification
describes a mixture or panel of 5 different specific binding members,
each comprising an antibody VH and/or VL variable domain and capable,
when displayed on the surface of filamentous bacteriophage particles or
in the case of a specific binding member comprising the D5 VH and/or VL
variable domain when bound to human serum amyloid protein, to pass
through a mammalian blood brain barrier (BBB). The panel is useful for
the selection of specific binding members with a desired property such as
ability to cross BBB, ability to bind endothelial cells or other brain
cell antigen, ability to bind areas of inflammation in the brain or BBB
breakdown or ability to bind intracellular adhesion molecules and to bind
transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
and treatment of human or animal body, including neurological diseases,
such as Alzheimer's disease, prion disease, AIDS-related dementia,
epilepsy and traumatic brain injury and any diseases involving
inflammation occurring within the brain or central nervous system
XX
SQ Sequence 20 AA;
  Query Match      70.8%; Score 17; DB 4; Length 20;
  Best Local Similarity 40.0%; Pred. No. 5.8e+03;
  Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXX 6
  | | |
Db 4 FSSSW 8

RESULT 16
ADR68284
ID ADR68284 standard; peptide; 5 AA.
XX
AC ADR68284;
XX
DT 02-DEC-2004 (first entry)
XX
DE Androgen receptor interacting peptide SEQ ID NO:2.
XX
KW androgen receptor binding peptide; androgen receptor interacting peptide;
  
```

KW androgen receptor; cytostatic; gene therapy; prostate cancer.

XX Mammalia.

OS Synthetic.

XX WO2004076473-A2.

XX 10-SEP-2004.

XX 10-FEB-2004; 2004WO-US003774.

XX 12-FEB-2003; 2003US-0446955P.

XX (KARO-) KARO BIO AB.

XX Buehrer BM, Barnett TR;

XX WPI; 2004-653365/63.

XX New polypeptides that bind to the androgen receptor, useful for
PT diagnosing or treating diseases associated with abnormal levels of
PT activation of androgen receptor, e.g. prostate cancer, or in biological
PT research.

XX Disclosure; SEQ ID NO 2; 46pp; English.

XX The present invention describes a polypeptide that binds to the androgen
CC receptor, or a polypeptide that comprises at least 50% amino acid
CC sequence identity to the polypeptide. Also described: (1) methods of
CC analysing the surface conformation of a protein using one or more of the
CC polypeptide sequences mentioned above; (2) methods of identifying
CC modulators of protein function using one or more of the polypeptide
CC sequences mentioned above; (3) a pharmaceutical composition comprising a
CC pharmaceutical carrier and one or more of the polypeptide sequences
CC described above; (4) a peptide that binds to the androgen receptor, the
CC binding being competitively inhibited by the polypeptide and at least a
CC (5) a chimeric protein comprising the above polypeptide and at least a
CC portion of a filamentous phage protein, the portion of the filamentous
CC phage protein being sufficient for integration of the chimeric protein
CC into the coat of phage particles to display the polypeptide; (6) a
CC filamentous phage displaying the above polypeptide; (7) a method of
CC diagnosing a disease in a patient characterised by abnormal levels of
CC activation of androgen receptor, comprising providing a sample of body
CC fluid or tissue of the patient, administering a diagnostic amount of the
CC pharmaceutical composition described above, and assaying the amount of
CC activated androgen receptor in the body fluid or tissue of the patient;
CC and (8) a method of treating a patient suffering from a disease
CC characterised by abnormal levels of activation of androgen receptor,
CC comprising administering to the patient a therapeutic amount of the
CC pharmaceutical composition described above. The androgen receptor
CC interacting polypeptide has cytostatic activity, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing or
CC treating patients suffering from diseases characterised by abnormal
CC levels of activation of androgen receptor, such as prostate cancer. They
CC may also be used in biological research, as therapeutics or for in vitro
CC or in vivo classification of compounds. The present sequence represents
CC an androgen receptor interacting peptide, which is used in the
CC exemplification of the present invention.

XX SQ Sequence 5 AA;

Query Match 66.7%; Score 16; DB 8; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 1 FAALW 5

RESULT 17

AAW76953

ID AAW76953 standard; peptide; 6 AA.

XX AAW76953;

XX 25-JAN-1999 (first entry)

XX Fusion immunoglobulin heavy chain HIV gp120 B cell epitope #93.

XX B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IgH;
KW human immune deficiency virus; HIV; tolerance; treatment; therapy;
KW prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;
KW microbial infection; autoimmune disease; antibody; apoptosis;
KW antiviral T cell immunity.

XX Mus sp.

OS Homo sapiens.

XX WO9836087-A1.

XX 20-AUG-1998.

XX 13-FEB-1998; 98WO-US002766.

XX 13-FEB-1997; 97US-0040581P.

XX (AMNA-) AMERICAN NAT RED CROSS.

XX Scott D, Zambidis E;

XX WPI; 1998-506315/43.

XX New fusion immunoglobulin heavy chain including gp120 epitopes and
PT related complete antibodies - DNA, vectors and transformed cells, used to
PT induce tolerance to the epitopes for treatment of human immune deficiency
PT virus infection.

XX Disclosure; Page 40; 154pp; English.

XX This sequence is an epitope used in the construction of a novel fusion
CC immunoglobulin heavy chain (IgH) protein with a mammalian, especially
CC human, IgH chain fused in frame at its N-terminus to one or more human
CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or
CC transfected cells are used to tolerate subjects to gp120 epitopes and to
CC maintain this tolerance, particularly for treatment of HIV infection,
CC optionally together with other therapeutic/prophylactic agents such as
CC vaccines, chemotherapeutic agents and immune response modifiers. Such
CC proteins can be used against other diseases where an immune response is
CC deleterious, e.g. microbial infection, tumours or autoimmune disease.
CC Induction of tolerance suppresses production of antibodies against gp120,
CC so prevents or inhibits 'bystander' apoptosis of uninfected T cells that
CC are bound to gp120 protein, maximising induction of protective antiviral
CC T cell immunity

XX SQ Sequence 6 AA;

Query Match 66.7%; Score 16; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 2 FNSTW 6

RESULT 18

ABR46309

ID ABR46309 standard; peptide; 6 AA.

XX ABR46309;

XX 10-JUN-2003 (first entry)

XX Staphylococcus aureus CHIPS-related peptide #1499.

XX

KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; skin disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 PN 23-JAN-2003.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 PA Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 16; 89pp; English.
 PS The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 SQ Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXW 6
 | |
 Db 1 FFSW 5
 RESULT 19
 ABR46270
 ID ABR46270 standard; peptide; 6 AA.
 XX ABR46270;
 AC 10-JUN-2003 (first entry)
 DT Staphylococcus aureus CHIPS-related peptide #1460.
 DE CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; skin disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 PN 23-JAN-2003.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 PA Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 16; 89pp; English.
 PS The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 SQ Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXW 6
 | |
 Db 1 FFSW 5
 RESULT 20
 ABR46702
 ID ABR46702 standard; peptide; 6 AA.
 XX ABR46702;
 AC 10-JUN-2003 (first entry)
 DT Staphylococcus aureus CHIPS-related peptide #1892.
 DE CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; skin disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 PN 23-JAN-2003.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 PA Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 16; 89pp; English.
 PS The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 SQ Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXW 6
 | |
 Db 1 FFSW 5

XX 11-JUL-2001; 2001WO-EP008004.
 PR (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 17; 89pp; English.
 XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 XX Query Match 66.7%; Score 16; DB 6; Length 6;
 XX Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 XX Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 FXXXX 6
 Db 1 FFSW 5
 RESULT 21
 ABR47093
 ID ABR47093 standard; peptide; 6 AA.
 XX ABR47093;
 AC ABR47093;
 DT 10-JUN-2003 (first entry)
 XX Staphylococcus aureus CHIPS-related peptide #2283.
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX Staphylococcus aureus.
 OS Synthetic.
 OS WO2003006048-A1.
 XX 23-JAN-2003.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 11; 89pp; English.

DR WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 19; 89pp; English.
 XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 XX Query Match 66.7%; Score 16; DB 6; Length 6;
 XX Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 XX Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 FXXXX 6
 Db 1 FFSW 5
 RESULT 22
 ABR45149
 ID ABR45149 standard; peptide; 6 AA.
 XX ABR45149;
 AC ABR45149;
 DT 10-JUN-2003 (first entry)
 XX Staphylococcus aureus CHIPS-related peptide #339.
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX Staphylococcus aureus.
 OS Synthetic.
 OS WO2003006048-A1.
 XX 23-JAN-2003.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 11; 89pp; English.

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 SQ

Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXW 6
 DB 1 FSPW 5

RESULT 23
 ABR45486
 ID ABR45486 standard; peptide; 6 AA.
 XX AC ABR45486;
 XX DT 10-JUN-2003 (first entry)
 XX DE Staphylococcus aureus CHIPS-related peptide #576.
 XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX OS Staphylococcus aureus.
 XX OS Synthetic.
 XX PN WO2003006048-A1.
 XX PD 23-JAN-2003.
 XX PF 11-JUL-2001; 2001WO-EP008004.
 XX PR 11-JUL-2001; 2001WO-EP008004.
 XX PA (JARI-) JARI PHARM BV.
 XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX PI Van Strijp JAG;
 XX DR WPI; 2003-256333/25.
 XX CC Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX PS Disclosure; Page 13; 89pp; English.
 XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 SQ

CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 SQ

Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXW 6
 DB 1 FTFW 5

RESULT 24
 ABR45878
 ID ABR45878 standard; peptide; 6 AA.
 XX AC ABR45878;
 XX DT 10-JUN-2003 (first entry)
 XX DE Staphylococcus aureus CHIPS-related peptide #1068.
 XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX OS Staphylococcus aureus.
 XX OS Synthetic.
 XX PN WO2003006048-A1.
 XX PD 23-JAN-2003.
 XX PF 11-JUL-2001; 2001WO-EP008004.
 XX PR 11-JUL-2001; 2001WO-EP008004.
 XX PA (JARI-) JARI PHARM BV.
 XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX PI Van Strijp JAG;
 XX DR WPI; 2003-256333/25.
 XX CC Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX PS Disclosure; Page 14; 89pp; English.
 XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 SQ

Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXW 6
 DB 1 FTFW 5

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 1 FTFW 5

RESULT 25

ID ABR46661 standard; peptide; 6 AA.

XX AC ABR46661;

XX DT 10-JUN-2003 (first entry)

XX DE Staphylococcus aureus CHIPS-related peptide #1851.

XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiant; cerebroprotective; neuroprotective; nootropic; dermatological; gynecological; immunosuppressive; anti-HIV.

XX OS Staphylococcus aureus.

OS Synthetic.

XX PN W02003006048-A1.

XX PD 23-JAN-2003.

XX PF 11-JUL-2001; 2001WO-EP008004.

XX PR 11-JUL-2001; 2001WO-EP008004.

XX PA (JARI-) JARI PHARM BV.

XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtz JAW;

XX PI Van Strijp JAG;

XX DR WPI; 2003-256333/25.

XX CC Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases.

XX PS Disclosure; Page 17; 89pp; English.

XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164 -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

Qy Sequence 6 AA;

Query Match 66.7%; Score 16; DB 6; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 1 FTFW 5

RESULT 26

XX DE Staphylococcus aureus CHIPS-related peptide #380.

ABR47053

ID ABR47053 standard; peptide; 6 AA.

XX AC ABR47053;

XX DT 10-JUN-2003 (first entry)

XX DE Staphylococcus aureus CHIPS-related peptide #2243.

XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiant; cerebroprotective; neuroprotective; nootropic; dermatological; gynecological; immunosuppressive; anti-HIV.

XX OS Staphylococcus aureus.

OS Synthetic.

XX PN W02003006048-A1.

XX PD 23-JAN-2003.

XX PF 11-JUL-2001; 2001WO-EP008004.

XX PR 11-JUL-2001; 2001WO-EP008004.

XX PA (JARI-) JARI PHARM BV.

XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtz JAW;

XX PI Van Strijp JAG;

XX DR WPI; 2003-256333/25.

XX CC Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases.

XX PS Disclosure; Page 19; 89pp; English.

XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164 -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection

Qy Query Match 66.7%; Score 16; DB 6; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 1 FTFW 5

RESULT 27

ABR45190

ID ABR45190 standard; peptide; 6 AA.

XX AC ABR45190;

XX DT 10-JUN-2003 (first entry)

XX DE Staphylococcus aureus CHIPS-related peptide #380.

PF 11-JUL-2001; 2001WO-EP008004.
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 DR WPI; 2003-256333/25.
 XX
 CC Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 PS Disclosure; Page 16; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX
 SQ Sequence 6 AA;
 Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 FXXW 6
 Db 1 FTFSW 5

RESULT 30
 ABR47094
 ID ABR47094 standard; peptide; 6 AA.
 XX
 AC ABR47094;
 XX
 DT 10-JUN-2003 (first entry)
 DE Staphylococcus aureus CHIPS-related peptide #2284.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 FN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP008004.
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 DR WPI; 2003-256333/25.
 XX
 CC Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 PS Disclosure; Page 16; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX
 SQ Sequence 6 AA;
 Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 FXXW 6
 Db 1 FTFSW 5

RESULT 30
 ABR47094
 ID ABR47094 standard; peptide; 6 AA.
 XX
 AC ABR47094;
 XX
 DT 10-JUN-2003 (first entry)
 DE Staphylococcus aureus CHIPS-related peptide #2284.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 FN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP008004.
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX

XX WPI; 2003-256333/25.
 XX
 CC Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 PS Disclosure; Page 19; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX
 SQ Sequence 6 AA;
 Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 FXXW 6
 Db 1 FTFSW 5

RESULT 31
 ABR46701
 ID ABR46701 standard; peptide; 6 AA.
 XX
 AC ABR46701;
 XX
 DT 10-JUN-2003 (first entry)
 DE Staphylococcus aureus CHIPS-related peptide #1891.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 FN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP008004.
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 DR WPI; 2003-256333/25.
 XX
 CC Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX

PS Disclosure; Page 17; 89pp; English.

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164

CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from

CC Staphylococcus aureus. The peptide fragments are useful in the

CC prophylaxis or treatment of diseases or disorders involving the C5a-

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,

CC monocytes and endothelial cells or involving acute or chronic

CC inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, disease of the central nervous system, gastrointestinal

CC diseases, skin diseases, genitourinary diseases, joint diseases,

CC respiratory diseases and HIV infection

XX Sequence 6 AA;

XX Query Match 66.7%; Score 16; DB 6; Length 6;

XX Best Local Similarity 40.0%; Pred. No. 1.8e+06;

XX Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXX 6

Db | |

1 FSPSW 5

RESULT 32

ABR47054

ID ABR47054 standard; peptide; 6 AA.

AC ABR47054;

XX 10-JUN-2003 (first entry)

DT 10-JUN-2003 (first entry)

XX Staphylococcus aureus CHIPS-related peptide #2244.

XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;

XX formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;

XX inflammation; cardiovascular disease; central nervous system disease;

XX gastrointestinal disease; skin disease; genitourinary disease;

XX joint disease; respiratory disease; HIV infection; antiinflammatory;

XX cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;

XX gynecological; immunosuppressive; anti-HIV.

XX Staphylococcus aureus.

OS Synthetic.

OS WO2003006048-A1.

XX 23-JAN-2003.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX (JARI-) JARI PHARM BV.

XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;

XX Van Strijp JAG;

XX WPI; 2003-256333/25.

XX Combination of peptides derived from chemotaxis inhibiting protein from

XX Staphylococcus aureus (CHIPS) having CHIPS activity, useful in

XX prophylaxis and treatment of inflammation, cardiovascular, skin and

XX kidney diseases.

XX Disclosure; Page 19; 89pp; English.

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164

CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from

CC Staphylococcus aureus. The peptide fragments are useful in the

CC prophylaxis or treatment of diseases or disorders involving the C5a-

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,

CC monocytes and endothelial cells or involving acute or chronic

XX inflammation reactions. The diseases or disorders include cardiovascular

XX diseases, disease of the central nervous system, gastrointestinal

XX diseases, skin diseases, genitourinary diseases, joint diseases,

XX respiratory diseases and HIV infection

XX Sequence 6 AA;

XX Query Match 66.7%; Score 16; DB 6; Length 6;

XX Best Local Similarity 40.0%; Pred. No. 1.8e+06;

XX Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXX 6

Db | |

1 FSPSW 5

RESULT 33

ABR45525

ID ABR45525 standard; peptide; 6 AA.

AC ABR45525;

XX 10-JUN-2003 (first entry)

DT 10-JUN-2003 (first entry)

XX Staphylococcus aureus CHIPS-related peptide #715.

XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;

XX formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;

XX inflammation; cardiovascular disease; central nervous system disease;

XX gastrointestinal disease; skin disease; genitourinary disease;

XX joint disease; respiratory disease; HIV infection; antiinflammatory;

XX cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;

XX gynecological; immunosuppressive; anti-HIV.

XX Staphylococcus aureus.

OS Synthetic.

OS WO2003006048-A1.

XX 23-JAN-2003.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX (JARI-) JARI PHARM BV.

XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;

XX Van Strijp JAG;

XX WPI; 2003-256333/25.

XX Combination of peptides derived from chemotaxis inhibiting protein from

XX Staphylococcus aureus (CHIPS) having CHIPS activity, useful in

XX prophylaxis and treatment of inflammation, cardiovascular, skin and

XX kidney diseases.

XX Disclosure; Page 13; 89pp; English.

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164

CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from

CC Staphylococcus aureus. The peptide fragments are useful in the

CC prophylaxis or treatment of diseases or disorders involving the C5a-

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,

CC monocytes and endothelial cells or involving acute or chronic

XX inflammation reactions. The diseases or disorders include cardiovascular

XX diseases, disease of the central nervous system, gastrointestinal

XX diseases, skin diseases, genitourinary diseases, joint diseases,

XX respiratory diseases and HIV infection

XX Sequence 6 AA;

XX Query Match 66.7%; Score 16; DB 6; Length 6;

XX Best Local Similarity 40.0%; Pred. No. 1.8e+06;

XX Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXX 6

Db | |

1 FSPSW 5

Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 1 FFSW 5

RESULT 34

ABR45918

ID ABR45918 standard; peptide; 6 AA.

AC ABR45918;

DT 10-JUN-2003 (first entry)

DE Staphylococcus aureus CHIPS-related peptide #1108.

XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.

OS Staphylococcus aureus.

OS Synthetic.

PN WO2003006048-A1.

PD 23-JAN-2003.

PF 11-JUL-2001; 2001WO-EP008004.

PR 11-JUL-2001; 2001WO-EP008004.

XX (JARI-) JARI PHARM BV.

XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtz JAW;

PI Van Strijp JAG;

XX WPI; 2003-256333/25.

XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.

PS Disclosure; Page 14; 89pp; English.

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection

SQ Sequence 6 AA;

Query Match 66.7%; Score 16; DB 6; Length 6;

Best Local Similarity 40.0%; Pred. No. 1.8e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 1 FFSW 5

RESULT 35

ABR45189

ID ABR45189 standard; peptide; 6 AA.

XX ABR45189;

DT 10-JUN-2003 (first entry)

DE Staphylococcus aureus CHIPS-related peptide #379.

XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.

OS Staphylococcus aureus.

OS Synthetic.

PN WO2003006048-A1.

PD 23-JAN-2003.

PF 11-JUL-2001; 2001WO-EP008004.

PR 11-JUL-2001; 2001WO-EP008004.

XX (JARI-) JARI PHARM BV.

XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtz JAW;

PI Van Strijp JAG;

XX WPI; 2003-256333/25.

XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.

PS Disclosure; Page 12; 89pp; English.

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection

SQ Sequence 6 AA;

Query Match 66.7%; Score 16; DB 6; Length 6;

Best Local Similarity 40.0%; Pred. No. 1.8e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 1 FFSW 5

RESULT 36

ABR45485

ID ABR45485 standard; peptide; 6 AA.

XX ABR45485;

DT 10-JUN-2003 (first entry)

XX

DE Staphylococcus aureus CHIPS-related peptide #675.
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 XX 23-JAN-2003.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 13; 89pp; English.
 XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 QY 2 FXXW 6
 DB 1 FSPAW 5
 Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DE ABR45150 standard; peptide; 6 AA.
 XX ABR45150;
 XX 10-JUN-2003 (first entry)
 XX Staphylococcus aureus CHIPS-related peptide #340.
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 XX 23-JAN-2003.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 13; 89pp; English.
 XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 QY 2 FXXW 6
 DB 1 FSPAW 5
 Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DE ABR45150 standard; peptide; 6 AA.
 XX ABR45150;
 XX 10-JUN-2003 (first entry)
 XX Staphylococcus aureus CHIPS-related peptide #716.
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 XX 23-JAN-2003.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 11; 89pp; English.
 XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 QY 2 FXXW 6
 DB 1 FTFAM 5
 Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DE ABR45526 standard; peptide; 6 AA.
 XX ABR45526;
 XX 10-JUN-2003 (first entry)
 XX Staphylococcus aureus CHIPS-related peptide #716.
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 XX 23-JAN-2003.

XX PF 11-JUL-2001; 2001WO-EP008004.
 XX PR 11-JUL-2001; 2001WO-EP008004.
 XX PA (JARI-) JARI PHARM BV,
 XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX PI Van Strijp JAG;
 XX DR WPI; 2003-256333/25.
 XX CC Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX PS Disclosure; Page 13; 89pp; English.
 XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX SQ Sequence 6 AA;
 Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 FXXW 6
 |
 Db 1 FTFSW 5
 RESULT 39
 ABR46269
 ID ABR46269 standard; peptide; 6 AA.
 XX AC ABR46269;
 XX DT 10-JUN-2003 (first entry)
 XX DE Staphylococcus aureus CHIPS-related peptide #1459.
 XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nontropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX OS Staphylococcus aureus.
 XX OS Synthetic.
 XX PN WO2003006048-A1.
 XX PD 23-JAN-2003.
 XX PF 11-JUL-2001; 2001WO-EP008004.
 XX PR 11-JUL-2001; 2001WO-EP008004.
 XX PA (JARI-) JARI PHARM BV.
 XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX PI Van Strijp JAG;
 XX DR WPI; 2003-256333/25.
 XX CC Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX PS Disclosure; Page 13; 89pp; English.
 XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX SQ Sequence 6 AA;
 Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 FXXW 6
 |
 Db 1 FTFSW 5
 RESULT 39
 ABR46269
 ID ABR46269 standard; peptide; 6 AA.
 XX AC ABR46269;
 XX DT 10-JUN-2003 (first entry)
 XX DE Staphylococcus aureus CHIPS-related peptide #1459.
 XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nontropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX OS Staphylococcus aureus.
 XX OS Synthetic.
 XX PN WO2003006048-A1.
 XX PD 23-JAN-2003.
 XX PF 11-JUL-2001; 2001WO-EP008004.
 XX PR 11-JUL-2001; 2001WO-EP008004.
 XX PA (JARI-) JARI PHARM BV.
 XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX PI Van Strijp JAG;
 XX DR WPI; 2003-256333/25.
 XX CC Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX PS Disclosure; Page 16; 89pp; English.
 XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX SQ Sequence 6 AA;
 Query Match 66.7%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 FXXW 6
 |
 Db 1 FSPAW 5
 RESULT 40
 ABR46662
 ID ABR46662 standard; peptide; 6 AA.
 XX AC ABR46662;
 XX DT 10-JUN-2003 (first entry)
 XX DE Staphylococcus aureus CHIPS-related peptide #1852.
 XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nontropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX OS Staphylococcus aureus.
 XX OS Synthetic.
 XX PN WO2003006048-A1.
 XX PD 23-JAN-2003.
 XX PF 11-JUL-2001; 2001WO-EP008004.
 XX PR 11-JUL-2001; 2001WO-EP008004.
 XX PA (JARI-) JARI PHARM BV.
 XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX PI Van Strijp JAG;
 XX DR WPI; 2003-256333/25.
 XX CC Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.

XX Disclosure; Page 17; 89pp; English.
PS
XX
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection
XX
SQ Sequence 6 AA;

Query Match 66.7%; Score 16; DB 6; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
| |
Db 1 FTFW 5

Search completed: October 18, 2005, 15:54:57
Job time : 123.824 secs

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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:46:49 ; Search time 31.2353 Seconds
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21.509 Million cell updates/sec

Title: US-09-214-371-11
Perfect score: 24
Sequence: 1 XFXXXXXXX 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 196327

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	70.8	13	3	US-09-085-072-7
2	17	70.8	15	4	US-09-142-524D-87
3	17	70.8	15	4	US-09-142-524D-88
4	16	66.7	6	1	US-07-920-519-10
5	16	66.7	6	1	US-08-086-410-7
6	16	66.7	6	1	US-08-314-596-10
7	16	66.7	7	4	US-09-774-639-284
8	16	66.7	9	4	US-09-702-114A-28
9	16	66.7	10	1	US-08-208-886C-87
10	16	66.7	10	1	US-08-704-744-89
11	16	66.7	10	1	US-08-469-557-68
12	16	66.7	10	2	US-08-290-793B-68
13	16	66.7	11	1	US-08-277-660A-16
14	16	66.7	11	1	US-08-277-660A-17
15	16	66.7	11	1	US-08-424-957-29
16	16	66.7	11	3	US-08-424-957-30
17	16	66.7	11	3	US-09-035-686-29
18	16	66.7	11	3	US-09-035-686-30
19	16	66.7	12	2	US-08-406-330-32
20	16	66.7	12	2	US-08-556-597-32
21	16	66.7	13	1	US-08-305-871A-23
22	16	66.7	13	3	US-08-912-560-11
23	16	66.7	13	4	US-08-788-822A-27
24	16	66.7	13	4	US-09-543-608A-27
25	16	66.7	13	4	US-09-556-818-65
26	16	66.7	13	6	5185431-25
27	16	66.7	13	6	5185431-25

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102	15	62.5	9	1	US-08-638-911A-15	Sequence 13, Appl	175	15	62.5	11	3	US-09-035-686-43	Sequence 43, Appl
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104	15	62.5	9	1	US-08-638-911A-21	Sequence 21, Appl	177	15	62.5	11	3	US-09-035-686-45	Sequence 45, Appl
105	15	62.5	9	2	US-08-709-177-8	Sequence 5, Appl	178	15	62.5	11	3	US-09-035-686-46	Sequence 46, Appl
106	15	62.5	9	2	US-08-709-177-8	Sequence 8, Appl	179	15	62.5	11	4	US-09-603-053-5	Sequence 5, Appl
107	15	62.5	9	2	US-08-709-177-11	Sequence 11, Appl	180	15	62.5	11	4	US-09-069-827A-45	Sequence 46, Appl
108	15	62.5	9	2	US-08-709-177-14	Sequence 14, Appl	181	15	62.5	11	4	US-09-069-827A-172	Sequence 172, App
109	15	62.5	9	3	US-08-396-385-7	Sequence 7, Appl	182	15	62.5	11	4	US-09-620-091-444	Sequence 2, Appl
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111	15	62.5	9	3	US-09-287-221-7	Sequence 7, Appl	184	15	62.5	12	1	US-08-439-114-4	Sequence 5, Appl
112	15	62.5	9	4	US-09-225-322B-12	Sequence 12, Appl	185	15	62.5	12	1	US-08-200-011-5	Sequence 6, Appl
113	15	62.5	9	4	US-09-764-304-12	Sequence 12, Appl	186	15	62.5	12	3	US-08-665-643A-6	Sequence 70, Appl
114	15	62.5	9	4	US-08-634-332A-71	Sequence 71, Appl	187	15	62.5	12	4	US-08-634-332A-70	Sequence 131, App
115	15	62.5	9	4	US-09-555-790A-7	Sequence 7, Appl	188	15	62.5	12	4	US-09-428-082B-131	Sequence 132, App
116	15	62.5	9	4	US-09-555-790A-9	Sequence 9, Appl	189	15	62.5	12	4	US-09-428-082B-132	Sequence 133, App
117	15	62.5	9	4	US-09-771-415-16	Sequence 16, Appl	190	15	62.5	12	4	US-09-428-082B-133	Sequence 134, App
118	15	62.5	9	4	US-09-239-043D-2374	Sequence 2374, Ap	191	15	62.5	12	4	US-09-428-082B-134	Sequence 137, App
119	15	62.5	10	1	US-08-221-580-2	Sequence 2, Appl	192	15	62.5	12	4	US-09-428-082B-137	Sequence 143, App
120	15	62.5	10	1	US-08-208-886C-83	Sequence 83, Appl	193	15	62.5	12	4	US-09-428-082B-143	Sequence 144, App
121	15	62.5	10	1	US-08-277-660A-7	Sequence 7, Appl	194	15	62.5	12	4	US-09-428-082B-144	Sequence 145, App
122	15	62.5	10	1	US-08-277-660A-8	Sequence 8, Appl	195	15	62.5	12	4	US-09-428-082B-145	Sequence 146, App
123	15	62.5	10	1	US-08-704-744-85	Sequence 85, Appl	196	15	62.5	12	4	US-09-428-082B-146	Sequence 102, App
124	15	62.5	10	1	US-08-424-957-11	Sequence 11, Appl	197	15	62.5	13	1	US-08-463-115-102	Sequence 102, App
125	15	62.5	10	1	US-08-424-957-12	Sequence 12, Appl	198	15	62.5	13	1	US-08-463-115-102	Sequence 102, App
126	15	62.5	10	1	US-08-424-957-18	Sequence 18, Appl	199	15	62.5	13	2	US-08-480-190-26	Sequence 26, Appl
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131	15	62.5	10	3	US-08-974-899-10	Sequence 10, Appl	204	15	62.5	13	4	US-09-695-437A-23	Sequence 23, Appl
132	15	62.5	10	3	US-09-035-686-11	Sequence 11, Appl	205	15	62.5	13	4	US-09-695-437A-42	Sequence 42, Appl
133	15	62.5	10	3	US-09-035-686-12	Sequence 12, Appl	206	15	62.5	13	5	PCT-US93-07545-26	Sequence 26, Appl
134	15	62.5	10	3	US-09-035-686-18	Sequence 18, Appl	207	15	62.5	14	2	US-08-764-640-33	Sequence 33, Appl
135	15	62.5	10	4	US-09-490-702B-53	Sequence 53, Appl	208	15	62.5	14	3	US-08-973-225-33	Sequence 33, Appl
136	15	62.5	10	4	US-09-490-702B-72	Sequence 72, Appl	209	15	62.5	14	3	US-08-973-225-213	Sequence 213, App
137	15	62.5	10	4	US-09-795-798-10	Sequence 10, Appl	210	15	62.5	14	3	US-09-244-298A-33	Sequence 33, Appl
138	15	62.5	10	5	PCT-US95-04018-64	Sequence 64, Appl	211	15	62.5	14	3	US-09-516-704-33	Sequence 33, Appl
139	15	62.5	11	1	US-08-277-660A-9	Sequence 9, Appl	212	15	62.5	14	4	US-09-549-090-33	Sequence 33, Appl
140	15	62.5	11	1	US-08-277-660A-10	Sequence 10, Appl	213	15	62.5	14	4	US-09-549-090-213	Sequence 213, App
141	15	62.5	11	1	US-08-277-660A-11	Sequence 11, Appl	214	15	62.5	14	4	US-09-832-230A-33	Sequence 33, Appl
142	15	62.5	11	1	US-08-277-660A-12	Sequence 12, Appl	215	15	62.5	14	4	US-09-428-082B-68	Sequence 68, Appl
143	15	62.5	11	1	US-08-277-660A-13	Sequence 13, Appl	216	15	62.5	14	4	US-09-695-437A-18	Sequence 18, Appl
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145	15	62.5	11	1	US-08-277-660A-19	Sequence 19, Appl	218	15	62.5	14	4	US-09-695-437A-25	Sequence 25, Appl
146	15	62.5	11	1	US-08-277-660A-20	Sequence 20, Appl	219	15	62.5	14	4	US-09-695-437A-26	Sequence 26, Appl
147	15	62.5	11	1	US-08-424-957-17	Sequence 17, Appl	220	15	62.5	15	1	US-08-277-660A-1	Sequence 1, Appl
148	15	62.5	11	1	US-08-424-957-23	Sequence 23, Appl	221	15	62.5	15	1	US-08-277-660A-4	Sequence 4, Appl
149	15	62.5	11	1	US-08-424-957-24	Sequence 24, Appl	222	15	62.5	15	1	US-08-277-660A-5	Sequence 5, Appl
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153	15	62.5	11	1	US-08-424-957-32	Sequence 32, Appl	226	15	62.5	15	1	US-08-424-957-21	Sequence 21, Appl
154	15	62.5	11	1	US-08-424-957-33	Sequence 33, Appl	227	15	62.5	15	1	US-08-424-957-22	Sequence 22, Appl
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156	15	62.5	11	1	US-08-424-957-36	Sequence 36, Appl	229	15	62.5	15	3	US-09-280-047-6	Sequence 6, Appl
157	15	62.5	11	1	US-08-424-957-40	Sequence 40, Appl	230	15	62.5	15	3	US-09-165-042-16	Sequence 16, Appl
158	15	62.5	11	1	US-08-424-957-42	Sequence 42, Appl	231	15	62.5	15	3	US-09-035-686-1	Sequence 1, Appl
159	15	62.5	11	1	US-08-424-957-43	Sequence 43, Appl	232	15	62.5	15	3	US-09-035-686-20	Sequence 20, Appl
160	15	62.5	11	1	US-08-424-957-44	Sequence 44, Appl	233	15	62.5	15	3	US-09-035-686-21	Sequence 21, Appl
161	15	62.5	11	1	US-08-424-957-45	Sequence 45, Appl	234	15	62.5	15	3	US-09-035-686-22	Sequence 22, Appl
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163	15	62.5	11	3	US-09-035-686-17	Sequence 17, Appl	236	15	62.5	15	4	US-09-314-259-165	Sequence 165, App
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165	15	62.5	11	3	US-09-035-686-24	Sequence 24, Appl	238	15	62.5	15	4	US-08-634-332A-69	Sequence 69, Appl
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168	15	62.5	11	3	US-09-035-686-28	Sequence 28, Appl	241	15	62.5	15	4	US-09-157-689-52	Sequence 52, Appl
169	15	62.5	11	3	US-09-035-686-32	Sequence 32, Appl	242	15	62.5	15	4	US-08-268-981-3	Sequence 3, Appl
170	15	62.5	11	3	US-09-035-686-33	Sequence 33, Appl	243	15	62.5	15	4	US-09-428-082B-139	Sequence 139, App
171	15	62.5	11	3	US-09-035-686-34	Sequence 34, Appl	244	15	62.5	15	4	US-09-428-082B-140	Sequence 140, App
172	15	62.5	11	3	US-09-035-686-36	Sequence 36, Appl	245	15	62.5	15	4	US-09-428-082B-141	Sequence 141, App
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254	15	62.5	15	4	US-09-695-437A-17	Sequence 17, Appli	Sequence 101, App
255	15	62.5	15	4	US-09-695-437A-20	Sequence 20, Appli	Sequence 102, App
256	15	62.5	15	4	US-09-695-437A-21	Sequence 21, Appli	Sequence 103, App
257	15	62.5	15	4	US-09-695-437A-22	Sequence 22, Appli	Sequence 104, App
258	15	62.5	15	4	US-09-695-437A-32	Sequence 32, Appli	Sequence 105, App
259	15	62.5	15	4	US-09-695-437A-33	Sequence 33, Appli	Sequence 106, App
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275	15	62.5	17	2	US-08-637-759B-238	Sequence 238, App	Sequence 30, Appli
276	15	62.5	17	3	US-08-671-353A-238	Sequence 238, App	Sequence 30, Appli
277	15	62.5	17	3	US-09-201-945-238	Sequence 238, App	Sequence 30, Appli
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311	15	62.5	20	4	US-09-081-975-20	Sequence 20, Appli	Patent No. 5318899
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317	15	62.5	20	4	US-09-476-498A-234	Sequence 234, App	Sequence 4, Appli
318	15	62.5	20	4	US-09-630-940B-234	Sequence 234, App	Sequence 71, Appli
319	15	62.5	20	4	US-09-471-276-1481	Sequence 1481, Ap	Sequence 8, Appli
320	15	62.5	20	5	PCT-US95-09307-11	Sequence 11, Appli	Sequence 71, Appli

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394	14	58.3	7	3	US-09-258-754-402	Sequence 402, App	467	14	58.3	10	2	US-08-751-300-97	Sequence 97, Appl
395	14	58.3	7	3	US-09-181-083-26	Sequence 26, Appl	468	14	58.3	10	2	US-08-751-300-98	Sequence 98, Appl
396	14	58.3	7	3	US-09-181-083-70	Sequence 70, Appl	469	14	58.3	10	2	US-08-751-300-99	Sequence 99, Appl
397	14	58.3	7	3	US-09-181-083-79	Sequence 79, Appl	470	14	58.3	10	3	US-08-485-324-16	Sequence 16, Appl
398	14	58.3	7	3	US-09-042-107-402	Sequence 402, App	471	14	58.3	10	3	US-08-447-506-16	Sequence 16, Appl
399	14	58.3	7	3	US-09-099-053-7	Sequence 7, Appli	472	14	58.3	10	3	US-08-235-437-16	Sequence 16, Appl
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403	14	58.3	7	4	US-09-750-754-70	Sequence 70, Appl	476	14	58.3	10	3	US-09-268-347-2	Sequence 2, Appli
404	14	58.3	7	4	US-09-750-754-79	Sequence 79, Appl	477	14	58.3	10	3	US-09-261-182-2	Sequence 2, Appli
405	14	58.3	7	4	US-09-676-475A-402	Sequence 402, App	478	14	58.3	10	4	US-09-490-702B-40	Sequence 40, Appl
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407	14	58.3	8	3	US-09-063-894B-31	Sequence 31, Appl	480	14	58.3	10	4	US-09-428-082B-142	Sequence 142, App
408	14	58.3	8	3	US-09-063-893A-8	Sequence 8, Appli	481	14	58.3	10	4	US-09-239-043D-2392	Sequence 2392, App
409	14	58.3	8	3	US-08-444-818-323	Sequence 323, App	482	14	58.3	10	4	US-09-620-091-46	Sequence 46, Appl
410	14	58.3	8	3	US-08-444-818-346	Sequence 346, App	483	14	58.3	10	4	US-09-043-813-2	Sequence 2, Appli
411	14	58.3	8	3	US-08-444-818-347	Sequence 347, App	484	14	58.3	10	4	US-09-043-813-5	Sequence 5, Appli
412	14	58.3	8	3	US-08-444-818-348	Sequence 348, App	485	14	58.3	10	4	US-09-043-813-8	Sequence 8, Appli
413	14	58.3	8	3	US-08-444-818-384	Sequence 384, App	486	14	58.3	10	4	US-09-043-813-11	Sequence 11, Appl
414	14	58.3	8	3	US-08-444-818-385	Sequence 385, App	487	14	58.3	10	4	US-09-043-813-14	Sequence 14, Appl
415	14	58.3	8	3	US-08-444-818-386	Sequence 386, App	488	14	58.3	10	4	US-09-043-813-17	Sequence 17, Appl
416	14	58.3	8	3	US-09-314-242-4	Sequence 4, Appli	489	14	58.3	10	4	US-09-043-813-20	Sequence 20, Appl
417	14	58.3	8	4	US-09-402-641-3	Sequence 3, Appli	490	14	58.3	10	4	US-09-043-813-23	Sequence 23, Appl
418	14	58.3	8	4	US-09-601-729-168	Sequence 168, App	491	14	58.3	10	4	US-09-043-813-26	Sequence 26, Appl
419	14	58.3	8	4	US-09-620-091-484	Sequence 484, App	492	14	58.3	10	4	US-09-043-813-29	Sequence 29, Appl
420	14	58.3	9	1	US-08-318-970B-23	Sequence 23, Appl	493	14	58.3	10	4	US-09-043-813-32	Sequence 32, Appl
421	14	58.3	9	2	US-08-417-174-77	Sequence 77, Appl	494	14	58.3	10	4	US-09-043-813-35	Sequence 35, Appl
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424	14	58.3	9	3	US-09-407-549-16	Sequence 16, Appl	497	14	58.3	10	4	US-09-043-813-44	Sequence 44, Appl
425	14	58.3	9	4	US-09-402-641-5	Sequence 5, Appli	498	14	58.3	10	4	US-09-043-813-57	Sequence 57, Appl
426	14	58.3	9	4	US-09-073-138-77	Sequence 77, Appl	499	14	58.3	10	4	US-09-043-813-59	Sequence 59, Appl
427	14	58.3	9	4	US-09-870-089B-3	Sequence 3, Appli	500	14	58.3	10	4	US-09-043-813-63	Sequence 63, Appl
428	14	58.3	9	4	US-09-870-089B-7	Sequence 7, Appli	501	14	58.3	10	4	US-09-043-813-65	Sequence 65, Appl
429	14	58.3	9	4	US-08-870-089B-9	Sequence 9, Appli	502	14	58.3	10	4	US-09-043-813-76	Sequence 76, Appl
430	14	58.3	10	1	US-08-321-625-74	Sequence 74, Appl	503	14	58.3	10	4	US-09-756-247-16	Sequence 16, Appl
431	14	58.3	10	1	US-08-242-678D-5	Sequence 5, Appli	504	14	58.3	10	4	US-09-756-247-36	Sequence 36, Appl
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436	14	58.3	10	2	US-08-902-623-37	Sequence 37, Appl	509	14	58.3	11	3	US-08-485-324-14	Sequence 14, Appl
437	14	58.3	10	2	US-08-902-623-40	Sequence 40, Appl	510	14	58.3	11	3	US-08-151-011-9	Sequence 9, Appli
438	14	58.3	10	2	US-08-902-623-72	Sequence 72, Appl	511	14	58.3	11	3	US-08-447-506-14	Sequence 14, Appl
439	14	58.3	10	2	US-08-747-137-122	Sequence 122, App	512	14	58.3	11	3	US-08-235-437-14	Sequence 14, Appl
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442	14	58.3	10	2	US-08-751-300-8	Sequence 8, Appli	515	14	58.3	11	3	US-09-181-083-10	Sequence 10, Appl
443	14	58.3	10	2	US-08-751-300-11	Sequence 11, Appl	516	14	58.3	11	3	US-09-224-785-5	Sequence 5, Appli
444	14	58.3	10	2	US-08-751-300-14	Sequence 14, Appl	517	14	58.3	11	3	US-09-186-958-5	Sequence 5, Appli
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446	14	58.3	10	2	US-08-751-300-20	Sequence 20, Appl	519	14	58.3	11	3	US-09-186-958-9	Sequence 9, Appli
447	14	58.3	10	2	US-08-751-300-23	Sequence 23, Appl	520	14	58.3	11	3	US-09-186-958-9	Sequence 9, Appli
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449	14	58.3	10	2	US-08-751-300-29	Sequence 29, Appl	522	14	58.3	11	3	US-09-669-271A-6	Sequence 6, Appli
450	14	58.3	10	2	US-08-751-300-32	Sequence 32, Appl	523	14	58.3	11	3	US-09-669-271A-8	Sequence 8, Appli
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453	14	58.3	10	2	US-08-751-300-41	Sequence 41, Appl	526	14	58.3	11	4	US-09-081-975-21	Sequence 21, Appl
454	14	58.3	10	2	US-08-751-300-44	Sequence 44, Appl	527	14	58.3	11	4	US-09-461-325-504	Sequence 504, App
455	14	58.3	10	2	US-08-751-300-57	Sequence 57, Appl	528	14	58.3	11	4	US-09-881-276-5	Sequence 5, Appli
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457	14	58.3	10	2	US-08-751-300-63	Sequence 63, Appl	530	14	58.3	11	4	US-09-881-276-9	Sequence 9, Appli
458	14	58.3	10	2	US-08-751-300-65	Sequence 65, Appl	531	14	58.3	11	4	US-09-881-276-8	Sequence 8, Appli
459	14	58.3	10	2	US-08-751-300-77	Sequence 77, Appl	532	14	58.3	11	4	US-09-756-594-5	Sequence 5, Appli
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462	14	58.3	10	2	US-08-751-300-92	Sequence 92, Appl	535	14	58.3	11	4	US-09-069-827A-47	Sequence 47, Appl
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464	14	58.3	10	2	US-08-751-300-94	Sequence 94, Appl	537	14	58.3	11	4	US-09-750-754-10	Sequence 10, Appl
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542	14	58.3	12	3	US-09-315-444-45	Sequence 45, App	615	14	58.3	15	4	US-09-441-992-51	Sequence 51, App
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550	14	58.3	12	4	US-09-428-082B-135	Sequence 135, App	623	14	58.3	15	5	PCT-US94-02465-51	Sequence 51, App
551	14	58.3	12	4	US-09-428-082B-136	Sequence 136, App	624	14	58.3	15	5	PCT-US94-10356-2	Sequence 2, App
552	14	58.3	13	1	US-08-487-568-87	Sequence 87, App	625	14	58.3	15	5	PCT-US94-10356-3	Sequence 3, App
553	14	58.3	13	3	US-08-702-054B-35	Sequence 35, App	626	14	58.3	15	5	PCT-US94-10356-6	Sequence 6, App
554	14	58.3	13	3	US-09-236-415-5	Sequence 5, App	627	14	58.3	15	5	PCT-US94-10356-7	Sequence 7, App
555	14	58.3	13	4	US-09-081-975-9	Sequence 9, App	628	14	58.3	15	5	PCT-US94-10356-20	Sequence 20, App
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561	14	58.3	14	2	US-08-954-470-10	Sequence 10, App	634	14	58.3	16	1	US-08-321-625-20	Sequence 20, App
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577	14	58.3	15	1	US-08-372-783-51	Sequence 51, App	650	14	58.3	16	3	US-09-181-083-20	Sequence 20, App
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582	14	58.3	15	1	US-08-625-691-10	Sequence 10, App	655	14	58.3	16	3	US-09-181-083-34	Sequence 34, App
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587	14	58.3	15	2	US-08-553-257A-51	Sequence 51, App	660	14	58.3	16	3	US-09-181-083-68	Sequence 68, App
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592	14	58.3	15	3	US-08-818-112-57	Sequence 57, App	665	14	58.3	16	4	US-09-081-975-23	Sequence 23, App
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597	14	58.3	15	3	US-09-056-556-123	Sequence 123, App	670	14	58.3	16	4	US-09-750-754-20	Sequence 20, App
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611	14	58.3	15	4	US-09-072-596-57	Sequence 57, App	684	14	58.3	16	4	US-09-541-345-20	Sequence 20, App

685	14	58.3	16	4	US-09-541-345-35	Sequence 35, Appl	758	14	58.3	17	4	US-09-350-641C-814	Sequence 814, App
686	14	58.3	16	4	US-09-541-345-37	Sequence 37, Appl	759	14	58.3	17	4	US-09-428-082B-209	Sequence 209, App
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689	14	58.3	16	4	US-09-541-345-40	Sequence 40, Appl	762	14	58.3	17	4	US-09-490-070A-228	Sequence 228, App
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693	14	58.3	16	4	US-09-541-345-44	Sequence 44, Appl	766	14	58.3	17	4	US-09-490-153-228	Sequence 228, App
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695	14	58.3	16	4	US-09-541-345-46	Sequence 46, Appl	768	14	58.3	17	4	US-09-490-153-262	Sequence 262, App
696	14	58.3	16	4	US-09-541-345-47	Sequence 47, Appl	769	14	58.3	17	4	US-09-350-841A-814	Sequence 814, App
697	14	58.3	16	4	US-09-541-345-48	Sequence 48, Appl	770	14	58.3	17	4	US-09-695-437A-40	Sequence 40, Appl
698	14	58.3	16	4	US-09-541-345-50	Sequence 50, Appl	771	14	58.3	17	4	US-09-490-324-222	Sequence 222, App
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702	14	58.3	16	4	US-09-541-345-55	Sequence 55, Appl	775	14	58.3	17	5	PCT-US93-07545-123	Sequence 123, App
703	14	58.3	16	4	US-09-541-345-57	Sequence 57, Appl	776	14	58.3	17	5	PCT-US94-05684-7	Sequence 7, Appl
704	14	58.3	16	4	US-09-541-345-58	Sequence 58, Appl	777	14	58.3	17	5	PCT-US94-10356-19	Sequence 19, Appl
705	14	58.3	16	4	US-09-541-345-59	Sequence 59, Appl	778	14	58.3	17	5	PCT-US94-10356-21	Sequence 21, Appl
706	14	58.3	16	4	US-09-541-345-61	Sequence 61, Appl	779	14	58.3	18	1	US-08-218-025A-3	Sequence 3, Appl
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713	14	58.3	16	4	US-09-541-345-73	Sequence 73, Appl	786	14	58.3	18	3	US-08-940-093-199	Sequence 199, App
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719	14	58.3	16	4	US-09-541-345-81	Sequence 81, Appl	792	14	58.3	18	3	US-09-082-279B-1147	Sequence 1147, Ap
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834	14	58.3	19	4	US-09-700-993-34	Sequence 34, Appl	907	14	58.3	20	3	US-09-119-263-59	Sequence 59, Appl
835	14	58.3	20	1	US-08-311-611A-54	Sequence 54, Appl	908	14	58.3	20	3	US-09-119-263-101	Sequence 101, App
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ALIGNMENTS

RESULT 1

US-09-085-072-7

; Sequence 7, Application US/09085072

; Patent No. 6265150

; GENERAL INFORMATION:

; APPLICANT: L. Terstappen et al.

; TITLE OF INVENTION: PHAGE ANTIBODIES

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hoffmann & Baron, LLP

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; ZIP: 11753

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; ATTORNEY/AGENT INFORMATION:

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; TELECOMMUNICATION INFORMATION:

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; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-085-072-7

Query Match 70.8%; Score 17; DB 3; Length 13;

Best Local Similarity 40.0%; Pred. No. 1.9e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 2 FXXW 6
DB 6 FASSW 10

RESULT 2

US-09-142-524D-87

; Sequence 87, Application US/09142524D

; Patent No. 6719976

; GENERAL INFORMATION:

; APPLICANT: Sone, Toshio

; APPLICANT: Kume, Akinori

; APPLICANT: Dairiki, Kazuo

; APPLICANT: Iwama, Akiko

; APPLICANT: Kino, Kohsuke

; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease

; FILE REFERENCE: SPO-103

; CURRENT APPLICATION NUMBER: US/09/142,524D

; CURRENT FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: PCT/JP97/00740

; PRIOR FILING DATE: 1997-03-10

; NUMBER OF SEQ ID NOS: 174

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 87

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Cryptomeria japonica

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)-(15)

; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4

US-09-142-524D-87

Query Match 70.8%; Score 17; DB 4; Length 15;

Best Local Similarity 40.0%; Pred. No. 2e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
DB 9 FSTAW 13

RESULT 3

US-09-142-524D-88

; Sequence 88, Application US/09142524D

; Patent No. 6719976

; GENERAL INFORMATION:

; APPLICANT: Sone, Toshio

; APPLICANT: Kume, Akinori

; APPLICANT: Dairiki, Kazuo

; APPLICANT: Iwama, Akiko

; APPLICANT: Kino, Kohsuke

; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease

; FILE REFERENCE: SPO-103

; CURRENT APPLICATION NUMBER: US/09/142,524D

; CURRENT FILING DATE: 1998-09-09

; PRIOR APPLICATION NUMBER: PCT/JP97/00740

; PRIOR FILING DATE: 1997-03-10

; NUMBER OF SEQ ID NOS: 174

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 88

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Cryptomeria japonica

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)-(15)

; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5

US-09-142-524D-88

Query Match 70.8%; Score 17; DB 4; Length 15;

Best Local Similarity 40.0%; Pred. No. 2e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 FXXXW 6
|
Db 4 FSTAW 8

RESULT 4

US-07-920-519-10
; Sequence 10, Application US/07920519
; Patent No. 5382518
; GENERAL INFORMATION:
; APPLICANT: CAPUT, DANIEL
; APPLICANT: FERRARA, PASQUAL
; APPLICANT: GUILLEMOT, JEAN-CLAUDE
; APPLICANT: KAGHAD, MOURAD
; APPLICANT: LEGOUX, RICHARD
; APPLICANT: LOISON, GERARD
; APPLICANT: LARBRE, ELIZABETH
; APPLICANT: LUPKER, JOHANNES
; APPLICANT: LEPLATOIS, PASCUAL
; APPLICANT: SALOME, MARK
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
; TITLE OF INVENTION: MICRO-ORGANISMS AND TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/920,519
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/659,408
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16781/276 BEDL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: Hydrolysis product T 23

US-07-920-519-10

Query Match 66.7%; Score 16; DB 1; Length 6;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 FXXXW 6
|
Db 1 FDATAW 5

RESULT 5

US-08-086-410-7
; Sequence 7, Application US/08086410
; Patent No. 5407822
; GENERAL INFORMATION:
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: LOISON, Gerard
; APPLICANT: PESSEGUE, Bernard
; APPLICANT: SHIRE, David
; TITLE OF INVENTION: Artificial promoter for the expression
; TITLE OF INVENTION: of proteins in yeast
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: King Street Station, Suite 500, 1800 Diagonal
; STREET: Road, PO Box 299
; CITY: ALEXANDRIA
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,410
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,083
; FILING DATE: 02-OCT-1991
; APPLICATION NUMBER: FR 89 17467
; FILING DATE: 29-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/318
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: hydrolysis product T23

Query Match 66.7%; Score 16; DB 1; Length 6;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 FXXXW 6
|
Db 1 FDATAW 5

RESULT 6

US-08-314-586-10
; Sequence 10, Application US/08314586
; Patent No. 5541098
; GENERAL INFORMATION:
; APPLICANT: CAPUT, DANIEL
; APPLICANT: FERRARA, PASQUAL
; APPLICANT: GUILLEMOT, JEAN-CLAUDE
; APPLICANT: KAGHAD, MOURAD
; APPLICANT: LEGOUX, RICHARD
; APPLICANT: LOISON, GERARD
; APPLICANT: LARBRE, ELIZABETH

; APPLICANT: LUPKER, JOHANNES
; APPLICANT: LEPLATOIS, PASCUAL
; APPLICANT: SALOME, MARK
; APPLICANT: LAURENT, PATRICK
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
; TITLE OF INVENTION: MICROORGANISMS AND TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/314,586
; APPLICATION NUMBER: US/08/314,586
; FILING DATE: 28-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/659,408
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16781/509/BEDL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: Hydrolysis product T 23
; US-08-314-586-10

Query Match 66.7%; Score 16; DB 1; Length 6;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 1 FDTW 5

RESULT 7
US-09-774-639-284
; Sequence 284, Application US/09774639
; Patent No. 6806351
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774, 639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 284
; LENGTH: 7
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-774-639-284
Query Match 66.7%; Score 16; DB 4; Length 7;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 2 FGTSW 6

RESULT 8
US-09-702-114A-28
; Sequence 28, Application US/09702114A
; Patent No. 6566078
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Paris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: 36PGD5: SECRETED TUMOR ANTIGEN
; FILE REFERENCE: 129.22-US-U1
; CURRENT APPLICATION NUMBER: US/09/702,114A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/162,417
; PRIOR FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-702-114A-28

Query Match 66.7%; Score 16; DB 4; Length 9;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FRSSW 8

RESULT 9
US-08-208-886C-87
; Sequence 87, Application US/08208886C
; Patent No. 5597710
; GENERAL INFORMATION:
; APPLICANT: Dalié, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,886C
; FILING DATE: March 10, 1994
; CLASSIFICATION: 424

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Foulke, Cynthia L.
;; REGISTRATION NUMBER: 32,364
;; REFERENCE/DOCKET NUMBER: JB0429
;; TELEPHONE: 908 298 2987
;; TELEFAX: 908 298 5388
;; INFORMATION FOR SEQ ID NO: 87:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-208-886C-87

Query Match 66.7%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 4 FSSW 8

RESULT 10

US-08-704-744-89
; Sequence 89, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-704-744-89

Query Match 66.7%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 4 FSSW 8

RESULT 11

US-08-469-557-68
; Sequence 68, Application US/08469557
; Patent No. 5770403
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Le, Hung
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Nguyen, Hanh
; APPLICANT: Tindall, Stephen
; APPLICANT: Zavodny, Paul
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; TITLE OF INVENTION: Against Human Interleukin-4
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,557
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290,793
; FILING DATE: August 16, 1994
; APPLICATION NUMBER: PCT/US93/01301
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/841,659
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/782,784
; FILING DATE: 24-OCT-1991
; APPLICATION NUMBER: US 07/499,327
; FILING DATE: 21-MAY-1990
; APPLICATION NUMBER: PCT/US88/03631
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: US 07/655,966
; FILING DATE: 14-FEB-1991
; APPLICATION NUMBER: US 07/113,623
; FILING DATE: 26-OCT-1987
; APPLICATION NUMBER: US 06/881,553
; FILING DATE: 03-JUL-1986
; APPLICATION NUMBER: US 06/843,958
; FILING DATE: 25-MAR-1986
; APPLICATION NUMBER: US 06/799,668
; FILING DATE: 19-NOV-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: 2409K7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908 298-2987
; TELEFAX: 908-298-5388

; INFORMATION FOR SEQ ID NO: 68:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-469-557-68

Query Match 66.7%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FSSW 8

RESULT 12

US-08-290-793B-68
; Sequence 68, Application US/08290793B
; Patent No. 5863537

; GENERAL INFORMATION:

; APPLICANT: Dalié, Barbara
; APPLICANT: Le, Hung
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Nguyen, Hanh
; APPLICANT: Tindall, Stephen
; APPLICANT: Zavodny, Paul
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; TITLE OF INVENTION: Against Human Interleukin-4
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schering-Plough Corporation

; STREET: 2000 Galloping Hill Road

; CITY: Kenilworth

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07033-0530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 6.0.5

; SOFTWARE: Microsoft Word 5.1A

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/290,793B

; FILING DATE: August 16, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/01301

; FILING DATE: 19-FEB-1992

; APPLICATION NUMBER: US 07/841,659

; FILING DATE: 19-FEB-1992

; APPLICATION NUMBER: US 07/782,784

; FILING DATE: 24-OCT-1991

; APPLICATION NUMBER: US 07/499,327

; FILING DATE: 21-MAY-1990

; APPLICATION NUMBER: PCT/US88/03631

; FILING DATE: 21-OCT-1988

; APPLICATION NUMBER: US 07/655,966

; FILING DATE: 14-FEB-1991

; APPLICATION NUMBER: US 07/113,623

; FILING DATE: 26-OCT-1987

; APPLICATION NUMBER: US 06/881,553

; FILING DATE: 03-JUL-1986

; APPLICATION NUMBER: US 06/843,958

; FILING DATE: 25-MAR-1986

; APPLICATION NUMBER: US 06/799,668

; FILING DATE: 19-NOV-1985

; ATTORNEY/AGENT INFORMATION:

; NAME: Foulke, Cynthia L.

; REGISTRATION NUMBER: 32,364

; REFERENCE/DOCKET NUMBER: 2409K7

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 908 298-2987

; TELEFAX: 908-298-5388

; INFORMATION FOR SEQ ID NO: 68:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-290-793B-68

Query Match 66.7%; Score 16; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FSSW 8

RESULT 13

US-08-277-660A-16

; Sequence 16, Application US/08277660A

; Patent No. 5702908

; GENERAL INFORMATION:

; APPLICANT: Pickley, Steven M.

; APPLICANT: Lane, David P.

; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53

; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/277,660A

; FILING DATE: 20-JUL-1994

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190

; REFERENCE/DOCKET NUMBER: A-60244/WHD

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

US-08-277-660A-16

Query Match 66.7%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 5 FSALW 9

RESULT 14

US-08-277-660A-17

; Sequence 17, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Pickaley, Steven M.
; ATTORNEY/AGENT INFORMATION:
; FILING DATE: 20-JUL-1994
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHO
; TELEPHONE: (415) 781-1989
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-277-660A-17

Query Match 66.7%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 5 FSDAW 9

RESULT 15
US-08-424-957-29
; Sequence 29, Application US/08424957
; Patent No. 570377
; GENERAL INFORMATION:
; APPLICANT: Pickaley, Steven M.
; ATTORNEY/AGENT INFORMATION:
; FILING DATE: 20-JUL-1994
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957

; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-29

Query Match 66.7%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 5 FSALM 9

RESULT 16
US-08-424-957-30
; Sequence 30, Application US/08424957
; Patent No. 570377
; GENERAL INFORMATION:
; APPLICANT: Pickaley, Steven M.
; ATTORNEY/AGENT INFORMATION:
; FILING DATE: 20-JUL-1994
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown

US-08-424-957-30

Query Match 66.7%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 5 FSDAW 9

RESULT 17

US-09-035-686-29
; Sequence 29, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/09/035.686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-09-035-686-29

Query Match 66.7%; Score 16; DB 3; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 5 FSALW 9

RESULT 18

US-09-035-686-30
; Sequence 30, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.

; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/09/035.686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-09-035-686-30

Query Match 66.7%; Score 16; DB 3; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 5 FSDAW 9

RESULT 19

US-08-406-330-32
; Sequence 32, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/406.330
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/100
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-32

Query Match 66.7%; Score 16; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 3 PSSW 7

RESULT 20
US-08-556-597-32
Sequence 32, Application US/08556597
Patent No. 597155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
HUMAN PLATELET GLYCOPROTEIN Ib/IX
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556.597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406.330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-32

Query Match 66.7%; Score 16; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 3 PSSW 7

RESULT 21
US-08-305-871A-23
Sequence 23, Application US/08305871A
Patent No. 5736142
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Gaeta, Federico
APPLICANT: Grey, Howard M.
APPLICANT: Sidney, John
APPLICANT: Alexander, Jeffrey L.
TITLE OF INVENTION: Alteration of Immune Response Using Pan
DR-Binding Peptides
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/305.871A
FILING DATE: 14-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,101
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-0062-10
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..13
OTHER INFORMATION: /note= "Peptide wherein X is
tyrosine or phenylalanine."
US-08-305-871A-23

Query Match 66.7%; Score 16; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 3 FVAW 7

RESULT 22
US-08-192-560-11

```
; Sequence 11, Application US/08912560A
; Patent No. 6066484
; GENERAL INFORMATION:
; APPLICANT: HATANAKA, Haruyo
; APPLICANT: ASHIKARI, Toshiniko
; APPLICANT: OGAWA, Jun
; APPLICANT: SHIMIZU, Sakayu
; TITLE OF INVENTION: NOVEL PURINE NUCLEOSIDASE
; FILE REFERENCE: 001560-309
; CURRENT APPLICATION NUMBER: US/08/912,560A
; CURRENT FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: JP 8-216421
; EARLIER FILING DATE: 1996-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Ochrobactrum anthropi
US-08-912-560-11

Query Match          66.7%; Score 16; DB 3; Length 13;
Best Local Similarity 40.0%; Pred. NO. 2.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
      |
Db      2 FDSW 6

RESULT 23
US-08-788-822A-27
; Sequence 27, Application US/08788822A
; Patent No. 6413935
; GENERAL INFORMATION:
; APPLICANT: Alexander, Jeffrey L.
; APPLICANT: Defrees, Shawn
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Induction of Immune Response Against
; TITLE OF INVENTION: Desired Determinants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,822A
; FILING DATE: 23-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,510
; FILING DATE: 24-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 014137-009210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-788-822A-27

Query Match          66.7%; Score 16; DB 4; Length 13;
Best Local Similarity 40.0%; Pred. NO. 2.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
      |
Db      3 FVAW 7

RESULT 24
US-09-543-608A-27
; Sequence 27, Application US/09543608A
; Patent No. 6602510
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa A.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
; TITLE OF INVENTION: Peptides and Vaccine Compositions
; FILE REFERENCE: 018623-015710US
; CURRENT APPLICATION NUMBER: US/09/543,608A
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PanDR binding peptide (PADRE)
US-09-543-608A-27

Query Match          66.7%; Score 16; DB 4; Length 13;
Best Local Similarity 40.0%; Pred. NO. 2.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
      |
Db      3 FVAW 7

RESULT 25
US-09-556-818-65
; Sequence 65, Application US/09556818
; Patent No. 6746669
; GENERAL INFORMATION:
; APPLICANT: Klynsner, Steen
; TITLE OF INVENTION: Method For Down-Regulating IL5 Activity
; FILE REFERENCE: 0459-0428P
; CURRENT APPLICATION NUMBER: US/09/556,818
; CURRENT FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Promiscuous T
; OTHER INFORMATION: helper epitope derived from Homo sapiens
US-09-556-818-65

Query Match          66.7%; Score 16; DB 4; Length 13;
Best Local Similarity 40.0%; Pred. NO. 2.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 2 FXXXW 6
|
Db 3 FVAAW 7

RESULT 26
5185431-25
; Patent No. 5185431
; APPLICANT: YOSHIMATSU, KENTARO; SHIKATA, YASUSHI; TANAKA, ISAO;
; HASEGAWA, YOSHIKAZU; SETO, TOSHIO; OSAWA, TOSHIO
; TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392.841
; FILING DATE: 11-AUG-1989
; SEQ ID NO: 25
; LENGTH: 13
5185431-25

Query Match 66.7%; Score 16; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 5 FSQAW 9

RESULT 27
5185431-25
; Patent No. 5185431
; APPLICANT: YOSHIMATSU, KENTARO; SHIKATA, YASUSHI; TANAKA, ISAO;
; HASEGAWA, YOSHIKAZU; SETO, TOSHIO; OSAWA, TOSHIO
; TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392.841
; FILING DATE: 11-AUG-1989
; SEQ ID NO: 25
; LENGTH: 13
5185431-25

Query Match 66.7%; Score 16; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 5 FSQAW 9

RESULT 28
US-08-025A-139
; Sequence 139, Application US/08218025A
; Patent No. 5556744
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Ugen, Kenneth E.
; APPLICANT: Williams, William V.
; TITLE OF INVENTION: Methods and Compositions for Diagnosing
; TITLE OF INVENTION: and Treating Certain HIV Infected Patients
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: P.O. Box 457, 321 No. 5556744ristown Road
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218.025A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,451
FILING DATE: 29-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST33A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-218-025A-139

Query Match 66.7%; Score 16; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 1 FNSTW 5

RESULT 29
US-08-847-844A-22
; Sequence 22, Application US/08847844A
; Patent No. 6150160
; GENERAL INFORMATION:
; APPLICANT: KAZAZIAN JR., HAIG H.
; APPLICANT: BOEKE, JEF D.
; APPLICANT: MORAN, JOHN V.
; APPLICANT: DOMBROSKI, BETH A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
; TITLE OF INVENTION: MAMMALIAN RETROTRANSPOSONS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,844A
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/749,805
; FILING DATE: 16-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,831
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-23U2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020

```
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-847-844A-22

Query Match 66.7%; Score 16; DB 3; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
| |
Db 6 FIATW 10

RESULT 30
PCT-US93-08699-1
; Sequence 1, Application PC/TUS9308699
; GENERAL INFORMATION:
; APPLICANT: JOHNSON & JOHNSON AND GEORGETOWN UNIVERSITY
; TITLE OF INVENTION: IMMUNOREACTIVE PEPTIDES FROM
; TITLE OF INVENTION: EPSTEIN-BARR VIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08699
; FILING DATE: 15-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD-3033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
PCT-US93-08699-1

Query Match 66.7%; Score 16; DB 5; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
| |
Db 3 FTETW 7

RESULT 31
US-09-330-914A-11

; Sequence 11, Application US/09330914A
; Patent No. 6432671
; GENERAL INFORMATION:
; APPLICANT: Flohe, Leopold
; No. 6432671ecke, Everson
; Kalisz, Henryk
; Montemartini, Marisa
; TITLE OF INVENTION: TRYPARADOXIN, EXPRESSION PLASMID, PROCESS OF
; PRODUCTION, METHOD OF USE, TEST KIT, AND
; PHARMACEUTICAL COMPOSITION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Brown
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: Unites States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,914A
; FILING DATE: 11-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/06983
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, James P.
; REGISTRATION NUMBER: 28,491
; REFERENCE/DOCKET NUMBER: 29473/35678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-330-914A-11

Query Match 66.7%; Score 16; DB 4; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
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Db 8 FAQSW 12

RESULT 32
US-08-413-233-3
; Sequence 3, Application US/08413233
; Patent No. 6508553
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard S.
; APPLICANT: Parks, D. Ellio
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS OF EPSTEIN-BARR
; TITLE OF INVENTION: VIRUS ASSOCIATED DISEASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOEB AND LOEB
; STREET: 1880 Century Park East, 5th Floor
; CITY: Los Angeles
; STATE: California
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; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413.233
; FILING DATE: 30-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Yang, Wei-ning
; REGISTRATION NUMBER: 38,690
; REFERENCE/DOCKET NUMBER: 7586D.4007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 553-5050
; TELEFAX: (310) 553-4619
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..16
; US-08-413-233-3

Query Match 66.7%; Score 16; DB 4; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 3 FTETW 7

RESULT 33
US-09-690-454-88
; Sequence 88, Application US/09690454
; Patent No. 6531447
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/09/690,454
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 16
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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-690-454-88

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Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 8 FRSAW 12

RESULT 34
US-09-170-496D-285
; Sequence 285, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 285
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6555339e1 Sequence
; US-09-170-496D-285

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Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 5 FMSTW 9

RESULT 35
US-08-218-025A-115
; Sequence 115, Application US/08218025A
; Patent No. 5556744
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Ugen, Kenneth E.
; APPLICANT: Williams, William V.
; TITLE OF INVENTION: Methods and Compositions for Diagnosing
; TITLE OF INVENTION: and Treating Certain HIV Infected Patients
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: P.O. Box 457, 321 No. 5556744ristown Road
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-218-025A-115

Query Match 66.7%; Score 16; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 13 FNSTW 17

RESULT 36
US-08-746-283-7
; Sequence 7, Application US/08746283
; Patent No. 5834280
; GENERAL INFORMATION:
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Si, Joan Q.
; APPLICANT: Aagaard, Jesper
; TITLE OF INVENTION: Glucose Oxidases
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5834280 No. 5834280disk of No. 5834280th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,283
; FILING DATE: 07-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Agria, Dr. Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4158.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5834280e
US-08-746-283-7

Query Match 66.7%; Score 16; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
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Db 3 FTSVW 7

RESULT 37
US-08-746-257A-5
; Sequence 5, Application US/08746257A
; Patent No. 5879921
; GENERAL INFORMATION:
; APPLICANT: Cherry, Joel
; APPLICANT: Berka, Randy
; APPLICANT: Halkier, Torben
; TITLE OF INVENTION: Glucose Oxidases
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5879921 No. 5879921disk of No. 5879921th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,257A
; FILING DATE: 07-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Starnes, Robert L.
; REGISTRATION NUMBER: 41,324
; REFERENCE/DOCKET NUMBER: 4700.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5879921e
US-08-746-257A-5

Query Match 66.7%; Score 16; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 3 FTSVW 7

RESULT 38
US-08-987-743-11
; Sequence 11, Application US/08987743
; Patent No. 6123938
; GENERAL INFORMATION:
; APPLICANT: Stern, Robert
; APPLICANT: Csoka, Anthony
; APPLICANT: Frost, Gregory I.
; APPLICANT: Wong, Tim M.
; TITLE OF INVENTION: Purification and Microsequencing of
; FILE REFERENCE: 9076/088CIP2
; CURRENT APPLICATION NUMBER: US/08/987,743
; CURRENT FILING DATE: 1997-12-09
; EARLIER APPLICATION NUMBER: 08/733,360
; EARLIER FILING DATE: 1996-10-17
; NUMBER OF SEQ ID NOS: 16
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 17
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; ORGANISM: H. sapiens
US-08-987-743-11

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Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXW 6
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Db      11 FTTW 15

RESULT 39
US-09-170-496D-286
; Sequence 286, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: 1998-10-13
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 286
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 655339el Sequence
US-09-170-496D-286

Query Match      66.7%; Score 16; DB 4; Length 17;
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Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXW 6
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Db      5 FMSTW 9

RESULT 40
US-08-934-915-125
; Sequence 125, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-125

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Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db      7 FSRTW 11

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Job time : 32.2353 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2005, 15:58:45 ; Search time 115.412 Seconds
(without alignments)
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Title: US-09-214-371-11

Perfect score: 24

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	17	70.8	8 18 US-10-818-036-30	Sequence 30, Appl
5	17	70.8	9 14 US-10-072-419-3	Sequence 3, Appli
6	17	70.8	9 14 US-10-072-419-8	Sequence 8, Appli
7	17	70.8	9 16 US-10-869-768-3	Sequence 3, Appli
8	17	70.8	9 15 US-10-869-768-8	Sequence 8, Appli
9	17	70.8	9 18 US-10-818-036-14	Sequence 14, Appl
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11	17	70.8	9 18 US-10-818-036-23	Sequence 23, Appl

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13	17	70.8	9 18	US-10-818-036-26	Sequence 26, Appl
14	17	70.8	9 18	US-10-818-036-29	Sequence 29, Appl
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16	17	70.8	10 11	US-10-996-316-139	Sequence 139, Appl
17	17	70.8	11 14	US-10-072-419-37	Sequence 37, Appl
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22	17	70.8	19 14	US-10-145-586-59	Sequence 59, Appl
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46	16	66.7	8 15	US-10-367-668-264	Sequence 264, Appl
47	16	66.7	8 16	US-10-367-674-260	Sequence 260, Appl
48	16	66.7	8 16	US-10-367-674-264	Sequence 264, Appl
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54	16	66.7	8 16	US-10-869-768-30	Sequence 30, Appl
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74	16	66.7	8 18	US-10-820-067A-243	Sequence 243, Appl
75	16	66.7	8 18	US-10-820-067A-725	Sequence 725, Appl
76	16	66.7	8 18	US-10-818-036-17	Sequence 17, Appl
77	16	66.7	9 13	US-10-046-922-59	Sequence 59, Appl
78	16	66.7	9 15	US-10-365-254-28	Sequence 28, Appl
79	16	66.7	9 15	US-10-398-104-98	Sequence 98, Appl
80	16	66.7	10 9	US-09-836-290-453	Sequence 453, Appl
81	16	66.7	10 14	US-10-076-047A-47	Sequence 47, Appl
82	16	66.7	10 14	US-10-072-419-34	Sequence 34, Appl
83	16	66.7	10 14	US-10-072-419-36	Sequence 36, Appl
84	16	66.7	10 14	US-10-320-231A-55	Sequence 55, Appl

85	15	66.7	10	15	US-10-264-309-128	Sequence 128, App	158	16	66.7	16	14	US-10-191-795-11	Sequence 11, Appl
86	16	66.7	10	15	US-10-436-782-6	Sequence 6, Appl	159	16	66.7	16	14	US-10-251-385-285	Sequence 285, App
87	16	66.7	10	15	US-10-239-656-14	Sequence 14, Appl	160	16	66.7	16	14	US-10-062-831-88	Sequence 88, Appl
88	16	66.7	10	15	US-10-128-520-367	Sequence 367, App	161	16	66.7	16	14	US-10-224-356-36	Sequence 36, Appl
89	16	66.7	10	16	US-10-468-250A-109	Sequence 109, App	162	16	66.7	16	14	US-10-062-599-88	Sequence 88, Appl
90	16	66.7	10	16	US-10-869-768-34	Sequence 34, Appl	163	16	66.7	16	18	US-10-963-760-11	Sequence 11, Appl
91	16	66.7	10	16	US-10-869-768-36	Sequence 36, Appl	164	16	66.7	16	18	US-10-963-760-11	Sequence 11, Appl
92	16	66.7	10	16	US-10-729-441-53	Sequence 53, Appl	165	16	66.7	17	14	US-10-059-271-20	Sequence 20, Appl
93	16	66.7	10	17	US-10-769-348-31	Sequence 30, Appl	166	16	66.7	17	14	US-10-251-385-286	Sequence 286, App
94	16	66.7	10	17	US-10-725-962-62	Sequence 62, Appl	167	16	66.7	17	14	US-10-031-874A-59	Sequence 59, Appl
95	16	66.7	10	17	US-10-725-962-65	Sequence 65, Appl	168	16	66.7	17	14	US-10-029-386-29993	Sequence 29993, A
96	16	66.7	10	17	US-10-638-265-89	Sequence 89, Appl	169	16	66.7	17	14	US-10-029-386-31536	Sequence 31536, A
97	16	66.7	10	17	US-10-879-994-19	Sequence 19, Appl	170	16	66.7	18	9	US-10-450-036A-59	Sequence 59, Appl
98	16	66.7	10	17	US-10-726-332-54	Sequence 54, Appl	171	16	66.7	18	9	US-09-205-658-283	Sequence 283, App
99	16	66.7	10	17	US-10-726-332-72	Sequence 72, Appl	172	16	66.7	18	9	US-09-205-658-285	Sequence 285, App
100	16	66.7	10	17	US-10-726-332-87	Sequence 87, Appl	173	16	66.7	18	10	US-09-963-693-283	Sequence 283, App
101	16	66.7	10	17	US-10-726-332-90	Sequence 90, Appl	174	16	66.7	18	10	US-09-963-693-285	Sequence 285, App
102	16	66.7	10	17	US-10-726-333-107	Sequence 107, App	175	16	66.7	18	11	US-09-833-245-1958	Sequence 1958, App
103	16	66.7	10	17	US-10-769-074-30	Sequence 30, Appl	176	16	66.7	18	11	US-09-833-245-1959	Sequence 1959, App
104	16	66.7	10	17	US-10-867-506-55	Sequence 55, Appl	177	16	66.7	18	14	US-10-224-356-17	Sequence 17, Appl
105	16	66.7	10	18	US-10-981-738-17	Sequence 17, Appl	178	16	66.7	19	9	US-09-864-761-41546	Sequence 41546, A
106	16	66.7	10	18	US-10-727-737-20	Sequence 20, Appl	179	16	66.7	20	9	US-09-812-528-19	Sequence 19, Appl
107	16	66.7	10	18	US-10-727-737-23	Sequence 23, Appl	180	16	66.7	20	9	US-09-884-441-411	Sequence 411, App
108	16	66.7	10	18	US-10-727-737-24	Sequence 24, Appl	181	16	66.7	20	9	US-09-884-441-412	Sequence 412, App
109	16	66.7	10	18	US-10-264-309-128	Sequence 128, App	182	16	66.7	20	10	US-09-907-969-411	Sequence 411, App
110	16	66.7	10	18	US-10-897-406-53	Sequence 53, Appl	183	16	66.7	20	10	US-09-907-969-412	Sequence 412, App
111	16	66.7	10	20	US-11-004-795A-6	Sequence 6, Appl	184	16	66.7	20	10	US-09-827-271-411	Sequence 411, App
112	16	66.7	10	20	US-11-004-794A-6	Sequence 6, Appl	185	16	66.7	20	10	US-09-827-271-412	Sequence 412, App
113	16	66.7	11	14	US-10-097-175-70	Sequence 70, Appl	186	16	66.7	20	10	US-09-933-767-744	Sequence 744, App
114	16	66.7	11	14	US-10-097-175-90	Sequence 90, Appl	187	16	66.7	20	14	US-10-004-860-744	Sequence 744, App
115	16	66.7	11	14	US-10-193-651-11	Sequence 11, Appl	188	16	66.7	20	14	US-10-023-282-744	Sequence 744, App
116	16	66.7	11	15	US-10-398-104-238	Sequence 238, App	189	16	66.7	20	14	US-10-174-613-14	Sequence 14, Appl
117	16	66.7	11	15	US-10-879-994-83	Sequence 83, App	190	16	66.7	20	14	US-10-198-053-411	Sequence 411, App
118	16	66.7	11	17	US-10-879-994-99	Sequence 99, App	191	16	66.7	20	14	US-10-198-053-412	Sequence 412, App
119	16	66.7	12	10	US-09-954-385-391	Sequence 391, App	192	16	66.7	20	14	US-10-198-053-617	Sequence 617, App
120	16	66.7	12	14	US-10-092-908-22	Sequence 22, App	193	16	66.7	20	14	US-10-198-053-618	Sequence 618, App
121	16	66.7	12	14	US-10-092-908-42	Sequence 42, App	194	16	66.7	20	15	US-10-280-066-400	Sequence 400, App
122	16	66.7	12	14	US-10-075-869-36	Sequence 36, Appl	195	16	66.7	20	16	US-10-023-339-26	Sequence 26, Appl
123	16	66.7	12	15	US-10-366-493-36	Sequence 36, Appl	196	16	66.7	20	16	US-10-725-952-19	Sequence 19, Appl
124	16	66.7	12	16	US-10-467-758-26	Sequence 26, Appl	197	16	66.7	20	17	US-10-860-790-411	Sequence 411, App
125	16	66.7	12	17	US-10-912-512-391	Sequence 391, App	198	16	66.7	20	17	US-10-860-790-617	Sequence 617, App
126	16	66.7	12	17	US-10-235-043-391	Sequence 391, App	199	16	66.7	20	17	US-10-860-790-618	Sequence 618, App
127	16	66.7	12	17	US-10-926-893-36	Sequence 36, Appl	200	15	62.5	5	10	US-09-894-594-11	Sequence 11, Appl
128	16	66.7	12	20	US-11-003-951-32	Sequence 32, Appl	201	15	62.5	5	20	US-11-081-198-114	Sequence 114, App
129	16	66.7	13	9	US-09-894-018-69	Sequence 69, App	202	15	62.5	6	9	US-09-214-371-83	Sequence 83, Appl
130	16	66.7	13	9	US-09-949-375A-18	Sequence 18, App	203	15	62.5	6	9	US-09-732-384-4	Sequence 4, Appl
131	16	66.7	13	9	US-09-785-215-19	Sequence 19, App	204	15	62.5	6	9	US-09-732-384-5	Sequence 5, Appl
132	16	66.7	13	14	US-10-116-118-36	Sequence 36, Appl	205	15	62.5	6	9	US-09-486-734A-34	Sequence 34, Appl
133	16	66.7	13	14	US-10-223-809A-17	Sequence 17, App	206	15	62.5	6	13	US-10-155-059-1	Sequence 1, Appl
134	16	66.7	13	14	US-10-295-074-7	Sequence 7, Appl	207	15	62.5	6	15	US-10-609-217-130	Sequence 130, App
135	16	66.7	13	14	US-10-295-074-20	Sequence 20, Appl	208	15	62.5	6	15	US-10-632-388-130	Sequence 130, App
136	16	66.7	13	15	US-10-371-069-52	Sequence 52, App	209	15	62.5	6	15	US-10-651-723-130	Sequence 130, App
137	16	66.7	13	15	US-10-371-645-52	Sequence 52, App	210	15	62.5	6	15	US-10-645-761-130	Sequence 130, App
138	16	66.7	13	15	US-10-371-260-52	Sequence 52, App	211	15	62.5	6	15	US-10-666-696-130	Sequence 130, App
139	16	66.7	13	16	US-10-441-779C-33	Sequence 33, App	212	15	62.5	6	15	US-10-653-048-130	Sequence 130, App
140	16	66.7	13	16	US-10-363-954B-18	Sequence 18, App	213	15	62.5	6	18	US-10-645-784-130	Sequence 130, App
141	16	66.7	13	16	US-10-643-103-3	Sequence 3, Appl	214	15	62.5	6	18	US-10-927-262A-83	Sequence 83, Appl
142	16	66.7	13	16	US-10-474-960B-69	Sequence 69, App	215	15	62.5	7	9	US-09-096-749A-36	Sequence 36, Appl
143	16	66.7	13	16	US-10-846-911-7	Sequence 7, Appl	216	15	62.5	7	10	US-09-912-414-28	Sequence 28, Appl
144	16	66.7	13	16	US-10-846-911-20	Sequence 20, App	217	15	62.5	7	10	US-09-903-412-36	Sequence 36, Appl
145	16	66.7	13	17	US-10-893-018-15	Sequence 15, App	218	15	62.5	7	14	US-10-174-717A-36	Sequence 36, Appl
146	16	66.7	13	18	US-10-732-862B-233	Sequence 233, App	219	15	62.5	7	14	US-10-165-155-36	Sequence 36, Appl
147	16	66.7	13	18	US-10-783-317A-17	Sequence 17, App	220	15	62.5	7	14	US-10-190-082-27	Sequence 27, Appl
148	16	66.7	13	18	US-10-939-107-7	Sequence 7, Appl	221	15	62.5	7	14	US-10-190-082-30	Sequence 30, Appl
149	16	66.7	13	18	US-10-939-107-20	Sequence 20, App	222	15	62.5	7	14	US-10-190-082-81	Sequence 81, Appl
150	16	66.7	14	16	US-10-387-955-49	Sequence 49, App	223	15	62.5	7	14	US-10-190-082-98	Sequence 98, Appl
151	16	66.7	15	9	US-09-205-658-284	Sequence 284, App	224	15	62.5	7	14	US-10-190-082-128	Sequence 128, App
152	16	66.7	15	10	US-09-963-693-284	Sequence 284, App	225	15	62.5	7	14	US-10-190-082-179	Sequence 179, App
153	16	66.7	15	14	US-10-216-122-22	Sequence 22, App	226	15	62.5	7	14	US-10-197-927-5	Sequence 5, Appl
154	16	66.7	15	15	US-10-442-456-1	Sequence 1, Appl	227	15	62.5	7	14	US-10-190-163-36	Sequence 36, Appl
155	16	66.7	15	18	US-10-946-647-790	Sequence 790, App	228	15	62.5	7	18	US-10-953-901-680	Sequence 680, App
156	16	66.7	15	18	US-10-946-647-957	Sequence 957, App	229	15	62.5	8	8	US-08-424-550B-252	Sequence 252, App
157	16	66.7	15	18	US-10-705-165-9	Sequence 9, Appl	230	15	62.5	8	9	US-09-214-371-12	Sequence 12, Appl

231	15	62.5	8	9	US-09-214-371-13	Sequence 13, Appl	304	15	62.5	8	18	US-10-927-262A-22	Sequence 22, Appl
232	15	62.5	8	9	US-09-214-371-21	Sequence 21, Appl	305	15	62.5	8	18	US-10-927-262A-46	Sequence 46, Appl
233	15	62.5	8	9	US-09-214-371-22	Sequence 22, Appl	306	15	62.5	8	18	US-10-927-262A-47	Sequence 47, Appl
234	15	62.5	8	9	US-09-214-371-46	Sequence 46, Appl	307	15	62.5	8	18	US-10-927-262A-48	Sequence 48, Appl
235	15	62.5	8	9	US-09-214-371-47	Sequence 47, Appl	308	15	62.5	8	18	US-10-927-262A-49	Sequence 49, Appl
236	15	62.5	8	9	US-09-214-371-48	Sequence 48, Appl	309	15	62.5	8	18	US-10-927-262A-52	Sequence 52, Appl
237	15	62.5	8	9	US-09-214-371-49	Sequence 49, Appl	310	15	62.5	8	18	US-10-946-647-346	Sequence 346, App
238	15	62.5	8	9	US-09-214-371-52	Sequence 52, Appl	311	15	62.5	8	18	US-10-946-647-621	Sequence 621, App
239	15	62.5	8	9	US-09-908-322-83	Sequence 83, Appl	312	15	62.5	8	18	US-10-776-521B-338	Sequence 338, App
240	15	62.5	8	10	US-09-783-931-83	Sequence 83, Appl	313	15	62.5	8	18	US-10-820-067A-848	Sequence 338, App
241	15	62.5	8	14	US-10-209-372-31	Sequence 31, Appl	314	15	62.5	8	20	US-11-051-411-203	Sequence 203, App
242	15	62.5	8	14	US-10-190-082-265	Sequence 265, App	315	15	62.5	8	20	US-11-051-411-345	Sequence 345, App
243	15	62.5	8	14	US-10-072-419-16	Sequence 16, Appl	316	15	62.5	8	20	US-11-051-411-475	Sequence 475, App
244	15	62.5	8	14	US-10-072-419-17	Sequence 17, Appl	317	15	62.5	8	20	US-11-051-411-690	Sequence 690, App
245	15	62.5	8	15	US-10-325-810-154	Sequence 154, App	318	15	62.5	8	20	US-11-051-411-902	Sequence 902, App
246	15	62.5	8	15	US-10-387-934-37	Sequence 37, Appl	319	15	62.5	8	20	US-11-051-411-1052	Sequence 1052, Ap
247	15	62.5	8	15	US-10-387-957-36	Sequence 36, Appl	320	15	62.5	8	20	US-11-013-537-39	Sequence 39, Appl
248	15	62.5	8	15	US-10-387-957-37	Sequence 37, Appl	321	15	62.5	9	8	US-08-821-739A-49	Sequence 49, Appl
249	15	62.5	8	15	US-10-387-957-38	Sequence 38, Appl	322	15	62.5	9	8	US-08-821-739A-53	Sequence 53, Appl
250	15	62.5	8	15	US-10-387-957-39	Sequence 39, Appl	323	15	62.5	9	9	US-09-214-371-37	Sequence 37, Appl
251	15	62.5	8	15	US-10-387-934-36	Sequence 36, Appl	324	15	62.5	9	9	US-09-214-371-38	Sequence 38, Appl
252	15	62.5	8	15	US-10-387-934-37	Sequence 37, Appl	325	15	62.5	9	9	US-09-764-304-12	Sequence 12, Appl
253	15	62.5	8	15	US-10-387-934-38	Sequence 38, Appl	326	15	62.5	9	9	US-09-862-260A-13	Sequence 13, Appl
254	15	62.5	8	16	US-10-387-934-39	Sequence 39, Appl	327	15	62.5	9	9	US-09-780-053-130	Sequence 130, App
255	15	62.5	8	16	US-10-340-179-2	Sequence 2, Appl	328	15	62.5	9	9	US-09-771-415-16	Sequence 16, App
256	15	62.5	8	16	US-10-480-954-98	Sequence 98, Appl	329	15	62.5	9	10	US-09-884-456-5	Sequence 5, Appl
257	15	62.5	8	16	US-10-387-955-36	Sequence 36, Appl	330	15	62.5	9	10	US-09-884-456-8	Sequence 8, Appl
258	15	62.5	8	16	US-10-387-955-37	Sequence 37, Appl	331	15	62.5	9	10	US-09-884-456-11	Sequence 11, Appl
259	15	62.5	8	16	US-10-387-955-38	Sequence 38, Appl	332	15	62.5	9	10	US-09-884-456-14	Sequence 14, Appl
260	15	62.5	8	16	US-10-387-955-39	Sequence 39, Appl	333	15	62.5	9	10	US-09-809-638-117	Sequence 117, App
261	15	62.5	8	16	US-10-869-768-16	Sequence 16, Appl	334	15	62.5	9	10	US-09-809-638-255	Sequence 255, App
262	15	62.5	8	16	US-10-877-124-154	Sequence 154, App	335	15	62.5	9	10	US-09-809-638-347	Sequence 347, App
263	15	62.5	8	16	US-10-877-124-154	Sequence 154, App	336	15	62.5	9	10	US-09-884-455-5	Sequence 5, Appl
264	15	62.5	8	16	US-10-877-022-154	Sequence 36, Appl	337	15	62.5	9	10	US-09-884-455-8	Sequence 8, Appl
265	15	62.5	8	16	US-10-488-219-37	Sequence 37, Appl	338	15	62.5	9	10	US-09-884-455-11	Sequence 11, Appl
266	15	62.5	8	16	US-10-488-219-38	Sequence 38, Appl	339	15	62.5	9	10	US-09-884-455-14	Sequence 14, Appl
267	15	62.5	8	16	US-10-488-219-39	Sequence 39, Appl	340	15	62.5	9	10	US-09-865-548A-186	Sequence 186, App
268	15	62.5	8	17	US-10-877-146-154	Sequence 154, App	341	15	62.5	9	11	US-09-920-480B-3	Sequence 3, Appl
269	15	62.5	8	17	US-10-480-954-49	Sequence 49, Appl	342	15	62.5	9	12	US-09-957-806A-62	Sequence 62, Appl
270	15	62.5	8	17	US-10-480-954-84	Sequence 84, Appl	343	15	62.5	9	12	US-09-957-806A-69	Sequence 69, Appl
271	15	62.5	8	17	US-10-480-954-86	Sequence 86, Appl	344	15	62.5	9	13	US-10-047-539-13	Sequence 13, Appl
272	15	62.5	8	17	US-10-480-954-88	Sequence 88, Appl	345	15	62.5	9	14	US-10-265-713-12	Sequence 12, Appl
273	15	62.5	8	17	US-10-480-954-90	Sequence 90, Appl	346	15	62.5	9	14	US-10-190-082-169	Sequence 169, App
274	15	62.5	8	17	US-10-480-954-92	Sequence 92, Appl	347	15	62.5	9	14	US-10-190-082-180	Sequence 180, App
275	15	62.5	8	17	US-10-480-954-94	Sequence 94, Appl	348	15	62.5	9	14	US-10-190-082-212	Sequence 212, App
276	15	62.5	8	17	US-10-480-954-96	Sequence 96, Appl	349	15	62.5	9	14	US-10-166-626-12	Sequence 12, Appl
277	15	62.5	8	17	US-10-480-954-98	Sequence 98, Appl	350	15	62.5	9	15	US-10-245-871-297	Sequence 297, App
278	15	62.5	8	17	US-10-480-954-113	Sequence 113, App	351	15	62.5	9	15	US-10-363-204-198	Sequence 198, App
279	15	62.5	8	17	US-10-480-954-115	Sequence 115, App	352	15	62.5	9	15	US-10-398-104-22	Sequence 22, Appl
280	15	62.5	8	17	US-10-480-954-117	Sequence 117, App	353	15	62.5	9	15	US-10-363-208-237	Sequence 237, App
281	15	62.5	8	17	US-10-480-954-119	Sequence 119, App	354	15	62.5	9	15	US-10-253-286-297	Sequence 297, App
282	15	62.5	8	17	US-10-480-954-121	Sequence 121, App	355	15	62.5	9	16	US-10-657-363-16	Sequence 16, Appl
283	15	62.5	8	17	US-10-480-954-123	Sequence 123, App	356	15	62.5	9	16	US-10-340-179-1	Sequence 1, Appl
284	15	62.5	8	17	US-10-480-954-125	Sequence 125, App	357	15	62.5	9	16	US-10-793-943-7	Sequence 7, Appl
285	15	62.5	8	17	US-10-480-954-143	Sequence 143, App	358	15	62.5	9	17	US-10-705-459-186	Sequence 186, App
286	15	62.5	8	17	US-10-480-954-145	Sequence 145, App	359	15	62.5	9	17	US-10-654-601-2374	Sequence 2374, Ap
287	15	62.5	8	17	US-10-480-954-147	Sequence 147, App	360	15	62.5	9	18	US-10-927-262A-37	Sequence 37, Appl
288	15	62.5	8	17	US-10-480-954-149	Sequence 149, App	361	15	62.5	9	18	US-10-927-262A-38	Sequence 38, Appl
289	15	62.5	8	17	US-10-480-954-151	Sequence 151, App	362	15	62.5	9	18	US-10-149-137A-540	Sequence 540, App
290	15	62.5	8	17	US-10-480-954-153	Sequence 153, App	363	15	62.5	9	18	US-10-953-901-690	Sequence 690, App
291	15	62.5	8	17	US-10-480-954-155	Sequence 155, App	364	15	62.5	9	18	US-10-510-523-33	Sequence 33, Appl
292	15	62.5	8	17	US-10-480-954-157	Sequence 157, App	365	15	62.5	9	18	US-10-510-523-34	Sequence 34, Appl
293	15	62.5	8	17	US-10-480-954-166	Sequence 166, App	366	15	62.5	9	20	US-11-051-411-73	Sequence 73, Appl
294	15	62.5	8	17	US-10-480-954-168	Sequence 168, App	367	15	62.5	9	20	US-11-051-411-281	Sequence 281, App
295	15	62.5	8	17	US-10-480-954-170	Sequence 170, App	368	15	62.5	9	20	US-11-051-411-346	Sequence 346, App
296	15	62.5	8	17	US-10-480-954-172	Sequence 172, App	369	15	62.5	9	20	US-11-051-411-473	Sequence 473, App
297	15	62.5	8	17	US-10-480-954-174	Sequence 174, App	370	15	62.5	9	20	US-11-051-411-607	Sequence 607, App
298	15	62.5	8	17	US-10-480-954-176	Sequence 176, App	371	15	62.5	9	20	US-11-051-411-1053	Sequence 1053, Ap
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300	15	62.5	8	17	US-10-480-954-180	Sequence 180, App	373	15	62.5	10	9	US-09-214-371-36	Sequence 36, Appl
301	15	62.5	8	18	US-10-927-262A-12	Sequence 12, Appl	374	15	62.5	10	9	US-09-767-460-53	Sequence 53, Appl
302	15	62.5	8	18	US-10-927-262A-13	Sequence 13, Appl	375	15	62.5	10	9	US-09-767-460-53	Sequence 53, Appl
303	15	62.5	8	18	US-10-927-262A-21	Sequence 21, Appl	376	15	62.5	10	9	US-09-767-460-72	Sequence 72, Appl

377	15	62.5	10	9	US-09-780-053-175	Sequence 175, App	450	15	62.5	10	18	US-10-818-036-20	Sequence 20, App
378	15	62.5	10	9	US-09-826-290-390	Sequence 390, App	451	15	62.5	10	20	US-11-003-951-93	Sequence 93, App
379	15	62.5	10	10	US-09-809-638-187	Sequence 187, App	452	15	62.5	10	20	US-11-009-443-85	Sequence 85, App
380	15	62.5	10	10	US-09-809-638-273	Sequence 273, App	453	15	62.5	10	20	US-11-051-411-15	Sequence 15, App
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385	15	62.5	10	10	US-09-995-529-46	Sequence 46, App	458	15	62.5	11	10	US-09-840-085-31	Sequence 31, App
386	15	62.5	10	10	US-09-995-529-47	Sequence 47, App	459	15	62.5	11	14	US-10-014-340-216	Sequence 216, App
387	15	62.5	10	10	US-09-795-798-10	Sequence 10, App	460	15	62.5	11	15	US-10-398-104-162	Sequence 162, App
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390	15	62.5	10	11	US-09-995-529-44	Sequence 44, App	463	15	62.5	11	17	US-10-658-250-46	Sequence 46, App
391	15	62.5	10	11	US-09-995-529-45	Sequence 45, App	464	15	62.5	11	17	US-10-656-250-171	Sequence 171, App
392	15	62.5	10	11	US-09-995-529-46	Sequence 46, App	465	15	62.5	11	20	US-11-051-411-21	Sequence 21, App
393	15	62.5	10	11	US-09-995-529-47	Sequence 47, App	466	15	62.5	11	20	US-11-051-411-162	Sequence 162, App
394	15	62.5	10	14	US-10-094-401-172	Sequence 172, App	467	15	62.5	11	20	US-11-051-411-222	Sequence 222, App
395	15	62.5	10	14	US-10-190-082-167	Sequence 167, App	468	15	62.5	11	20	US-11-051-411-325	Sequence 325, App
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402	15	62.5	10	14	US-10-072-419-32	Sequence 32, App	475	15	62.5	12	9	US-09-214-371-20	Sequence 20, App
403	15	62.5	10	14	US-10-031-874A-16	Sequence 16, App	476	15	62.5	12	9	US-09-214-371-24	Sequence 24, App
404	15	62.5	10	15	US-10-462-262-140	Sequence 140, App	477	15	62.5	12	9	US-09-214-371-25	Sequence 25, App
405	15	62.5	10	15	US-10-264-309-407	Sequence 407, App	478	15	62.5	12	9	US-09-214-371-26	Sequence 26, App
406	15	62.5	10	16	US-10-449-379-29	Sequence 29, App	479	15	62.5	12	9	US-09-214-371-31	Sequence 31, App
407	15	62.5	10	16	US-10-338-553-35	Sequence 35, App	480	15	62.5	12	9	US-09-214-371-64	Sequence 64, App
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409	15	62.5	10	16	US-10-338-552-39	Sequence 39, App	482	15	62.5	12	14	US-10-032-818-31	Sequence 31, App
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411	15	62.5	10	16	US-10-338-627-35	Sequence 35, App	484	15	62.5	12	14	US-10-190-082-252	Sequence 252, App
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421	15	62.5	10	16	US-10-160-505-29	Sequence 29, App	494	15	62.5	12	15	US-10-609-217-146	Sequence 146, App
422	15	62.5	10	16	US-10-869-768-32	Sequence 32, App	495	15	62.5	12	15	US-10-632-388-131	Sequence 131, App
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427	15	62.5	10	17	US-10-823-253-26	Sequence 26, App	500	15	62.5	12	15	US-10-632-388-143	Sequence 143, App
428	15	62.5	10	17	US-10-769-308-29	Sequence 29, App	501	15	62.5	12	15	US-10-632-388-144	Sequence 144, App
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441	15	62.5	10	18	US-10-927-262A-36	Sequence 36, App	514	15	62.5	12	15	US-10-645-761-132	Sequence 132, App
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449	15	62.5	10	18	US-10-264-309-407	Sequence 407, App	522	15	62.5	12	15	US-10-666-696-131	Sequence 131, App

523	15	62.5	12	15	US-10-666-696-132	Sequence 132, App	596	15	62.5	14	15	US-10-632-388-68	Sequence 68, Appl
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525	15	62.5	12	15	US-10-666-696-134	Sequence 134, App	598	15	62.5	14	15	US-10-645-761-68	Sequence 68, Appl
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532	15	62.5	12	15	US-10-653-048-132	Sequence 132, App	605	15	62.5	14	16	US-10-712-447-160	Sequence 160, App
533	15	62.5	12	15	US-10-653-048-133	Sequence 133, App	606	15	62.5	14	16	US-10-712-447-194	Sequence 194, App
534	15	62.5	12	15	US-10-653-048-134	Sequence 134, App	607	15	62.5	14	16	US-10-712-447-195	Sequence 195, App
535	15	62.5	12	15	US-10-653-048-137	Sequence 137, App	608	15	62.5	14	16	US-10-712-447-196	Sequence 196, App
536	15	62.5	12	15	US-10-653-048-143	Sequence 143, App	609	15	62.5	14	16	US-10-712-447-204	Sequence 204, App
537	15	62.5	12	15	US-10-653-048-144	Sequence 144, App	610	15	62.5	14	16	US-10-865-478-854	Sequence 854, App
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543	15	62.5	12	16	US-10-467-758-36	Sequence 36, Appl	616	15	62.5	14	18	US-10-807-807-1052	Sequence 1052, App
544	15	62.5	12	16	US-10-363-204-228	Sequence 228, App	617	15	62.5	14	20	US-11-093-103-45	Sequence 45, Appl
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546	15	62.5	12	16	US-10-839-525-98	Sequence 98, Appl	619	15	62.5	15	9	US-09-214-371-29	Sequence 29, Appl
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548	15	62.5	12	18	US-10-645-784-131	Sequence 131, App	621	15	62.5	15	9	US-09-214-371-66	Sequence 66, Appl
549	15	62.5	12	18	US-10-645-784-132	Sequence 132, App	622	15	62.5	15	9	US-09-829-549A-23	Sequence 23, Appl
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552	15	62.5	12	18	US-10-645-784-137	Sequence 137, App	625	15	62.5	15	9	US-09-953-510-51	Sequence 51, Appl
553	15	62.5	12	18	US-10-645-784-143	Sequence 143, App	626	15	62.5	15	9	US-09-953-510-52	Sequence 52, Appl
554	15	62.5	12	18	US-10-645-784-144	Sequence 144, App	627	15	62.5	15	9	US-09-732-384-6	Sequence 6, Appl
555	15	62.5	12	18	US-10-645-784-145	Sequence 145, App	628	15	62.5	15	10	US-09-894-594-31	Sequence 31, Appl
556	15	62.5	12	18	US-10-645-784-146	Sequence 146, App	629	15	62.5	15	10	US-09-894-594-43	Sequence 43, Appl
557	15	62.5	12	18	US-10-927-262A-7	Sequence 7, Appl	630	15	62.5	15	10	US-09-952-680A-55	Sequence 55, Appl
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569	15	62.5	13	14	US-10-300-694A-18	Sequence 18, Appl	642	15	62.5	15	14	US-10-080-608A-165	Sequence 165, App
570	15	62.5	13	14	US-10-113-512-1	Sequence 1, Appl	643	15	62.5	15	14	US-10-295-693-90	Sequence 90, Appl
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572	15	62.5	13	16	US-10-468-496-692	Sequence 692, App	645	15	62.5	15	15	US-10-375-157-64	Sequence 64, Appl
573	15	62.5	13	16	US-10-468-496-693	Sequence 693, App	646	15	62.5	15	15	US-10-609-217-139	Sequence 139, App
574	15	62.5	13	16	US-10-468-496-694	Sequence 694, App	647	15	62.5	15	15	US-10-609-217-140	Sequence 140, App
575	15	62.5	13	16	US-10-468-496-695	Sequence 695, App	648	15	62.5	15	15	US-10-609-217-141	Sequence 141, App
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581	15	62.5	13	16	US-10-495-146-186	Sequence 186, App	654	15	62.5	15	15	US-10-651-723-140	Sequence 140, App
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583	15	62.5	13	16	US-10-495-146-188	Sequence 188, App	656	15	62.5	15	15	US-10-645-761-139	Sequence 139, App
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585	15	62.5	13	18	US-10-948-707-1379	Sequence 1379, App	658	15	62.5	15	15	US-10-645-761-141	Sequence 141, App
586	15	62.5	13	20	US-11-093-103-7	Sequence 7, Appl	659	15	62.5	15	15	US-10-666-696-139	Sequence 139, App
587	15	62.5	14	9	US-09-214-371-33	Sequence 33, Appl	660	15	62.5	15	15	US-10-666-696-140	Sequence 140, App
588	15	62.5	14	9	US-09-214-371-34	Sequence 34, Appl	661	15	62.5	15	15	US-10-666-696-141	Sequence 141, App
589	15	62.5	14	14	US-10-186-867-7	Sequence 7, Appl	662	15	62.5	15	15	US-10-653-048-139	Sequence 139, App
590	15	62.5	14	14	US-10-083-768-33	Sequence 33, Appl	663	15	62.5	15	15	US-10-653-048-140	Sequence 140, App
591	15	62.5	14	14	US-10-083-768-213	Sequence 213, App	664	15	62.5	15	15	US-10-653-048-141	Sequence 141, App
592	15	62.5	14	15	US-10-435-766-80	Sequence 80, Appl	665	15	62.5	15	16	US-10-775-965-74	Sequence 74, Appl
593	15	62.5	14	15	US-10-436-715-430	Sequence 430, App	666	15	62.5	15	16	US-10-215-982-55	Sequence 55, Appl
594	15	62.5	14	15	US-10-436-715-442	Sequence 442, App	667	15	62.5	15	16	US-10-695-155-51	Sequence 51, Appl
595	15	62.5	14	15	US-10-609-217-68	Sequence 68, Appl	668	15	62.5	15	16	US-10-695-155-52	Sequence 52, Appl

669	15	62.5	15	16	US-10-695-155-110	Sequence 110, App	742	15	62.5	18	20	US-11-093-103-47	Sequence 47, Appl
670	15	62.5	15	16	US-10-695-155-111	Sequence 111, App	743	15	62.5	18	20	US-11-093-103-48	Sequence 48, Appl
671	15	62.5	15	16	US-10-495-146-23	Sequence 23, Appl	744	15	62.5	19	9	US-09-214-371-1	Sequence 1, Appl
672	15	62.5	15	16	US-10-495-146-24	Sequence 24, Appl	745	15	62.5	19	9	US-09-732-357A-9	Sequence 9, Appl
673	15	62.5	15	16	US-10-495-146-25	Sequence 25, Appl	746	15	62.5	19	9	US-09-732-384-7	Sequence 7, Appl
674	15	62.5	15	16	US-10-495-146-26	Sequence 26, Appl	747	15	62.5	19	9	US-09-774-639-342	Sequence 342, App
675	15	62.5	15	16	US-10-793-943-3	Sequence 3, Appl	748	15	62.5	19	10	US-09-229-173-45	Sequence 45, Appl
676	15	62.5	15	17	US-10-182-613A-6	Sequence 6, Appl	749	15	62.5	19	10	US-09-977-797A-116	Sequence 116, App
677	15	62.5	15	17	US-10-182-613A-7	Sequence 7, Appl	750	15	62.5	19	10	US-09-969-730-289	Sequence 289, App
678	15	62.5	15	18	US-10-645-784-139	Sequence 139, App	751	15	62.5	19	13	US-10-155-059-13	Sequence 13, Appl
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680	15	62.5	15	18	US-10-645-784-141	Sequence 141, App	753	15	62.5	19	14	US-10-225-567A-1318	Sequence 1318, Ap
681	15	62.5	15	18	US-10-927-262A-8	Sequence 8, Appl	754	15	62.5	19	14	US-10-300-694A-42	Sequence 42, Appl
682	15	62.5	15	18	US-10-927-262A-29	Sequence 29, Appl	755	15	62.5	19	14	US-10-029-386-28258	Sequence 28258, A
683	15	62.5	15	18	US-10-927-262A-30	Sequence 30, Appl	756	15	62.5	19	14	US-10-029-386-33510	Sequence 33510, A
684	15	62.5	15	18	US-10-927-262A-66	Sequence 66, Appl	757	15	62.5	19	15	US-10-120-885A-45	Sequence 45, Appl
685	15	62.5	15	18	US-10-862-193-2239	Sequence 2239, Ap	758	15	62.5	19	15	US-10-144-929-231	Sequence 231, App
686	15	62.5	15	18	US-10-754-473-30	Sequence 30, Appl	759	15	62.5	19	15	US-10-621-363-289	Sequence 289, App
687	15	62.5	15	20	US-11-051-411-1069	Sequence 1069, Ap	760	15	62.5	19	15	US-10-616-279-9	Sequence 9, Appl
688	15	62.5	15	20	US-11-051-411-1109	Sequence 1109, Ap	761	15	62.5	19	15	US-10-257-864A-100	Sequence 100, App
689	15	62.5	15	20	US-11-051-411-1469	Sequence 1469, Ap	762	15	62.5	19	15	US-10-328-953-14	Sequence 14, Appl
690	15	62.5	16	9	US-09-214-371-39	Sequence 39, Appl	763	15	62.5	19	15	US-10-393-518-129	Sequence 129, App
691	15	62.5	16	9	US-09-214-371-40	Sequence 40, Appl	764	15	62.5	19	15	US-10-624-884-9	Sequence 9, Appl
692	15	62.5	16	9	US-09-214-371-41	Sequence 41, Appl	765	15	62.5	19	16	US-10-754-457-9	Sequence 9, Appl
693	15	62.5	16	9	US-09-019-679-3	Sequence 3, Appl	766	15	62.5	19	16	US-10-399-585-128	Sequence 128, App
694	15	62.5	16	9	US-09-962-805-13	Sequence 13, Appl	767	15	62.5	19	16	US-10-645-085A-100	Sequence 100, App
695	15	62.5	16	9	US-09-813-333-20	Sequence 20, Appl	768	15	62.5	19	17	US-10-895-183-9	Sequence 9, Appl
696	15	62.5	16	10	US-09-825-517A-56	Sequence 56, Appl	769	15	62.5	19	17	US-10-637-317-58	Sequence 58, Appl
697	15	62.5	16	10	US-09-825-517A-105	Sequence 105, App	770	15	62.5	19	17	US-10-866-831-231	Sequence 231, App
698	15	62.5	16	10	US-09-825-517A-130	Sequence 130, App	771	15	62.5	19	17	US-10-947-352-37	Sequence 37, Appl
699	15	62.5	16	10	US-09-825-517A-137	Sequence 137, App	772	15	62.5	19	18	US-10-927-262A-1	Sequence 1, Appl
700	15	62.5	16	13	US-10-044-703-20	Sequence 20, Appl	773	15	62.5	20	9	US-09-735-705-234	Sequence 234, App
701	15	62.5	16	14	US-10-223-047-19	Sequence 19, Appl	774	15	62.5	20	9	US-09-735-705-381	Sequence 381, App
702	15	62.5	16	14	US-10-094-401-220	Sequence 220, App	775	15	62.5	20	9	US-09-850-716A-381	Sequence 381, App
703	15	62.5	16	15	US-10-462-262-188	Sequence 188, App	776	15	62.5	20	9	US-09-850-716A-381	Sequence 381, App
704	15	62.5	16	15	US-10-239-103-20	Sequence 20, Appl	777	15	62.5	20	9	US-09-897-778-234	Sequence 234, App
705	15	62.5	16	16	US-10-467-758-14	Sequence 14, Appl	778	15	62.5	20	9	US-09-897-778-381	Sequence 381, App
706	15	62.5	16	18	US-10-927-262A-39	Sequence 39, Appl	779	15	62.5	20	10	US-09-764-891-4348	Sequence 4348, Ap
707	15	62.5	16	18	US-10-927-262A-40	Sequence 40, Appl	780	15	62.5	20	13	US-10-155-059-8	Sequence 8, Appl
708	15	62.5	16	18	US-10-927-262A-41	Sequence 41, Appl	781	15	62.5	20	13	US-10-155-059-10	Sequence 10, Appl
709	15	62.5	16	20	US-11-045-477-56	Sequence 56, Appl	782	15	62.5	20	13	US-10-155-059-11	Sequence 11, Appl
710	15	62.5	16	20	US-11-045-477-105	Sequence 105, App	783	15	62.5	20	13	US-10-155-059-14	Sequence 14, Appl
711	15	62.5	16	20	US-11-045-477-130	Sequence 130, App	784	15	62.5	20	13	US-10-155-059-15	Sequence 15, Appl
712	15	62.5	16	20	US-11-045-477-137	Sequence 137, App	785	15	62.5	20	13	US-10-155-059-16	Sequence 16, Appl
713	15	62.5	17	14	US-10-280-066-83	Sequence 83, Appl	786	15	62.5	20	13	US-10-155-059-19	Sequence 19, Appl
714	15	62.5	17	14	US-10-029-386-27504	Sequence 27504, A	787	15	62.5	20	14	US-10-155-059-20	Sequence 20, Appl
715	15	62.5	17	14	US-10-029-386-28133	Sequence 28133, A	788	15	62.5	20	14	US-10-007-700-234	Sequence 234, App
716	15	62.5	17	15	US-10-120-885A-44	Sequence 44, Appl	789	15	62.5	20	14	US-10-007-700-381	Sequence 381, App
717	15	62.5	17	16	US-10-258-144-248	Sequence 248, App	790	15	62.5	20	14	US-10-205-428-377	Sequence 377, App
718	15	62.5	17	16	US-10-258-144-258	Sequence 258, App	791	15	62.5	20	14	US-10-162-538-11	Sequence 11, Appl
719	15	62.5	17	16	US-10-258-144-442	Sequence 442, App	792	15	62.5	20	14	US-10-117-982-234	Sequence 234, App
720	15	62.5	17	16	US-10-258-144-442	Sequence 442, App	793	15	62.5	20	14	US-10-117-982-381	Sequence 381, App
721	15	62.5	17	17	US-10-695-155-155	Sequence 155, App	794	15	62.5	20	14	US-10-280-066-286	Sequence 286, App
722	15	62.5	17	18	US-10-946-647-66	Sequence 93, Appl	795	15	62.5	20	14	US-10-280-066-316	Sequence 316, App
723	15	62.5	18	9	US-09-214-371-74	Sequence 74, Appl	796	15	62.5	20	14	US-10-280-066-343	Sequence 343, App
724	15	62.5	18	10	US-09-896-841A-48	Sequence 48, Appl	797	15	62.5	20	14	US-10-029-386-33058	Sequence 33058, A
725	15	62.5	18	10	US-09-896-841A-49	Sequence 49, Appl	798	15	62.5	20	15	US-10-329-087-26	Sequence 26, Appl
726	15	62.5	18	14	US-10-225-567A-2147	Sequence 2147, Ap	799	15	62.5	20	15	US-10-329-087-31	Sequence 31, Appl
727	15	62.5	18	14	US-10-187-215-48	Sequence 48, Appl	800	15	62.5	20	15	US-10-313-986-234	Sequence 234, App
728	15	62.5	18	14	US-10-187-215-49	Sequence 49, Appl	801	15	62.5	20	15	US-10-313-986-381	Sequence 381, App
729	15	62.5	18	15	US-10-273-386-49	Sequence 49, Appl	802	15	62.5	20	15	US-10-644-703-14	Sequence 14, Appl
730	15	62.5	18	15	US-10-273-386-49	Sequence 49, Appl	803	15	62.5	20	16	US-10-666-480-5	Sequence 5, Appl
731	15	62.5	18	16	US-10-258-144-268	Sequence 268, App	804	15	62.5	20	16	US-10-467-758-8	Sequence 8, Appl
732	15	62.5	18	16	US-10-258-144-358	Sequence 358, App	805	15	62.5	20	16	US-10-467-758-9	Sequence 9, Appl
733	15	62.5	18	16	US-10-742-379-68	Sequence 68, App	806	15	62.5	20	16	US-10-467-758-10	Sequence 10, Appl
734	15	62.5	18	16	US-10-468-655-28	Sequence 28, Appl	807	15	62.5	20	16	US-10-775-972-234	Sequence 234, App
735	15	62.5	18	16	US-10-649-378A-51	Sequence 51, Appl	808	15	62.5	20	17	US-10-775-972-381	Sequence 381, App
736	15	62.5	18	16	US-10-649-378A-52	Sequence 52, Appl	809	15	62.5	20	17	US-10-660-370-154	Sequence 154, App
737	15	62.5	18	16	US-10-423-830-48	Sequence 48, Appl	810	15	62.5	20	17	US-10-661-156-181	Sequence 181, App
738	15	62.5	18	16	US-10-423-830-49	Sequence 49, Appl	811	15	62.5	20	17	US-10-661-156-182	Sequence 182, App
739	15	62.5	18	17	US-10-913-937-8	Sequence 8, Appl	812	15	62.5	20	17	US-10-926-683-1481	Sequence 1481, Ap
740	15	62.5	18	17	US-10-661-156-107	Sequence 107, App	813	15	62.5	20	17	US-10-690-276-394	Sequence 394, App
741	15	62.5	18	18	US-10-927-262A-74	Sequence 74, Appl	814	15	62.5	20	17	US-10-690-276-443	Sequence 443, App

815	15	62.5	20	18	US-10-922-124-234	Sequence 234, App	888	14	58.3	8	15	US-10-260-937-89	Sequence 89, Appl
816	15	62.5	20	18	US-10-922-124-381	Sequence 381, App	889	14	58.3	8	15	US-10-367-580-156	Sequence 156, App
817	15	62.5	20	18	US-10-792-582-456	Sequence 456, App	890	14	58.3	8	15	US-10-367-580-211	Sequence 211, App
818	15	62.5	20	18	US-10-518-358-1	Sequence 1, Appli	891	14	58.3	8	15	US-10-367-593-156	Sequence 156, App
819	15	62.5	20	18	US-10-518-358-2	Sequence 2, Appli	892	14	58.3	8	15	US-10-367-593-211	Sequence 211, App
820	15	62.5	20	18	US-10-518-358-3	Sequence 3, Appli	893	14	58.3	8	15	US-10-367-594-156	Sequence 156, App
821	15	62.5	20	18	US-11-066-697-1366	Sequence 1366, App	894	14	58.3	8	15	US-10-367-594-211	Sequence 211, App
822	15	62.5	20	20	US-11-065-970-27	Sequence 27, Appl	895	14	58.3	8	15	US-10-367-654-156	Sequence 156, App
823	15	62.5	20	20	US-11-075-234-257	Sequence 257, App	896	14	58.3	8	15	US-10-367-654-211	Sequence 211, App
824	15	62.5	20	20	US-11-127-702-5	Sequence 5, Appli	897	14	58.3	8	15	US-10-367-654-156	Sequence 156, App
825	14	58.3	5	9	US-09-214-371-2	Sequence 2, Appli	898	14	58.3	8	15	US-10-367-658-211	Sequence 211, App
826	14	58.3	5	9	US-09-281-717-3	Sequence 3, Appli	899	14	58.3	8	15	US-10-367-668-156	Sequence 156, App
827	14	58.3	5	12	US-09-957-806A-226	Sequence 226, App	900	14	58.3	8	15	US-10-367-668-211	Sequence 211, App
828	14	58.3	5	15	US-10-436-549-16	Sequence 16, Appl	901	14	58.3	8	16	US-10-440-390-52	Sequence 52, Appl
829	14	58.3	5	15	US-10-126-962-3	Sequence 3, Appli	902	14	58.3	8	16	US-10-440-390-89	Sequence 89, Appl
830	14	58.3	5	16	US-10-777-053-801	Sequence 801, App	903	14	58.3	8	16	US-10-367-674-156	Sequence 156, App
831	14	58.3	5	16	US-10-337-105-3	Sequence 3, Appli	904	14	58.3	8	16	US-10-367-674-211	Sequence 211, App
832	14	58.3	5	16	US-10-337-105-4	Sequence 4, Appli	905	14	58.3	8	16	US-10-712-425-1325	Sequence 1325, App
833	14	58.3	5	16	US-10-712-425-16	Sequence 16, Appl	906	14	58.3	8	16	US-10-869-768-5	Sequence 5, Appli
834	14	58.3	5	16	US-10-837-217-801	Sequence 801, App	907	14	58.3	8	16	US-10-869-768-6	Sequence 6, Appli
835	14	58.3	5	17	US-10-773-032-16	Sequence 16, Appl	908	14	58.3	8	16	US-10-869-768-7	Sequence 7, Appli
836	14	58.3	5	18	US-10-927-262A-2	Sequence 2, Appli	909	14	58.3	8	16	US-10-869-768-9	Sequence 9, Appli
837	14	58.3	5	18	US-10-705-165-21	Sequence 21, Appl	910	14	58.3	8	16	US-10-869-768-12	Sequence 12, Appl
838	14	58.3	6	10	US-09-813-153-232	Sequence 232, App	911	14	58.3	8	16	US-10-869-768-14	Sequence 14, Appl
839	14	58.3	6	10	US-09-750-754-27	Sequence 27, Appl	912	14	58.3	8	16	US-10-869-768-18	Sequence 18, Appl
840	14	58.3	6	10	US-09-750-754-28	Sequence 28, Appl	913	14	58.3	8	16	US-10-869-768-19	Sequence 19, Appl
841	14	58.3	6	10	US-09-750-754-29	Sequence 29, Appl	914	14	58.3	8	16	US-10-869-768-20	Sequence 20, Appl
842	14	58.3	6	10	US-09-750-754-30	Sequence 30, Appl	915	14	58.3	8	16	US-10-869-768-21	Sequence 21, Appl
843	14	58.3	6	12	US-09-957-806A-225	Sequence 225, App	916	14	58.3	8	16	US-10-869-768-22	Sequence 22, Appl
844	14	58.3	6	13	US-10-155-059-2	Sequence 2, Appli	917	14	58.3	8	16	US-10-869-768-23	Sequence 23, Appl
845	14	58.3	6	13	US-10-156-820-84	Sequence 84, Appl	918	14	58.3	8	16	US-10-869-768-26	Sequence 26, Appl
846	14	58.3	6	14	US-10-127-691-30	Sequence 30, Appl	919	14	58.3	8	16	US-10-869-768-38	Sequence 38, Appl
847	14	58.3	6	15	US-10-139-794-249	Sequence 249, App	920	14	58.3	8	16	US-10-771-232-1	Sequence 1, Appli
848	14	58.3	6	15	US-10-374-466-47	Sequence 47, Appl	921	14	58.3	8	17	US-10-480-954-2	Sequence 2, Appli
849	14	58.3	6	17	US-10-643-627-30	Sequence 30, Appl	922	14	58.3	8	17	US-10-480-954-4	Sequence 4, Appli
850	14	58.3	6	18	US-10-776-521B-190	Sequence 190, App	923	14	58.3	8	17	US-10-480-954-6	Sequence 6, Appli
851	14	58.3	6	18	US-10-820-067A-696	Sequence 696, App	924	14	58.3	8	17	US-10-480-954-17	Sequence 17, Appl
852	14	58.3	7	9	US-09-884-767A-93	Sequence 93, Appl	925	14	58.3	8	17	US-10-480-954-19	Sequence 19, Appl
853	14	58.3	7	10	US-09-750-754-26	Sequence 26, Appl	926	14	58.3	8	17	US-10-480-954-21	Sequence 21, Appl
854	14	58.3	7	10	US-09-750-754-70	Sequence 70, Appl	927	14	58.3	8	17	US-10-480-954-23	Sequence 23, Appl
855	14	58.3	7	10	US-09-750-754-79	Sequence 79, Appl	928	14	58.3	8	17	US-10-480-954-25	Sequence 25, Appl
856	14	58.3	7	14	US-10-190-082-61	Sequence 61, Appl	929	14	58.3	8	17	US-10-480-954-27	Sequence 27, Appl
857	14	58.3	7	15	US-10-363-208-253	Sequence 253, App	930	14	58.3	8	17	US-10-480-954-29	Sequence 29, Appl
858	14	58.3	7	15	US-10-126-962-7	Sequence 7, Appli	931	14	58.3	8	17	US-10-480-954-31	Sequence 31, Appl
859	14	58.3	7	16	US-10-789-450-15	Sequence 15, Appl	932	14	58.3	8	17	US-10-480-954-58	Sequence 58, Appl
860	14	58.3	7	17	US-10-935-254-6	Sequence 6, Appli	933	14	58.3	8	17	US-10-480-954-60	Sequence 60, Appl
861	14	58.3	7	17	US-10-607-595-402	Sequence 402, App	934	14	58.3	8	17	US-10-480-954-62	Sequence 62, Appl
862	14	58.3	7	18	US-10-589-462-182	Sequence 182, App	935	14	58.3	8	17	US-10-480-954-64	Sequence 64, Appl
863	14	58.3	7	20	US-11-030-348-93	Sequence 93, Appl	936	14	58.3	8	17	US-10-480-954-66	Sequence 66, Appl
864	14	58.3	8	9	US-09-214-371-10	Sequence 10, Appl	937	14	58.3	8	17	US-10-659-207-484	Sequence 484, App
865	14	58.3	8	9	US-09-214-371-14	Sequence 14, Appl	938	14	58.3	8	17	US-10-773-032-1325	Sequence 1325, App
866	14	58.3	8	9	US-09-214-371-16	Sequence 16, Appl	939	14	58.3	8	17	US-10-886-165-39	Sequence 39, Appl
867	14	58.3	8	9	US-09-214-371-23	Sequence 23, Appl	940	14	58.3	8	17	US-10-886-165-68	Sequence 68, Appl
868	14	58.3	8	9	US-09-214-371-50	Sequence 50, Appl	941	14	58.3	8	18	US-10-927-262A-10	Sequence 10, Appl
869	14	58.3	8	9	US-09-214-371-51	Sequence 51, Appl	942	14	58.3	8	18	US-10-927-262A-14	Sequence 14, Appl
870	14	58.3	8	9	US-09-214-371-53	Sequence 53, Appl	943	14	58.3	8	18	US-10-927-262A-16	Sequence 16, Appl
871	14	58.3	8	14	US-10-209-372-12	Sequence 12, Appl	944	14	58.3	8	18	US-10-927-262A-23	Sequence 23, Appl
872	14	58.3	8	14	US-10-209-372-37	Sequence 37, Appl	945	14	58.3	8	18	US-10-927-262A-50	Sequence 50, Appl
873	14	58.3	8	14	US-10-209-372-43	Sequence 43, Appl	946	14	58.3	8	18	US-10-927-262A-51	Sequence 51, Appl
874	14	58.3	8	14	US-10-072-419-5	Sequence 5, Appli	947	14	58.3	8	18	US-10-927-262A-53	Sequence 53, Appl
875	14	58.3	8	14	US-10-072-419-6	Sequence 6, Appli	948	14	58.3	8	18	US-10-927-262A-54	Sequence 54, Appl
876	14	58.3	8	14	US-10-072-419-7	Sequence 7, Appli	949	14	58.3	8	18	US-10-927-262A-57	Sequence 57, Appl
877	14	58.3	8	14	US-10-072-419-9	Sequence 9, Appli	950	14	58.3	8	18	US-10-927-262A-58	Sequence 58, Appl
878	14	58.3	8	14	US-10-072-419-12	Sequence 12, Appl	951	14	58.3	8	18	US-10-927-262A-60	Sequence 60, Appl
879	14	58.3	8	14	US-10-072-419-14	Sequence 14, Appl	952	14	58.3	8	18	US-10-927-262A-61	Sequence 61, Appl
880	14	58.3	8	14	US-10-072-419-18	Sequence 18, Appl	953	14	58.3	8	18	US-10-927-262A-62	Sequence 62, Appl
881	14	58.3	8	14	US-10-072-419-19	Sequence 19, Appl	954	14	58.3	8	18	US-10-838-135A-1	Sequence 1, Appli
882	14	58.3	8	14	US-10-072-419-20	Sequence 20, Appl	955	14	58.3	8	18	US-10-994-106-192	Sequence 192, App
883	14	58.3	8	14	US-10-072-419-21	Sequence 21, Appl	956	14	58.3	8	18	US-10-776-521B-228	Sequence 228, App
884	14	58.3	8	14	US-10-072-419-22	Sequence 22, Appl	957	14	58.3	8	18	US-10-776-521B-237	Sequence 237, App
885	14	58.3	8	14	US-10-072-419-23	Sequence 23, Appl	958	14	58.3	8	18	US-10-776-521B-264	Sequence 264, App
886	14	58.3	8	14	US-10-072-419-26	Sequence 26, Appl	959	14	58.3	8	18	US-10-776-521B-329	Sequence 329, App
887	14	58.3	8	14	US-10-072-419-38	Sequence 38, Appl	960	14	58.3	8	18	US-10-820-067A-135	Sequence 135, App


```
; Sequence 30, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818.036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD.RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; US-10-818-036-30

Query Match          70.8%; Score 17; DB 18; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
      | |
Db      4 FTSSW 8

RESULT 5
US-10-072-419-3
; Sequence 3, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Apis mellifera
; US-10-072-419-3

Query Match          70.8%; Score 17; DB 14; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
      | |
Db      4 FTSSW 8

RESULT 6
US-10-072-419-8
; Sequence 8, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
```

```
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
; US-10-072-419-8

Query Match          70.8%; Score 17; DB 14; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
      | |
Db      4 FTSSW 8

RESULT 7
US-10-869-768-3
; Sequence 3, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
; CURRENT FILING DATE: 2004-06-16
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Apis mellifera
; US-10-869-768-3

Query Match          70.8%; Score 17; DB 16; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
      | |
Db      4 FTSSW 8

RESULT 8
US-10-869-768-8
; Sequence 8, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
; CURRENT FILING DATE: 2004-06-16
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
; US-10-869-768-8

Query Match          70.8%; Score 17; DB 16; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
      | |
Db      4 FTSSW 8
```

```
RESULT 9
US-10-818-036-14
; Sequence 14, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-818-036-14

Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTASW 8

RESULT 10
US-10-818-036-15
; Sequence 15, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-818-036-15

Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTASW 8

RESULT 11
US-10-818-036-23
; Sequence 23, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
US-10-818-036-23

Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTASW 8

RESULT 12
US-10-818-036-25
; Sequence 25, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-818-036-25

Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTASW 8

RESULT 13
US-10-818-036-26
; Sequence 26, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
US-10-818-036-26

Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
   | |
Db 4 FTASW 8

RESULT 14
US-10-818-036-29
; Sequence 29, Application US/10818036
; Publication No. US2005022040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818.036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; NAME/KEY: MOD_RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
US-10-818-036-29

Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
   | |
Db 4 FTASW 8

RESULT 15
US-09-842-776A-28
; Sequence 28, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842.776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR1) of an
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease
; OTHER INFORMATION: epitope (alternative sequence)
US-09-842-776A-28

Query Match      70.8%; Score 17; DB 11; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
   | |
Db 4 FSTSW 8

RESULT 16
US-10-996-316-139
; Sequence 139, Application US/10996316
; Publication No. US20050129690A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: McWhirter, John
; APPLICANT: Kretz-Rommel, Anke
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC
; FILE REFERENCE: 60 CIP IV (1087-43 CIP IV)
; CURRENT APPLICATION NUMBER: US/10/996.316
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/894,672
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/736,188
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/379,151
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 10
; TYPE: PRT
; ORGANISM: murine
US-10-996-316-139

Query Match      70.8%; Score 17; DB 18; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
   | |
Db 4 FSAAW 8

RESULT 17
US-10-072-419-37
; Sequence 37, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072.419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanessa cardui
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US-10-072-419-37

Query Match 70.8%; Score 17; DB 14; Length 11;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FTSSW 8

RESULT 18

US-10-869-768-37
; Sequence 37, Application US/10859768
; Publication No. US20040224896A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-869-768-37

Query Match 70.8%; Score 17; DB 16; Length 11;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FTSSW 8

RESULT 19

US-10-354-240-87
; Sequence 87, Application US/10354240
; Publication No. US20030185847A1
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Diseases
; FILE REFERENCE: SPO-103D1
; CURRENT APPLICATION NUMBER: US/10/354,240
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 09/142,524
; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)_(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4
US-10-354-240-87

Query Match 70.8%; Score 17; DB 14; Length 15;
Best Local Similarity 40.0%; Pred. No. 8e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 9 FSTAW 13

RESULT 20

US-10-354-240-88
; Sequence 88, Application US/10354240
; Publication No. US20030185847A1
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Diseases
; FILE REFERENCE: SPO-103D1
; CURRENT APPLICATION NUMBER: US/10/354,240
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 09/142,524
; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)_(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5
US-10-354-240-88

Query Match 70.8%; Score 17; DB 14; Length 15;
Best Local Similarity 40.0%; Pred. No. 8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FSTAW 8

RESULT 21

US-09-963-339-10
; Sequence 10, Application US/09963339
; Publication No. US20030049700A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN
; TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-090001
; CURRENT APPLICATION NUMBER: US/09/963,339
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/235,049
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-339-10

Query Match 70.8%; Score 17; DB 10; Length 19;
Best Local Similarity 40.0%; Pred. No. 9.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |

Db 4 FSATW 8

RESULT 22

US-10-145-586-59

Sequence 59, Application US/10145586

Publication No. US20030138890A1

GENERAL INFORMATION:

APPLICANT: Alexandra Glucksmann, Maria

APPLICANT: Silos-Santiago, Inmaculada

APPLICANT: M. Galvin, Katherine

APPLICANT: Weich, Nadine

APPLICANT: Curtis, Rory A.J.

APPLICANT: Bandaru, Rajasekhar

APPLICANT: Kapeller-Libermann, Rosana

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,

TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH

TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER

FILE REFERENCE: 10448-188001

CURRENT APPLICATION NUMBER: US/10/145.586

Prior Filing Date: 2002-05-14

Number of SEQ ID NOS: 95

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 59

LENGTH: 19

TYPE: PRT

ORGANISM: Homo sapiens

US-10-145-586-59

Query Match 70.8%; Score 17; DB 14; Length 19;

Best Local Similarity 40.0%; Pred. No. 9.3e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

Db 4 FSATW 8

RESULT 23

US-10-931-260-265

Sequence 265, Application US/10931260

Publication No. US20050152927A1

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;

Pollock, Joanne;

Bond, Julian F.;

Garman, Richard D.;

Kuo, Mei-Chang;

Powers, Stephen P.;

Exley, Mark A.;

Chen, Xian;

Shaked, Ze'ev

TITLE OF INVENTION: Allergenic Proteins And Peptides From

Japanese Cedar Pollen

NUMBER OF SEQUENCES: 283

CORRESPONDENCE ADDRESS:

ADDRESSEE: Labive & Cockfield, LLP

STREET: 28 State St

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/931.260

FILING DATE: 30-Aug-2004

CLASSIFICATION: <Unknown>

Prior Application Data:

US-09-214-371-11.max.rapb

APPLICATION NUMBER: US/09/240.203

FILING DATE: 29-Jan-1999

APPLICATION NUMBER: 08/467,023

FILING DATE: 1995-JUN-06

APPLICATION NUMBER: 08/350,225

FILING DATE: 1994-DEC-06

APPLICATION NUMBER: 08/226,248

FILING DATE: 1994-APR-08

APPLICATION NUMBER: PCT/US93/00139

FILING DATE: 1993-JAN-15

APPLICATION NUMBER: 07/938,990

FILING DATE: 1992-SEP-01

APPLICATION NUMBER: 07/730,452

FILING DATE: 1991-JUL-15

APPLICATION NUMBER: 07/729,134

FILING DATE: 1991-JUL-12

APPLICATION NUMBER: 07/975,179

FILING DATE: 1992-NOV-12

APPLICATION NUMBER: PCT/US92/05661

FILING DATE: 1992-JUL-10

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragoutas, Esq.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-10-931-260-265

Query Match 70.8%; Score 17; DB 18; Length 20;

Best Local Similarity 40.0%; Pred. No. 9.6e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

Db 12 FSTAW 16

RESULT 24

US-10-190-082-36

Sequence 36, Application US/10190082

Publication No. US20030148264A1

GENERAL INFORMATION:

APPLICANT: Lasky, Lawrence A.

APPLICANT: Sidhu, Sachdev S.

APPLICANT: Held, Heike A.

TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS

FILE REFERENCE: P1905R1

CURRENT APPLICATION NUMBER: US/10/190.082

CURRENT FILING DATE: 2002-07-03

Prior Application Number: US 60/303,634

Prior Filing Date: 2001-07-06

NUMBER OF SEQ ID NOS: 683

SEQ ID NO 36

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-190-082-36

Query Match 66.7%; Score 16; DB 14; Length 6;

Best Local Similarity 40.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
Db 1 FSDTW 5

RESULT 25

US-09-774-639-284
; Sequence 284, Application US/09774639
; Publication No. US2003000355A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-284

Query Match 66.7%; Score 16; DB 10; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
Db 2 FGTSW 5

RESULT 26

US-09-969-730-267
; Sequence 267, Application US/09969730
; Publication No. US2003005443A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2
; CURRENT APPLICATION NUMBER: US/09/969,730
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,367
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,365
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,731
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,557
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,563
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/055,970

; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,986
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,311
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,808
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,803
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,809
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,806
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,310
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,798
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,309
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,312
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,807
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,386
; PRIOR FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 267
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-730-267

Query Match 66.7%; Score 16; DB 10; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
Db 2 FGTSW 6

RESULT 27

US-10-046-922-48
; Sequence 48, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 7
; TYPE: PRT
; ORGANISM: peptide
US-10-046-922-48

Query Match 66.7%; Score 16; DB 13; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
Db 3 FEAAW 7

RESULT 28

US-10-621-363-267
; Sequence 267, Application US/10621363
; Publication No. US20040023283A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/621.363
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 267
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-621-363-267

Query Match 66.7%; Score 16; DB 15; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 2 FGTSW 6

RESULT 29

US-10-072-419-4
; Sequence 4, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072.419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Schistocerca gregaria
US-10-072-419-4

Query Match 66.7%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |

Db

4 FSTGW 8

RESULT 30

US-10-072-419-11
; Sequence 11, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072.419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Locusta migratoria
US-10-072-419-11

Query Match 66.7%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 4 FSAGW 8

RESULT 31

US-10-072-419-15
; Sequence 15, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072.419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Phymateus leprosus
US-10-072-419-15

Query Match 66.7%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 4 FSTGW 8

RESULT 32

US-10-072-419-24
; Sequence 24, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072.419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24

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; LENGTH: 8
; TYPE: PRT
; ORGANISM: Gryllobates sigillatus
US-10-072-419-24

Query Match      66.7%  Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
      | |
Db      4 FSTGW 8

RESULT 33
US-10-072-419-25
; Sequence 25, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Libanasidus vittatus
US-10-072-419-25

Query Match      66.7%  Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
      | |
Db      4 FSTGW 8

RESULT 34
US-10-072-419-30
; Sequence 30, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Onitis sp.
US-10-072-419-30

Query Match      66.7%  Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
      | |
Db      4 FSTGW 8

RESULT 35
US-10-367-580-260
; Sequence 260, Application US/10367580
; Publication No. US20040071720A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461061
; CURRENT APPLICATION NUMBER: US/10/367,580
; CURRENT FILING DATE: 2003-02-14
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 260
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-580-260

Query Match      66.7%  Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
      | |
Db      2 FLSSW 6

RESULT 36
US-10-367-580-264
; Sequence 264, Application US/10367580
; Publication No. US20040071720A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461061
; CURRENT APPLICATION NUMBER: US/10/367,580
; CURRENT FILING DATE: 2003-02-14
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 264
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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```
; OTHER INFORMATION: synthetic peptide
US-10-367-593-264

Query Match      66.7%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXW 6
Db      2 FLSSW 6

RESULT 37
US-10-367-593-260
; Sequence 260, Application US/10367593
; Publication No. US20040071722A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 260
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-593-260

Query Match      66.7%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXW 6
Db      2 FLSSW 6

RESULT 38
US-10-367-593-264
; Sequence 264, Application US/10367593
; Publication No. US20040071722A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 260
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-593-260

Query Match      66.7%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXW 6
Db      2 FLSSW 6

RESULT 39
US-10-367-594-260
; Sequence 260, Application US/10367594
; Publication No. US20040071722A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461041
; CURRENT APPLICATION NUMBER: US/10/367,594
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/680,806
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 260
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-594-260

Query Match      66.7%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXW 6
Db      2 FLSSW 6

RESULT 40
US-10-367-594-264
; Sequence 264, Application US/10367594
; Publication No. US20040071722A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
```

```

; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461041
; CURRENT APPLICATION NUMBER: US/10/367,594
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/680,806
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 264
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-594-264

Query Match          66.7% Score 16; DB 15; Length 8;
Best Local Similarity 40.0% Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
      |
Db      2 FLSSW 6

Search completed: October 18, 2005, 16:17:19
Job time : 116.412 secs

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GenCore version 5.1.6
Copyright: (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2005, 15:44:54 ; Search time 24.3529 Seconds
(without alignments)
35.558 Million cell updates/sec

Title: US-09-214-371-11
Perfect score: 24
Sequence: 1 XFXXXXXXX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	70.8	9	2	A24244
2	16	66.7	8	2	A28004
3	16	66.7	10	2	A31571
4	15	62.5	8	2	S10596
5	15	62.5	9	2	D57444
6	15	62.5	10	2	T17063
7	15	62.5	10	2	T12325
8	15	62.5	10	2	S53789
9	15	62.5	15	2	PH1613
10	15	62.5	17	2	A34704
11	15	62.5	20	2	S77981
12	15	62.5	20	2	PN0171
13	15	62.5	20	2	PH1380
14	14	58.3	8	2	A33995
15	14	58.3	8	2	A4960
16	14	58.3	8	2	B4960
17	14	58.3	8	2	A58620
18	14	58.3	8	2	S11545
19	14	58.3	8	2	S55310
20	14	58.3	8	2	A61348
21	14	58.3	8	2	S08995
22	14	58.3	8	2	S08996
23	14	58.3	8	2	A49823
24	14	58.3	8	2	B49823
25	14	58.3	8	2	A43976
26	14	58.3	8	2	B43976
27	14	58.3	8	2	A05169
28	14	58.3	10	2	B33995
29	14	58.3	10	2	S08997

30	14	58.3	10	2	A60421	hypertrehalosemic
31	14	58.3	10	2	S08998	hypertrehalosemic
32	14	58.3	10	2	A26381	hypertrehalosemic
33	14	58.3	10	2	JC1416	hypertrehalosemic
34	14	58.3	10	2	S09118	hypertrehalosemic
35	14	58.3	10	2	C39191	hypothetical prote
36	14	58.3	10	2	PT0332	Ig heavy chain CRD
37	14	58.3	10	2	T17066	cytochrome-c oxida
38	14	58.3	10	2	T17069	cytochrome-c oxida
39	14	58.3	10	2	T12329	cytochrome-c oxida
40	14	58.3	12	2	PT0274	Ig heavy chain CRD
41	14	58.3	12	2	PH1324	Ig heavy chain DJ
42	14	58.3	13	2	PC4391	cysteine proteinas
43	14	58.3	16	2	C37290	homeotic protein G
44	14	58.3	19	2	S32675	nitrogen fixation
45	14	58.3	20	2	PC1240	calcium-binding pr
46	13	54.2	9	2	PT0288	Ig heavy chain CRD
47	13	54.2	9	2	T46023	growth hormone rec
48	13	54.2	11	2	C53652	rhIR protein - pse
49	13	54.2	11	2	PT0302	Ig heavy chain CRD
50	12	50.0	8	2	T13818	cytochrome oxidase
51	12	50.0	10	1	RHLMGS	gonadoliberin - se
52	12	50.0	11	2	S05002	corazonin - Americ
53	12	50.0	18	2	S39009	oviductin - golden
54	11	45.8	3	3	F37196	bradykinin-potent
55	11	45.8	4	2	A34626	RPCH-related neuro
56	11	45.8	4	2	B53284	T-cell receptor be
57	11	45.8	4	2	PT0661	T-cell receptor be
58	11	45.8	5	2	A32516	cholecystokinin-5
59	11	45.8	5	2	A60803	neuropeptide - sea
60	11	45.8	5	2	JH0253	gut pentapeptide -
61	11	45.8	5	2	PT0281	Ig heavy chain CRD
62	11	45.8	5	2	PT0308	Ig heavy chain CRD
63	11	45.8	5	2	PT0729	T-cell receptor be
64	11	45.8	5	2	PT0580	T-cell receptor be
65	11	45.8	5	2	G37196	bradykinin-potent
66	11	45.8	6	2	S66195	alcohol dehydrogen
67	11	45.8	6	2	B34835	dnaA protein - pse
68	11	45.8	6	2	A31263	dihydrofolate redu
69	11	45.8	6	2	B31263	dihydrofolate redu
70	11	45.8	6	2	B35640	cerebellar degener
71	11	45.8	6	2	PT0629	T-cell receptor be
72	11	45.8	6	2	PT0532	T-cell receptor be
73	11	45.8	6	2	PT0519	T-cell receptor be
74	11	45.8	6	2	PT0637	T-cell receptor be
75	11	45.8	6	2	PT0641	T-cell receptor be
76	11	45.8	6	2	PT0726	T-cell receptor be
77	11	45.8	6	2	F41946	T-cell receptor ga
78	11	45.8	6	2	PD0028	T-cell receptor ga
79	11	45.8	6	2	A61068	pev-kinin 2 - pena
80	11	45.8	6	4	I79564	locustakinin - mig
81	11	45.8	7	2	S21230	hypothetical TCU3
82	11	45.8	7	2	S09652	dermorphin (trp-4,
83	11	45.8	7	2	PQ0727	hypothetical prote
84	11	45.8	7	2	E48394	H2 class I protein
85	11	45.8	7	2	PH1602	glycoprotein compo
86	11	45.8	7	2	PT0536	Ig H chain V-D-J r
87	11	45.8	7	2	PT0628	T-cell receptor be
88	11	45.8	7	2	PT0642	T-cell receptor be
89	11	45.8	7	2	PT0722	T-cell receptor be
90	11	45.8	7	2	PT0688	T-cell receptor be
91	11	45.8	7	2	PT0586	T-cell receptor be
92	11	45.8	7	2	PT0728	T-cell receptor be
93	11	45.8	7	2	PK0008	glucuronosyltransf
94	11	45.8	7	2	B48394	major fat-globule
95	11	45.8	7	2	PD0029	pev-kinin 1 - pena
96	11	45.8	7	2	PN0649	pullulanase (EC 3.
97	11	45.8	7	2	S57274	triacylglycerol li
98	11	45.8	7	2	S33244	neuromodulatory pe
99	11	45.8	7	2	S33245	neuromodulatory pe
100	11	45.8	7	2	S33246	neuromodulatory pe
101	11	45.8	7	2	S33567	tubulin beta-3 cha
102	11	45.8	7	2	A58512	venom heptapeptide

103	11	45.8	7	2	A61081	tryptophyllin, bas	176	11	45.8	10	2	B38887	T-cell receptor ga
104	11	45.8	7	4	I55382	hypothetical pepti	177	11	45.8	10	2	PH0916	T-cell receptor be
105	11	45.8	7	4	A58725	viotoxin - destro	178	11	45.8	10	2	PH0923	T-cell receptor be
106	11	45.8	8	2	S15422	adipokinetic hormo	179	11	45.8	10	2	A40753	aldenhyde ferredoxi
107	11	45.8	8	2	A58641	adipokinetic hormo	180	11	45.8	10	2	A59272	peptida-N4 - (N-acet
108	11	45.8	8	2	PQ0012	cholecystokinin -	181	11	45.8	10	2	S66248	processing enzyme,
109	11	45.8	8	2	A43001	cholecystokinin -	182	11	45.8	10	2	A27617	triose-phosphate i
110	11	45.8	8	2	PT0724	T-cell receptor be	183	11	45.8	10	2	A46030	gonadoliberin I -
111	11	45.8	8	2	A38887	T-cell receptor ga	184	11	45.8	10	2	A21114	gonadoliberin - ch
112	11	45.8	8	2	A59495	Vesicle associated	185	11	45.8	10	2	B37196	bradykinin-potentl
113	11	45.8	8	2	S19288	acylase - Kluuvera	186	11	45.8	10	2	H37196	bradykinin-potentl
114	11	45.8	8	2	A39308	glycine reductase	187	11	45.8	10	2	F33932	Ig mu chain J regi
115	11	45.8	8	2	C61512	variant surface gl	188	11	45.8	10	2	T17054	cytochrome-c oxida
116	11	45.8	8	2	D61512	variant surface gl	189	11	45.8	10	2	T17075	cytochrome-c oxida
117	11	45.8	8	2	JS0315	leucokinin V - Mad	190	11	45.8	10	2	T13976	cytochrome-c oxida
118	11	45.8	8	2	JS0316	leucokinin VI - Ma	191	11	45.8	10	2	T17057	cytochrome-c oxida
119	11	45.8	8	2	JS0317	leucokinin VII - M	192	11	45.8	10	2	T12303	cytochrome-c oxida
120	11	45.8	8	2	JS0318	leucokinin VIII -	193	11	45.8	10	2	T14019	cytochrome-c oxida
121	11	45.8	8	2	S21663	neuropeptide - flo	194	11	45.8	10	2	T17060	cytochrome-c oxida
122	11	45.8	8	2	A41117	acetylcholinestera	195	11	45.8	10	2	T14043	cytochrome-c oxida
123	11	45.8	8	2	A31570	angiotensin-conver	196	11	45.8	10	2	T14054	cytochrome-c oxida
124	11	45.8	9	1	AKLQIM	locustamyoynhibiti	197	11	45.8	10	2	T12308	cytochrome-c oxida
125	11	45.8	9	1	S07205	litorin 2-Glu - Au	198	11	45.8	10	2	T17072	cytochrome-c oxida
126	11	45.8	9	2	S07204	litorin I - Austra	199	11	45.8	10	2	T12312	cytochrome-c oxida
127	11	45.8	9	2	S07241	litorin - Rohde's	200	11	45.8	10	2	T12316	cytochrome-c oxida
128	11	45.8	9	2	A61357	phyllocaerulein -	201	11	45.8	10	2	T14212	cytochrome-c oxida
129	11	45.8	9	2	JS0302	xenopsin-related p	202	11	45.8	10	2	T12321	cytochrome-c oxida
130	11	45.8	9	2	A60320	xenopsin-related p	203	11	45.8	10	2	T14215	cytochrome-c oxida
131	11	45.8	9	2	PT0231	Ig heavy chain CDR	204	11	45.8	10	2	T14223	cytochrome-c oxida
132	11	45.8	9	2	PT0270	Ig heavy chain CDR	205	11	45.8	10	2	T14219	cytochrome-c oxida
133	11	45.8	9	2	PT0272	Ig heavy chain CDR	206	11	45.8	10	2	A59173	cytochrome-c oxida
134	11	45.8	9	2	PT0299	Ig heavy chain CDR	207	11	45.8	10	2	S39030	lysyl-bradykinin -
135	11	45.8	9	2	PT0324	Ig heavy chain CDR	208	11	45.8	11	1	LFTWWE	probable trpEG lea
136	11	45.8	9	2	PT0634	Ig heavy chain CDR	209	11	45.8	11	2	B49164	alcohol dehydrogen
137	11	45.8	9	2	PT0562	T-cell receptor be	210	11	45.8	11	2	S66196	chromogranin-B - r
138	11	45.8	9	2	S58350	gene c-mpl protein	211	11	45.8	11	2	S32575	ribosomal protein
139	11	45.8	9	2	S78426	52.5K protein - sp	212	11	45.8	11	2	H54346	pyruvate synthase
140	11	45.8	9	2	S56004	Glucan 1,3-beta-gl	213	11	45.8	11	2	PT0249	Ig heavy chain CRD
141	11	45.8	9	2	A43848	cell surface adhes	214	11	45.8	11	2	PH1343	Ig heavy chain DJ
142	11	45.8	9	2	A57444	neuropeptide Grb-A	215	11	45.8	11	2	S68549	spermatidhesin AQN-3
143	11	45.8	9	2	B57444	neuropeptide Grb-A	216	11	45.8	11	2	A33571	folliculathesin - bovi
144	11	45.8	9	2	C57444	neuropeptide Grb-A	217	11	45.8	11	2	D41946	T-cell receptor ga
145	11	45.8	9	2	A37027	macrophage chemota	218	11	45.8	11	2	B41946	T-cell receptor ga
146	11	45.8	9	2	QDRB	delta sleep-induci	219	11	45.8	11	2	C38887	T-cell receptor ga
147	11	45.8	9	2	A60522	sperm-activating p	220	11	45.8	11	2	A41946	T-cell receptor ga
148	11	45.8	10	1	XASNPC	angiotensin-conver	221	11	45.8	11	2	A49037	TcR gamma V-J regi
149	11	45.8	10	1	XAVI6B	angiotensin-conver	222	11	45.8	11	2	B49037	TcR gamma V-J regi
150	11	45.8	10	1	RHPGG	gonadoliberin - pi	223	11	45.8	11	2	C49037	napin small chain
151	11	45.8	10	1	RHSHG	gonadoliberin - sh	224	11	45.8	11	2	S70338	protein-tyrosine k
152	11	45.8	10	1	A61126	gonadoliberin - sp	225	11	45.8	11	2	C59151	hypothetical 1.5K
153	11	45.8	10	1	RHAQ1	gonadoliberin I -	226	11	45.8	11	2	JQ2307	hypothetical 1.5K
154	11	45.8	10	1	RHAQ2	gonadoliberin II -	227	11	45.8	11	2	JQ2317	hypothetical 1.5K
155	11	45.8	10	2	B71868	glutathione transf	228	11	45.8	11	2	PQ0731	unidentified 5.7/3
156	11	45.8	10	2	B46030	gonadoliberin II -	229	11	45.8	11	2	S45698	gamma-MSH-like pro
157	11	45.8	10	2	JC1367	thyroliberin poten	230	11	45.8	11	2	A34662	acharins cardio-ex
158	11	45.8	10	2	A60647	neuromedin C - bov	231	11	45.8	11	2	A59146	conotoxin ausb - c
159	11	45.8	10	2	PQ0177	neuromedin C - lau	232	11	45.8	11	2	B59146	conotoxin-c oxida
160	11	45.8	10	2	A61337	caerulein - frog (233	11	45.8	11	2	T12264	cytochrome-c oxida
161	11	45.8	10	2	A13687	caerulein-like pep	234	11	45.8	11	2	T12253	cytochrome-c oxida
162	11	45.8	10	2	S59625	beta-galactosidase	235	11	45.8	11	2	T12244	cytochrome-c oxida
163	11	45.8	10	2	PQ0753	beta-fructofuranos	236	11	45.8	11	2	T12248	cytochrome-c oxida
164	11	45.8	10	2	S63696	DNA polymerase - Y	237	11	45.8	11	2	T17081	cytochrome-c oxida
165	11	45.8	10	2	A49187	gonadotropin-relea	238	11	45.8	11	2	T17078	cytochrome-c oxida
166	11	45.8	10	2	A35556	hypothetical prote	239	11	45.8	11	2	UOGM2	cytochrome-c oxida
167	11	45.8	10	2	PT0245	Ig heavy chain CRD	240	11	45.8	12	1	A53709	alpha-conotoxin Im
168	11	45.8	10	2	PT0249	Ig heavy chain CRD	241	11	45.8	12	1	A29169	phospholipase A2 (
169	11	45.8	10	2	PH1344	Ig heavy chain DJ	242	11	45.8	12	2	I64829	gene HEXA protein
170	11	45.8	10	2	S23370	T-cell receptor al	243	11	45.8	12	2	JS0423	urotensin II-A pep
171	11	45.8	10	2	E49033	T-cell receptor ga	244	11	45.8	12	2	S42765	urotensin II - tel
172	11	45.8	10	2	F49033	T-cell receptor ga	245	11	45.8	12	2	PH1675	Ig heavy chain V r
173	11	45.8	10	2	E41946	T-cell receptor ga	246	11	45.8	12	2	S26548	T-cell receptor be
174	11	45.8	10	2	E41946	T-cell receptor ga	247	11	45.8	12	2	S26548	T-cell receptor be
175	11	45.8	10	2	C41946	T-cell receptor ga	248	11	45.8	12	2	S26553	T-cell receptor be

249	11	45.8	12	2	A26093	microbial collagen	322	11	45.8	14	2	S03530	Ig heavy chain J r
250	11	45.8	12	2	G64003	hypothetical prote	323	11	45.8	14	2	I54284	Cl-inhibitor - hum
251	11	45.8	12	2	S69123	proton-translocati	324	11	45.8	14	2	PT0223	Ig heavy chain CDR
252	11	45.8	12	2	A40763	sucrose-6-phosphat	325	11	45.8	14	2	PH1348	Ig heavy chain DJ
253	11	45.8	12	2	PH1308	Ig heavy chain DJ	326	11	45.8	14	2	PH1327	Ig heavy chain DJ
254	11	45.8	12	2	S43957	Ig mu chain V regi	327	11	45.8	14	2	PH1356	Ig heavy chain DJ
255	11	45.8	12	2	A49033	T-cell receptor de	328	11	45.8	14	2	PH1332	Ig heavy chain DJ
256	11	45.8	12	2	B49033	T-cell receptor de	329	11	45.8	14	2	PH1332	Ig heavy chain DJ
257	11	45.8	12	2	S25039	Ig heavy chain V r	330	11	45.8	14	2	PH1757	T cell receptor al
258	11	45.8	12	2	H41946	T-cell receptor ga	331	11	45.8	14	2	PH1758	T cell receptor al
259	11	45.8	12	2	A42324	cytochrome P450c27	332	11	45.8	14	2	PH1759	T cell receptor al
260	11	45.8	12	2	I57678	gene RPLP-A protei	333	11	45.8	14	2	PH1766	T cell receptor al
261	11	45.8	12	2	I41235	glutamine-tRNA lig	334	11	45.8	14	2	PH1767	T cell receptor al
262	11	45.8	12	2	J50424	urotensin II-B pep	335	11	45.8	14	2	PH1768	T cell receptor al
263	11	45.8	12	2	A49637	MHC class II histo	336	11	45.8	14	2	PH1769	T cell receptor al
264	11	45.8	12	2	I77529	estrogen receptor	337	11	45.8	14	2	S57572	T cell receptor V-
265	11	45.8	12	2	S43170	kinesin light chai	338	11	45.8	14	2	S58426	spermadhesin AWN h
266	11	45.8	12	2	PN0046	ATP synthase D cha	339	11	45.8	14	2	PH1625	Ig H chain V-D-J r
267	11	45.8	12	2	I58273	thyroglobulin - ra	340	11	45.8	14	2	PH1626	Ig H chain V-D-J r
268	11	45.8	12	2	P00776	NADH2 dehydrogenas	341	11	45.8	14	2	PH1627	Ig H chain V-D-J r
269	11	45.8	13	1	XAVI9B	angiotensin-conver	342	11	45.8	14	2	PH1594	Ig H chain V-D-J r
270	11	45.8	13	1	MTCMAD	melanotropin alpha	343	11	45.8	14	2	PH0801	T-cell receptor al
271	11	45.8	13	1	MTHOAD	melanotropin alpha	344	11	45.8	14	2	PH0747	T-cell receptor be
272	11	45.8	13	2	PQ0445	urotensin II - lau	345	11	45.8	14	2	P49037	Tcr delta chain V-
273	11	45.8	13	2	PH1676	Ig heavy chain V r	346	11	45.8	14	2	B44854	L-2,4-diaminobuty
274	11	45.8	13	2	B28810	glutathione transf	347	11	45.8	14	2	PT0026	calotropin DI - mu
275	11	45.8	13	2	PT0293	Ig heavy chain CRD	348	11	45.8	14	2	S33801	chaperone, TCPI-re
276	11	45.8	13	2	PT0304	Ig heavy chain CRD	349	11	45.8	14	2	S33802	chaperone, TCPI-re
277	11	45.8	13	2	S57567	T cell receptor V-	350	11	45.8	14	2	PT0029	karatsasin - karata
278	11	45.8	13	2	S23372	T-cell receptor al	351	11	45.8	14	2	S14336	mastoparan B - hor
279	11	45.8	13	2	PH0138	T-cell receptor be	352	11	45.8	14	2	A47421	leukotriene B-4 12
280	11	45.8	13	2	S61798	T-cell-specific tr	353	11	45.8	14	2	S68095	calcium-binding pr
281	11	45.8	13	2	B56864	dipeptidyl-peptida	354	11	45.8	14	2	S39931	s-allele-associate
282	11	45.8	13	2	B25448	Ig kappa-1 chain,	355	11	45.8	14	2	A44515	Trp EG leader pept
283	11	45.8	13	2	PH1636	Ig H chain V-D-J r	356	11	45.8	14	2	JH0328	probursin tetradec
284	11	45.8	13	2	PH1620	Ig H chain V-D-J r	357	11	45.8	14	2	B26997	unspecific monooxy
285	11	45.8	13	2	G37286	Ig heavy chain C r	358	11	45.8	15	2	A26997	Sfil-glycoprotein
286	11	45.8	13	2	D37267	Ig heavy chain C r	359	11	45.8	15	2	PQ0195	stylar glycoprotei
287	11	45.8	13	2	B26406	Ig kappa chain J r	360	11	45.8	15	2	PQ0174	stylar glycoprotei
288	11	45.8	13	2	PH0928	T-cell receptor be	361	11	45.8	15	2	PQ0175	glucan 1,4-alpha-g
289	11	45.8	13	2	A47630	Ig kappa chain J r	362	11	45.8	15	2	S21202	alpha-glucosidase
290	11	45.8	13	2	I51905	collecting duct wa	363	11	45.8	15	2	S21240	oligo-1,6-glucosid
291	11	45.8	13	2	S54344	glyceraldehyde-3-p	364	11	45.8	15	2	S21241	leukocyte elastase
292	11	45.8	13	2	A59491	epithelial dog all	365	11	45.8	15	2	S24159	cystatin CI-4a - m
293	11	45.8	13	2	I54984	aeg-46.5 protein -	366	11	45.8	15	2	PQ0232	Ig heavy chain DJ
294	11	45.8	13	2	PC2369	unidentified 85K p	367	11	45.8	15	2	PH1319	Ig heavy chain V r
295	11	45.8	13	2	S60046	early nodulin 40 -	368	11	45.8	15	2	S26791	Ig heavy chain J r
296	11	45.8	13	2	A61514	glutathione transf	369	11	45.8	15	2	P50382	proteinase - Therm
297	11	45.8	13	2	A60379	factor X activator	370	11	45.8	15	2	S39012	hypothetical prote
298	11	45.8	13	2	S32551	glutathione transf	371	11	45.8	15	2	T46625	hypothetical prote
299	11	45.8	13	2	S66558	serine proteinase	372	11	45.8	15	2	S08209	self-incompatibili
300	11	45.8	13	2	A86126	hypothetical prote	373	11	45.8	15	2	PQ0750	gamma 2 gliadin -
301	11	45.8	13	2	A60409	bombesin-like pept	374	11	45.8	15	2	B56891	Ig heavy chain J r
302	11	45.8	13	2	A05174	cryptophyllin-13 -	375	11	45.8	15	2	S10388	Ig heavy chain J r
303	11	45.8	14	1	B5TD	bombesin - fire-be	376	11	45.8	15	2	S10386	Fc gamma receptor
304	11	45.8	14	1	QMVHXX	mastoparan X - hor	377	11	45.8	15	2	A47628	Ig heavy chain DJ
305	11	45.8	14	1	QMWAPP	polistes mastopara	378	11	45.8	15	2	PH1365	Ig heavy chain DJ
306	11	45.8	14	1	LFEBWC	trp operon leader	379	11	45.8	15	2	PH1366	Ig heavy chain DJ
307	11	45.8	14	1	LFEBWT	trp operon leader	380	11	45.8	15	2	PH1342	Ig heavy chain DJ
308	11	45.8	14	1	LFECW	trp operon leader	381	11	45.8	15	2	PH1318	Ig heavy chain DJ
309	11	45.8	14	2	PC2373	probable IMP dehyd	382	11	45.8	15	2	PH1320	Ig mu chain V regi
310	11	45.8	14	2	A60622	somatostatin - spo	383	11	45.8	15	2	S43956	T cell receptor al
311	11	45.8	14	2	A60840	somatostatin I - E	384	11	45.8	15	2	PH1762	T cell receptor al
312	11	45.8	14	2	C60414	somatostatin - sli	385	11	45.8	15	2	PH1788	T-cell receptor be
313	11	45.8	14	2	B60842	somatostatin I - C	386	11	45.8	15	2	G49655	7 alpha-hydroxy-4-
314	11	45.8	14	2	S00172	somatostatin I - s	387	11	45.8	15	2	PQ0073	Ig H chain V-D-J r
315	11	45.8	14	2	PH1677	Ig heavy chain V r	388	11	45.8	15	2	A45103	Ig H chain V-D-J r
316	11	45.8	14	2	PH1705	Ig heavy chain V r	389	11	45.8	15	2	PH1590	Ig H chain V-D-J r
317	11	45.8	14	2	PT0077	proteochondroitin c	390	11	45.8	15	2	PH1590	Ig H chain V-D-J r
318	11	45.8	14	2	B90858	trp operon leader	391	11	45.8	15	2	PH1612	T-cell receptor al
319	11	45.8	14	2	B85761	trp operon leader	392	11	45.8	15	2	PH0782	Tcr delta chain V-
320	11	45.8	14	2	A35105	hypothetical prote	393	11	45.8	15	2	E49037	complement factor
321	11	45.8	14	2	PC1215	homeotic protein E	394	11	45.8	15	2	PL0109	

541 11 45.8 19 2 S02269 glycogen(starch) s
 542 11 45.8 19 2 B56613 virion morphogenes
 543 11 45.8 19 2 S63489 dissimilatory sulf
 544 11 45.8 19 2 T50329 wd-repeat protein
 545 11 45.8 19 2 S60110 hypothetical prote
 546 11 45.8 19 2 PH1352 Ig heavy chain DJ
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 548 11 45.8 19 2 PH1339 Ig heavy chain DJ
 549 11 45.8 19 2 PH1315 Ig heavy chain DJ
 550 11 45.8 19 2 PH1330 Ig heavy chain DJ
 551 11 45.8 19 2 S57515 T cell receptor be
 552 11 45.8 19 2 S57516 T cell receptor be
 553 11 45.8 19 2 S03519 T-cell receptor ga
 554 11 45.8 19 2 I46654 T-cell receptor de
 555 11 45.8 19 2 PH1624 Ig H chain V-D-J r
 556 11 45.8 19 2 PH0793 T-cell receptor al
 557 11 45.8 19 2 I49037 TcR delta chain V-
 558 11 45.8 19 2 B46592 lactase-phlorizin
 559 11 45.8 19 2 A48354 nonstructural prot
 560 11 45.8 19 2 I40063 shikimate 5-dehydr
 561 11 45.8 19 2 A44854 L-2,4-diaminobuty
 562 11 45.8 19 2 S29212 protein C - oat (f
 563 11 45.8 19 2 S19532 globin - polychaet
 564 11 45.8 19 2 S19613 tachyplesin I prec
 565 11 45.8 19 2 JX0124 globin - polychaet
 566 11 45.8 19 2 S12721 gene hMLH1 protein
 567 11 45.8 19 2 S12268 Qa-2 antigen - mou
 568 11 45.8 19 2 A60505 hemoglobin Ci beta
 569 11 45.8 19 2 A58700 actagardine [valid
 570 11 45.8 19 4 I54264 rhodopsin single b
 571 11 45.8 20 2 A23739 cytochrome P450 MU
 572 11 45.8 20 2 S21176 testosterone 6beta
 573 11 45.8 20 2 A60728 cytochrome P450 3A
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 582 11 45.8 20 2 PH0110 style glycoprotein
 583 11 45.8 20 2 PC2347 base nonspecific a
 584 11 45.8 20 2 S33787 pancreatic elastas
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 586 11 45.8 20 2 B61333 chymotrypsin (EC 3
 587 11 45.8 20 2 I49423 cytotoxic T-lympho
 588 11 45.8 20 2 S46205 comosain (EC 3.4.2
 589 11 45.8 20 2 S46204 ananain (EC 3.4.22
 590 11 45.8 20 2 C54052 phosphoribosyl-AMP
 591 11 45.8 20 2 A37111 ribulose-bisphosph
 592 11 45.8 20 2 C49164 chromogranin-B - r
 593 11 45.8 20 2 P70248 Ig heavy chain CDR
 594 11 45.8 20 2 F49048 T-cell receptor be
 595 11 45.8 20 2 A49048 T-cell receptor be
 596 11 45.8 20 2 PL0192 Ig lambda 2 chain
 597 11 45.8 20 2 S39049 cytotoxin-binding
 598 11 45.8 20 2 B33761 actin - Acanthamo
 599 11 45.8 20 2 A05313 apolipoprotein A-I
 600 11 45.8 20 2 A36045 thrombospondin hom
 601 11 45.8 20 2 S03335 photosystem II pho
 602 11 45.8 20 2 PH0003 chlorophyll a/b-bi
 603 11 45.8 20 2 S04988 gag core shell pro
 604 11 45.8 20 2 A44773 pollen allergen I
 605 11 45.8 20 2 A60372 pollen allergen Po
 606 11 45.8 20 2 D37396 pollen allergen Fe
 607 11 45.8 20 2 I64036 pollen allergen re
 608 11 45.8 20 2 T46626 hypothetical prote
 609 11 45.8 20 2 S16202 pyroline-5-carbox
 610 11 45.8 20 2 D25507 proteinase inhibi
 611 11 45.8 20 2 PC1152 equinatoxin 1D - s
 612 11 45.8 20 2 S10876 hypothetical prote
 613 11 45.8 20 2 S58382 hypothetical prote

614 11 45.8 20 2 PH1358 Ig heavy chain DJ
 615 11 45.8 20 2 PH1341 Ig heavy chain DJ
 616 11 45.8 20 2 PH1326 Ig heavy chain DJ
 617 11 45.8 20 2 PC2248 lambda 112 protein
 618 11 45.8 20 2 S60350 kallikrein, pankre
 619 11 45.8 20 2 S15861 estrogen receptor
 620 11 45.8 20 2 A38699 i-phosphatidylinos
 621 11 45.8 20 2 PQ0071 T-cell receptor be
 622 11 45.8 20 2 S56756 link protein - rat
 623 11 45.8 20 2 S68341 procatepsin L - g
 624 11 45.8 20 2 S66222 defensin: AMP2 - Da
 625 11 45.8 20 2 C56894 intracrystalline c
 626 11 45.8 20 2 D84716 hypothetical prote
 627 11 45.8 20 2 T44453 acetyl-CoA synthet
 628 11 45.8 20 2 A44927 major outer membra
 629 11 45.8 20 2 S45637 oxidoreductase - p
 630 11 45.8 20 2 S63490 dissimilatory sulf
 631 11 45.8 20 2 A40451 dormancy-related p
 632 11 45.8 20 2 S29636 jacalin beta-1 cha
 633 11 45.8 20 2 S29635 jacalin beta chain
 634 11 45.8 20 2 S03987 agglutinin beta-2
 635 11 45.8 20 2 S35460 alliin lyase (EC 4
 636 11 45.8 20 2 PC2084 serine proteinase
 637 11 45.8 20 2 S38763 S-adenosyl-L-methi
 638 11 45.8 20 2 A34817 collagenolytic pro
 639 11 45.8 20 2 A56899 serum heterodimer,
 640 11 45.8 20 2 A47105 dystroglycan - chi
 641 11 45.8 20 2 A61506 alpha-1-antitrypsi
 642 11 45.8 20 2 A56894 intracrystalline c
 643 11 45.8 20 2 B56894 intracrystalline c
 644 11 45.8 20 2 A85659 hypothetical prote
 645 11 45.8 20 2 AE0120 insertion element
 646 11 45.8 20 2 AC0269 probable trp opero
 647 11 45.8 20 2 B60505 hemoglobin A1-2 be
 648 11 45.8 20 2 S08605 hypothetical prote
 649 11 45.8 20 2 S27142 hypothetical prote
 650 11 45.8 20 2 DIRT dental fluid tra
 651 8 33.3 12 2 A28856 fructose-bisphosph
 652 7 29.2 15 2 E41383 23k variable histo
 653 7 29.2 20 2 I70108 microsomal triglyc
 654 6 25.0 3 3 S68328 blood cell protein
 655 6 25.0 4 1 ECXAA antho-RFamide neur
 656 6 25.0 4 2 D41654 hypothetical prote
 657 6 25.0 4 2 S53508 starvation-induced
 658 6 25.0 4 2 A25844 autho-RF amide neu
 659 6 25.0 4 2 S39390 myosin-light-chain
 660 6 25.0 4 2 J01273 neuropeptide Antho
 661 6 25.0 4 2 A35779 neuropeptide Antho
 662 6 25.0 4 2 A60418 FMRFamide - polych
 663 6 25.0 4 2 A32480 achatin-I - giant
 664 6 25.0 4 2 ECNK cardioexcitatory n
 665 6 25.0 5 2 A44955 alkanal monooxygen
 666 6 25.0 5 2 S70615 endo-1,4-beta-xyla
 667 6 25.0 5 2 PS0324 ribulose-bisphosph
 668 6 25.0 5 2 B45525 actin I - malaria
 669 6 25.0 5 2 B61445 Leu-enkephalin - b
 670 6 25.0 5 2 A61445 Met-enkephalin - b
 671 6 25.0 5 2 B61168 cocoonase (EC 3.4.
 672 6 25.0 5 2 PT0278 Ig heavy chain CDR
 673 6 25.0 5 2 A44692 fulicin - giant Af
 674 6 25.0 5 2 JS0319 subesophageal gang
 675 6 25.0 5 4 PT0644 T-cell receptor be
 676 6 25.0 5 4 A58728 serrawettin W2 - S
 677 6 25.0 6 2 A61049 halo-toxin - Pseud
 678 6 25.0 6 2 A60986 N-formyl oligopept
 679 6 25.0 6 2 S11024 hydrogensulfite re
 680 6 25.0 6 2 I51317 bHLH transcription
 681 6 25.0 6 2 I37263 Y protein - human
 682 6 25.0 6 2 I59142 platelet-derived g
 683 6 25.0 6 2 A41946 T-cell receptor ga
 684 6 25.0 6 2 A27696 contraction-inhibi
 685 6 25.0 6 2 B27696 contraction-inhibi
 686 6 25.0 6 2 A43129 neuropeptide GNFR

687	6	25.0	7	1	NYPG7	hypothalamic hepta	760	9	2	S36850	Ig heavy chain V r
688	6	25.0	7	1	A61324	dermorphin - Ronde	761	9	2	G41946	T-cell receptor ga
689	6	25.0	7	2	A60244	Met-enkephalin-Arg	762	9	2	A42266	peptidylglycine mo
690	6	25.0	7	2	S36662	dermorphin (Iys-7)	763	9	2	I52974	seminal vesicle pr
691	6	25.0	7	2	PH1408	Ig heavy chain V r	764	9	2	S39767	cardioactive pupti
692	6	25.0	7	2	B39127	phosphotransferase	765	6	25.0	S39040	lysine-conopressin
693	6	25.0	7	2	S39127	hypothetical prote	766	6	25.0	G58502	kidney and bladder
694	6	25.0	7	2	I40504	180K exoantigen -	767	9	2	S19523	orf AB protein - S
695	6	25.0	7	2	H33098	hucolin, 75K chain	768	6	25.0	A31576	xylose isomerase (
696	6	25.0	7	2	S68004	Ig mu chain D regi	769	6	25.0	S33333	alpha/beta-gliadin
697	6	25.0	7	2	E33932	T-cell receptor be	770	6	25.0	PC2021	oxytocin-related p
698	6	25.0	7	2	PT0665	protein kinase C i	771	6	25.0	A26363	cardioactive pupti
699	6	25.0	7	2	A59489	RNA-directed DNA p	772	6	25.0	A61620	locustamyotropin I
700	6	25.0	7	2	B35890	sex pheromone CAM3	773	6	25.0	S27233	cardioactive pepti
701	6	25.0	7	2	A25269	sex pheromone CCF1	774	6	25.0	A41978	callicliffamide 1 -
702	6	25.0	7	2	S17976	glucose isomerase	775	6	25.0	D44787	callicliffamide 10
703	6	25.0	7	2	PC2132	FMRFamide-related	776	6	25.0	D44787	callicliffamide 13
704	6	25.0	7	2	B44787	callicliffamide 11	777	6	25.0	B41978	callicliffamide 2 -
705	6	25.0	7	2	S08606	hypothetical prote	778	6	25.0	C41978	callicliffamide 3 -
706	6	25.0	8	2	A32523	peptidyl-di-peptida	779	6	25.0	D41978	callicliffamide 4 -
707	6	25.0	8	2	PH1407	Ig heavy chain V r	780	6	25.0	E41978	callicliffamide 5 -
708	6	25.0	8	2	FL0184	capsid protein VP-	781	6	25.0	F41978	callicliffamide 6 -
709	6	25.0	8	2	PA0032	protein QA300040 -	782	6	25.0	G41978	callicliffamide 7 -
710	6	25.0	8	2	S13661	polygalacturonase	783	6	25.0	S10920	venom protein HR-3
711	6	25.0	8	2	B33059	158K exoantigen -	784	6	25.0	JN0027	[Phe-6]-mosact - s
712	6	25.0	8	2	A39892	P element, P Cytot	785	6	25.0	B20569	serum amyloid P-co
713	6	25.0	8	2	B45800	serum albumin - do	786	6	25.0	S77984	cytochrome-c oxida
714	6	25.0	8	2	A42057	fibroblast growth	787	6	25.0	PT0080	60K Ca binding pro
715	6	25.0	8	2	PH0803	T-cell receptor al	788	6	25.0	A61386	macrophage inhibit
716	6	25.0	8	2	PC4372	telomeric and tetr	789	6	25.0	B39504	octamer-binding pr
717	6	25.0	8	2	S66296	Na+-transporting A	790	6	25.0	S66635	alpha-2-macroglobu
718	6	25.0	8	2	S37141	rpsA protein - Erw	791	6	25.0	S10784	enamelin i - bovin
719	6	25.0	8	2	S21273	cellulase (EC 3.2.	792	6	25.0	A28924	fructose-bisphosph
720	6	25.0	8	2	A37521	R-phycoerythrin ga	793	6	25.0	PD0443	3-oxoacid CoA-tran
721	6	25.0	8	2	S11078	glucose-6-phosphat	794	6	25.0	PC7074	translation elonga
722	6	25.0	8	2	PT0030	inulinase (EC 3.2.	795	6	25.0	A43065	hydroxyproline-3-b
723	6	25.0	8	2	A46306	spasmogenic toxin	796	6	25.0	PD0027	pev-tachykinin - p
724	6	25.0	8	2	A23967	leucopyrokinin - M	797	6	25.0	G85802	hypothetical prote
725	6	25.0	8	2	S66646	cardioacceleratory	798	6	25.0	S15850	vitamin D3 26-mono
726	6	25.0	8	2	B27867	homeotic protein U	799	6	25.0	A26744	bradykinin-like pe
727	6	25.0	8	2	H41978	callicliffamide 8 -	800	6	25.0	A61057	Thr-6 bradykinin -
728	6	25.0	8	2	D47393	neuropeptide calla	801	6	25.0	A60579	bradykinin-like pe
729	6	25.0	8	2	E47393	neuropeptide calla	802	6	25.0	S19329	sperm-activating p
730	6	25.0	8	2	S71919	alcohol dehydrogen	803	6	25.0	B60246	ornitho-kinin - ch
731	6	25.0	8	2	A14663	aspartate transami	804	6	25.0	A61363	bradykinin - commo
732	6	25.0	8	2	A61328	trypsin (EC 3.4.21	805	6	25.0	A61358	bradykinin-like pe
733	6	25.0	8	2	A28719	thymic humoral fac	806	6	25.0	ECLQ1M	tachykinin I - mig
734	6	25.0	8	2	S65381	cytochrome-c oxida	807	6	25.0	ECLQ3M	tachykinin III - m
735	6	25.0	8	2	PC4373	telomeric and tetr	808	6	25.0	ECLQ4M	tachykinin IV - m
736	6	25.0	8	2	A59028	MHC class I histoc	809	6	25.0	SPPGNK	neuromedin K - pig
737	6	25.0	8	2	S20162	leghemoglobin III	810	6	25.0	GMROL2	leucosulfakinin-II
738	6	25.0	8	2	F60588	sperm-activating p	811	6	25.0	S28055	cytochrome b559 co
739	6	25.0	8	2	B24749	neuropeptide B - b	812	6	25.0	S15118	dihydrofolate redu
740	6	25.0	8	2	B60588	sperm-activating p	813	6	25.0	S39392	calpain (EC 3.4.22
741	6	25.0	8	2	G60588	sperm-activating p	814	6	25.0	A60624	angiotensin I - Ja
742	6	25.0	8	2	S43972	tumor-associated a	815	6	25.0	A60410	beta-neoendorphin
743	6	25.0	8	2	S43971	tumor-associated a	816	6	25.0	JN0024	neurokinin A - chi
744	6	25.0	9	2	A28495	conopressin G - co	817	6	25.0	S39374	mannose receptor -
745	6	25.0	9	2	A61320	calsequestrin, car	818	6	25.0	A61617	ecdysteroid UDPglu
746	6	25.0	9	2	D24180	fibrinogen beta ch	819	6	25.0	S66458	ferradoxin - Rhizo
747	6	25.0	9	2	C24180	fibrinogen beta ch	820	6	25.0	S70721	heat shock protein
748	6	25.0	9	2	E28854	fibrinopeptide B -	821	6	25.0	S48182	bacterioferritin -
749	6	25.0	9	2	D28854	fibrinopeptide B -	822	6	25.0	H28027	protein P11 - curl
750	6	25.0	9	2	D28854	fibrinopeptide B -	823	6	25.0	C61440	polygalacturonase
751	6	25.0	9	2	D58503	translation elonga	824	6	25.0	S65432	angiotensin I - ho
752	6	25.0	9	2	S66607	quinoline 2-oxidor	825	6	25.0	PT0230	Ig heavy chain CDR
753	6	25.0	9	2	S63491	dissimilatory sulf	826	6	25.0	PT0251	Ig heavy chain CDR
754	6	25.0	9	2	S36898	ribosomal protein	827	6	25.0	PT0284	Ig heavy chain CDR
755	6	25.0	9	2	T31612	hypothetical prote	828	6	25.0	B45482	platelet activatin
756	6	25.0	9	2	S39766	cardioactive pepti	829	6	25.0	S23371	T-cell receptor al
757	6	25.0	9	2	S65433	bradykinin - horn	830	6	25.0	S66214	cartilage oligomer
758	6	25.0	9	2	PT0225	Ig heavy chain CDR	831	6	25.0	S71948	matrix metalloprot
759	6	25.0	9	2	PT0315	Ig heavy chain CDR	832	6	25.0	C39398	Fc mu (IgM) recept

833	6	25.0	10	2	A37268	Ig heavy chain C r	906	6	25.0	10	2	I60588	sperm-activating p
834	6	25.0	10	2	S36849	Ig heavy chain V r	907	6	25.0	10	2	B60589	sperm-activating p
835	6	25.0	10	2	PH0807	T-cell receptor al	908	6	25.0	10	2	C61033	ranatachykinin C -
836	6	25.0	10	2	PT0215	T-cell receptor be	909	6	25.0	10	2	B61033	ranatachykinin B -
837	6	25.0	10	2	S65385	cytochrome-C-oxida	910	6	25.0	10	2	S27178	neurokinin A-relat
838	6	25.0	10	2	S68033	cytochrome P450 1A	911	6	25.0	10	2	A32543	cardioexcitatory n
839	6	25.0	10	2	D37397	hypothetical prote	912	6	25.0	10	4	S14943	UGA3 leader peptid
840	6	25.0	10	2	B46453	e antigen p20e pre	913	6	25.0	11	1	ECLQ2M	tachykinin II - mi
841	6	25.0	10	2	G58501	48K bile/gallbladd	914	6	25.0	11	1	A60654	substance P - guin
842	6	25.0	10	2	I39702	nopaline synthase	915	6	25.0	11	1	EOCC	eledoisin - musky
843	6	25.0	10	2	S06964	hypothetical prote	916	6	25.0	11	1	EOCCC	eledoisin - curled
844	6	25.0	10	2	S18396	probable glucose-6	917	6	25.0	11	1	SPHO	substance P - hors
845	6	25.0	10	2	S70251	nitrogenase (EC 1.	918	6	25.0	11	1	GMROL	leucosulfakinin -
846	6	25.0	10	2	I40032	trpE protein - Bac	919	6	25.0	11	2	G42762	proteasome endopep
847	6	25.0	10	2	A60476	S-layer protein -	920	6	25.0	11	2	A33917	dihydroorotase (EC
848	6	25.0	10	2	I44644	neurotoxin-associ	921	6	25.0	11	2	JN0023	substance P - chic
849	6	25.0	10	2	A39745	endo-glucosylceram	922	6	25.0	11	2	A38841	rhodopsin homolog
850	6	25.0	10	2	PC2044	beta-kirilowin - M	923	6	25.0	11	2	D58502	27K bile and gallb
851	6	25.0	10	2	B52272	peptide-N4-(N-acet	924	6	25.0	11	2	A58502	38K kidney stone p
852	6	25.0	10	2	S38304	lectin GNL1 alpha	925	6	25.0	11	2	S33782	acetolactate synth
853	6	25.0	10	2	S38305	lectin GNL2 alpha	926	6	25.0	11	2	E06091	phycobilisome 8K 1
854	6	25.0	10	2	D28027	protein P7 - curle	927	6	25.0	11	2	D60691	phycobilisome 8K 1
855	6	25.0	10	2	B61440	polygalacturonase	928	6	25.0	11	2	PC2372	58K heat shock pro
856	6	25.0	10	2	D61440	polygalacturonase	929	6	25.0	11	2	B41835	translational elonga
857	6	25.0	10	2	PN0165	triase-phosphate i	930	6	25.0	11	2	S19301	endo-1,4-beta-xyla
858	6	25.0	10	2	A58365	neuropeptide FF/Ra	931	6	25.0	11	2	PA0028	protein QA300042 -
859	6	25.0	10	2	B60656	leucosulfakinin II	932	6	25.0	11	2	T06383	hypothetical prote
860	6	25.0	10	2	A43977	FMRFamide-like pro	933	6	25.0	11	2	PU0029	33K protein 3218 -
861	6	25.0	10	2	C44787	calliFMRFamide 12	934	6	25.0	11	2	S78026	ribosomal protein
862	6	25.0	10	2	A56633	neomycinopressin -	935	6	25.0	11	2	I33088	173K exoantigen -
863	6	25.0	10	2	D46285	formaldehyde dehyd	936	6	25.0	11	2	B60769	Ig H2 chain - Paci
864	6	25.0	10	2	A30823	bothropstoxin - ja	937	6	25.0	11	2	I52980	glucocerebrosidase
865	6	25.0	10	2	A09117	angiotensin precu	938	6	25.0	11	2	PT0250	Ig heavy chain CRD
866	6	25.0	10	2	A90345	angiotensin precu	939	6	25.0	11	2	PT0287	Ig heavy chain CRD
867	6	25.0	10	2	S65387	cytochrome-C-oxida	940	6	25.0	11	2	S57575	T-cell receptor V-
868	6	25.0	10	2	T13838	cytochrome-c oxida	941	6	25.0	11	2	S23364	T-cell receptor al
869	6	25.0	10	2	A44871	monodehydroascorba	942	6	25.0	11	2	S23373	T-cell receptor al
870	6	25.0	10	2	S74147	glyceraldehyde-3-p	943	6	25.0	11	2	S51732	N-acetylglucosamin
871	6	25.0	10	2	B33710	ornithine decarbox	944	6	25.0	11	2	A54348	T-cell receptor al
872	6	25.0	10	2	A60527	sperm-activating p	945	6	25.0	11	2	PD0442	NIPSNAP2 protein -
873	6	25.0	10	2	B49581	sialokinin II - ye	946	6	25.0	11	2	PH1376	T antigen variant
874	6	25.0	10	2	A49581	sialokinin I - yel	947	6	25.0	11	2	PT0214	T-cell receptor be
875	6	25.0	10	2	H60787	sperm-activating p	948	6	25.0	11	2	I60434	68kDa neurofilamen
876	6	25.0	10	2	G60787	sperm-activating p	949	6	25.0	11	2	S53436	beta-D-galactosida
877	6	25.0	10	2	F60787	sperm-activating p	950	6	25.0	11	2	PH0906	T-cell receptor be
878	6	25.0	10	2	G60787	sperm-activating p	951	6	25.0	11	2	C58501	42K bile stone pro
879	6	25.0	10	2	C60787	sperm-activating p	952	6	25.0	11	2	S58244	pyrroloquinoline q
880	6	25.0	10	2	A60787	sperm-activating p	953	6	25.0	11	2	S35490	type II site-speci
881	6	25.0	10	2	D60787	sperm-activating p	954	6	25.0	11	2	B39853	LuxC protein - Pho
882	6	25.0	10	2	B60787	sperm-activating p	955	6	25.0	11	2	PC2330	cycloinulooligosac
883	6	25.0	10	2	D60588	sperm-activating p	956	6	25.0	11	2	A44755	20alpha-hydroxyate
884	6	25.0	10	2	B60588	sperm-activating p	957	6	25.0	11	2	A35594	buccalin - Califor
885	6	25.0	10	2	G60588	sperm-activating p	958	6	25.0	11	2	S69349	neuropeptide FFami
886	6	25.0	10	2	I60527	sperm-activating p	959	6	25.0	11	2	A60656	perisulfakinin - A
887	6	25.0	10	2	A60588	sperm-activating p	960	6	25.0	11	2	I41978	calliFMRFamide 9 -
888	6	25.0	10	2	A60788	sperm-activating p	961	6	25.0	11	2	S33300	probable substance
889	6	25.0	10	2	D60527	sperm-activating p	962	6	25.0	11	2	D42965	talin - chicken (f
890	6	25.0	10	2	C39572	sperm-activating p	963	6	25.0	11	2	E57789	gallbladder stone
891	6	25.0	10	2	F60527	sperm-activating p	964	6	25.0	11	2	S13279	Ile-Ser-bradykinin
892	6	25.0	10	2	C60527	sperm-activating p	965	6	25.0	11	2	A32428	amine oxidase (cop
893	6	25.0	10	2	E60527	sperm-activating p	966	6	25.0	11	2	PN0042	stathmin - mouse (
894	6	25.0	10	2	G60527	sperm-activating p	967	6	25.0	11	2	A48973	glucosylase A1 (E
895	6	25.0	10	2	E39572	sperm-activating p	968	6	25.0	11	2	S09074	cytochrome P450-4b
896	6	25.0	10	2	D60788	sperm-activating p	969	6	25.0	11	2	A57458	gene Gax protein -
897	6	25.0	10	2	E60788	sperm-activating p	970	6	25.0	11	2	S07203	uperolein - frog (
898	6	25.0	10	2	C60788	sperm-activating p	971	6	25.0	11	2	B26744	megascollakinin -
899	6	25.0	10	2	A24867	scyllorhinin I - s	972	6	25.0	11	2	C60409	kassinin-like pept
900	6	25.0	10	2	S23307	neurokinin A - rai	973	6	25.0	11	2	E60409	substance P-like p
901	6	25.0	10	2	S23186	neurokinin A - Atl	974	6	25.0	11	2	B60409	kassinin-like pept
902	6	25.0	10	2	S07202	phyllomedulin - tw	975	6	25.0	11	2	F60409	substance P-like p
903	6	25.0	10	2	F60589	sperm-activating p	976	6	25.0	11	2	D60409	kassinin-like pept
904	6	25.0	10	2	C60589	sperm-activating p	977	6	25.0	11	2	YHHO	morphogenetic neur
905	6	25.0	10	2	D60589	sperm-activating p	978	6	25.0	11	2		morphogenetic neur

979 morphogenetic neur 6 25.0 11 2 YHJPHY
 980 morphogenetic neur 6 25.0 11 2 YHXAE
 981 substance P - rain 6 25.0 11 2 S23308
 982 substance P - Atla 6 25.0 11 2 S23306
 983 Crinia-angiotensin 6 25.0 11 2 S07207
 984 phyllalaemin - frog 6 25.0 11 2 S07201
 985 phyllokinin - Rohd 6 25.0 11 2 A61365
 986 ranatachykinin A - 6 25.0 11 2 A61033
 987 ranatachykinin D - 6 25.0 11 2 D61033
 988 morphogenetic neur 6 25.0 11 2 YHRT
 989 hypothetical prote 6 25.0 11 4 S41909
 990 aminotransferase c 6 25.0 11 4 PC2124
 991 hypothetical prote 6 25.0 11 4 S52252
 992 locustamyotropin - 6 25.0 12 1 A43975
 993 PyRE leader peptid 6 25.0 12 1 LFECPE
 994 glutathione transf 6 25.0 12 2 S17869
 995 1-aminocyclopropan 6 25.0 12 2 C36201
 996 glycoprotein hormo 6 25.0 12 2 A61309
 997 T-cell receptor be 6 25.0 12 2 S26552
 998 T-cell receptor be 6 25.0 12 2 S26549
 999 T-cell receptor be 6 25.0 12 2 S26544
 1000 Ig heavy chain - m 6 25.0 12 2 S25056

ALIGNMENTS

RESULT 1
 A24244
 adipokinetic hormone - bollworm
 N;Alternate names: Hez-AKH
 C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
 C;Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C;Accession: A24244
 R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
 Biochem. Biophys. Res. Commun. 135, 622-628, 1986
 A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helic
 A;Reference number: A24244; MUID:86186794; PMID:3964263
 A;Accession: A24244
 A;Molecule type: protein
 A;Residues: 1-9 <JAF>
 A;Cross-references: UNIPROT:P08901
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 70.8%; Score 17; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
 |
 Db 4 FTSSW 8

RESULT 2
 A28004
 adipokinetic hormone G - two-spotted cricket
 N;Alternate names: AKH-G
 C;Species: Gryllus bimaculatus (two-spotted cricket)
 C;Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
 C;Accession: A28004
 R;Gaede, G.; Rinehart, K.L.
 Biochem. Biophys. Res. Commun. 149, 908-914, 1987
 A;Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a pepti
 A;Reference number: A28004; MUID:88106553; PMID:3426616
 A;Accession: A28004
 A;Molecule type: protein
 A;Residues: 1-8 <GAE>
 A;Cross-references: UNIPROT:P14086
 A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental
 Query Match 66.7%; Score 16; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
 |
 Db 4 FSTGW 8

RESULT 3
 A31571
 hypertrehalosemic/adipokinetic hormone - bollworm
 N;Alternate names: Hez-HrTH
 C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
 C;Date: 30-Jun-1989 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C;Accession: A31571
 R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.
 Biochem. Biophys. Res. Commun. 155, 344-350, 1988
 A;Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea wit
 A;Reference number: A31571; MUID:88326324; PMID:3415690
 A;Accession: A31571
 A;Molecule type: protein
 A;Residues: 1-10 <JAF>
 A;Cross-references: UNIPROT:P16353
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;10/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 66.7%; Score 16; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 6.3e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
 |
 Db 4 FSSGW 8

RESULT 4
 S10596
 adipokinetic hormone - pond skimmer
 C;Species: Libellula auripennis
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S10596
 R;Gaede, G.
 Biol. Chem. Hoppe-Seyler 371, 475-483, 1990
 A;Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hor
 A;Reference number: S10596; MUID:90359055; PMID:2390213
 A;Accession: S10596
 A;Molecule type: protein
 A;Residues: 1-8 <BIO>
 A;Cross-references: UNIPROT:P25418
 C;Comment: This peptide has both adipokinetic and hypertrehalosemic activities.

C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 62.5%; Score 15; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
 |
 Db 4 FTFSW 8

RESULT 5
 D57444

neuropeptide Grb-AST B4 - two-spotted cricket
C:Species: Gryllus bimaculatus (two-spotted cricket)
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
C:Accession: D57444
R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket
A:Reference number: A57444; MUID:95403341; PMID:7673141
A:Accession: D57444
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <LOR>
A:Cross-references: UNIPROT:Q7M3N6

Query Match 62.5%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 5 FHGSW 9

RESULT 6
T17063
cytochrome-c oxidase (EC 1.9.3.1) chain I - Hoplocercus spinosus mitochondrion (fragment)
C:Species: mitochondrion Hoplocercus spinosus
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17063
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A:Title: Evolutionary shifts in three major structural features of the mitochondrial gene
A:Reference number: 218674; MUID:97315309; PMID:9169559
A:Accession: T17063
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <AC>
A:Cross-references: UNIPROT:Q79897; EMBL:U82683; NID:G3603124; PID:G3603127; PIDN:AAC622
C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 2 FISRW 6

RESULT 7
T12325
cytochrome-c oxidase (EC 1.9.3.1) chain I - Leiocephalus carinatus mitochondrion (fragment)
C:Species: mitochondrion Leiocephalus carinatus
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12325
R:Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A:Title: Molecular tests of phylogenetic taxonomies: A general procedure and example using
A:Reference number: 217488; MUID:99162288; PMID:10051389
A:Accession: T12325
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <SCH>
A:Cross-references: UNIPROT:Q92YT2; EMBL:AF049864; NID:G4105754; PID:G4105757; PIDN:AAD0
C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 62.5%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 2 FITRW 6

RESULT 8
S53789
neuropeptide Pec-HrTH - Platypieura capensis
C:Species: Platypieura capensis
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S53789
R:Gaede, G.; Janssens, M.P.E.
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
A:Title: Cicadas contain novel members of the AKH/rpCH family peptides with hypertrehalose
A:Reference number: S53789; MUID:95225985; PMID:7710694
A:Accession: S53789
A:Molecule type: protein
A:Residues: 1-10 <GAE>
A:Cross-references: UNIPROT:Q7M465
C:Keywords: blocked amino end; blocked carboxyl end

Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 4 FSPSW 8

RESULT 9
PH1613
Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1613
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1560; MUID:93301609; PMID:8315387
A:Accession: PH1613
A:Molecule type: DNA
A:Residues: 1-15 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 62.5%; Score 15; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 10 FTMLW 14

RESULT 10
A34704
protein-tyrosine kinase (EC 2.7.1.112) 1, neuron-specific - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C:Accession: A34704
R:Pyper, J.M.; Bolen, J.B.
Mol. Cell. Biol. 10, 2035-2040, 1990
A:Title: Identification of a novel neuronal C-SRC exon expressed in human brain.
A:Reference number: A34704; MUID:90220588; PMID:1691439
A:Accession: A34704
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17 <PYP>
A:Cross-references: UNIPROT:Q14925

C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 62.5%; Score 15; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
DB 10 FTRW 14

RESULT 11

S77981
cytochrome-c oxidase (EC 1.9.3.1) chain Va.1 - bigeye tuna (fragment)
C;Species: Thunnus obesus (bigeye tuna) 17-Sep-1997 #text_change 09-Jul-2004
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: S77981
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A;Reference number: S77980
A;Accession: S77981
A;Molecule type: protein
A;Residues: 1-20 <ARN>
A;Cross-references: UNIPROT:P80972
A;Experimental source: heart; liver
C;Genetics:
A;Genome: nuclear
C;Function:
A;Pathway: oxidative phosphorylation; respiratory chain
A;Superfamily: mammalian cytochrome-c oxidase chain Va
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 62.5%; Score 15; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
DB 11 FDRW 15

RESULT 12

PN0171
peptidylprolyl isomerase (EC 5.2.1.8) b, cytosolic - fungus (Fusarium sporotrichioides)
N;Contains: cyclophilin
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 02-Sep-2000
C;Accession: PN0171
R;Fukaya, N.; Chow, L.P.; Sugita, Y.; Taigita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PN0160
A;Accession: PN0171
A;Molecule type: protein
A;Residues: 1-20 <FUK>
A;Experimental source: strain M-1-1
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase; cyclosporin A binding; cytosol

Query Match 62.5%; Score 15; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
DB 6 FDIW 10

RESULT 13

PH1380
alpha-amylose (EC 3.2.1.1) (Haim sensitive) - Bacillus sp. (fragment)
C;Species: Bacillus sp.
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

C;Accession: PH1380
R;Kawaguchi, T.; Nagae, H.; Murao, S.; Arai, M.
BioSci. Biotechnol. Biochem. 56, 1792-1796, 1992
A;Title: Purification and some properties of a Haim-sensitive alpha-amylose from newly isolated *Bacillus* sp.
A;Reference number: PH1380; MUID:93113087; PMID:1369074
A;Accession: PH1380
A;Molecule type: protein
A;Residues: 1-20 <KAW>
A;Cross-references: UNIPROT:Q9R5E8
A;Experimental source: strain N0.195
C;Comment: This enzyme has an optimum pH of 7.0.
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 62.5%; Score 15; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
DB 13 FSWT 17

RESULT 14

A33995
adipokinetic hormone - black horse fly
C;Species: Tabanus atratus (black horse fly)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33995
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Y.
Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activities
A;Reference number: A33995; MUID:90046758; PMID:2813385
A;Accession: A33995
A;Molecule type: protein
A;Residues: 1-8 <JAF>
A;Cross-references: UNIPROT:P14595
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 58.3%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
DB 4 FPGW 8

RESULT 15

A44960
neuropeptide Led-CC-I - Colorado potato beetle
C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A44960
R;Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A;Title: The metabolic neuropeptides of the corpus cardiaca from the potato beetle and the Colorado potato beetle
A;Reference number: A44960; MUID:90160053; PMID:2576128
A;Accession: A44960
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P04548
C;Superfamily: adipokinetic hormone
C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;

QY 2 FXXW 6
DB 6 FDIW 10

Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 2 FXXW 6
| |
Db 4 FSPW 8

RESULT 16

B44960

C;Species: Leptinotarsa decemlineata (Colorado potato beetle)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B44960
R;Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and
A;Reference number: A44960; MUID:90160053; PMID:2576128
A;Accession: B44960

A;Molecule type: protein
A;Residues: 1-8 <GAE>

A;Cross-references: UNIPROT:P04549

C;Superfamily: adipokinetic hormone

C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
| |
Db 4 FSPW 8

RESULT 17

A58620

C;Species: Ischnura senegalensis
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004
C;Accession: A58620
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicu
A;Reference number: S55310; MUID:94379987; PMID:8093008

A;Accession: A58620

A;Molecule type: protein

A;Residues: 1-8 <JAN>

A;Cross-references: UNIPROT:Q7M4H6

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
| |
Db 4 FSPW 8

RESULT 18

S11545

C;Species: Protophormia terraenovae (nestling-sucking blowfly)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S11545
R;Gaede, G.; Wilps, H.; Kellner, R.
Biochem. J. 289, 309-313, 1990
A;Title: Isolation and structure of a novel charged member of the red-pigment-concentrat

erraenovae (Diptera).
A;Reference number: S11545; MUID:90351345; PMID:2386478

A;Accession: S11545

A;Molecule type: protein

A;Residues: 1-8 <GAE>

A;Cross-references: UNIPROT:P61856

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
| |
Db 4 FSPW 8

RESULT 19

S55310

C;Species: Pseudagrion inconspicu

C;Accession: S55310

C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004

R;Janssens, M.P.E.; Kellner, R.; Gaede, G.

Biochem. J. 302, 539-543, 1994

A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicu

A;Reference number: S55310; MUID:94379987; PMID:8093008

A;Accession: S55310

A;Molecule type: protein

A;Residues: 1-8 <JAN>

A;Cross-references: UNIPROT:Q7M4H7

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
| |
Db 4 FSPW 8

RESULT 20

A61348

C;Species: Pandalus borealis (northern shrimp)

C;Accession: A61348; S07139

C;Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004

R;Fornlund, P.; Josefsson, L.

Science 177, 173-175, 1972

A;Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.

A;Reference number: A61348; MUID:72228738; PMID:5041363

A;Accession: A61348

A;Molecule type: protein

A;Residues: 1-8 <FER1>

A;Cross-references: UNIPROT:P08939

R;Fornlund, P.

Biochim. Biophys. Acta 371, 304-311, 1974

A;Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus bore

A;Reference number: S07139; MUID:75054965; PMID:4433569

A;Accession: S07139

A;Molecule type: protein

A;Residues: 'E', 2-8 <FER2>

A;Note: The amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C;Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pic

zed pigment-containing cells.

C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6

DB 4 FSPGW 8

RESULT 21

hyperrehalosemic hormone I - oriental cockroach

N:Alternate names: Pea-CAH-I

C:Species: Blattella orientalis (oriental cockroach)

C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004

C:Accession: S08995

R:Gade, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hyperrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry

A:Reference number: S08995; PMID:90253659; PMID:2340112

A:Accession: S08995

A:Molecule type: protein

A:Residues: 1-8 <GAE>

A:Cross-references: UNIPROT:P04548

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have assigned the amino-terminal residue as pyroglutamic acid

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

QY 2 FXXW 6

DB 4 FSPNW 8

RESULT 22

hyperrehalosemic hormone II - oriental cockroach

N:Alternate names: Pea-CAH-II

C:Species: Blattella orientalis (oriental cockroach)

C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004

C:Accession: S08996

R:Gade, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hyperrehalosemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry

A:Reference number: S08996; PMID:90253659; PMID:2340112

A:Accession: S08996

A:Molecule type: protein

A:Residues: 1-8 <GAE>

A:Cross-references: UNIPROT:P04549

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have assigned the amino-terminal residue as pyroglutamic acid

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

QY 2 FXXW 6

DB 4 FSPNW 8

DB

4 FFPNW 8

RESULT 23

A49823

adipokinetic hormone I - American cockroach

N:Alternate names: periplanetin CC-1

C:Species: Periplaneta americana (American cockroach)

C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C:Accession: A49823

R:Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEntee, G.A.; Miller, C.F.

Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984

A:Title: Isolation and primary structure of two peptides with cardioacceleratory and hypotensive activities

A:Reference number: A49823; PMID:84298179; PMID:6591205

A:Accession: A49823

A:Molecule type: protein

A:Residues: 1-8 <SCA>

A:Cross-references: UNIPROT:P04548

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6

DB 4 FSPNW 8

RESULT 24

B49823

adipokinetic hormone II - American cockroach

N:Alternate names: neuropeptide M-II; periplanetin CC-1

C:Species: Periplaneta americana (American cockroach)

C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C:Accession: B49823; A05170

R:Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEntee, G.A.; Miller, C.F.

Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984

A:Title: Isolation and primary structure of two peptides with cardioacceleratory and hypotensive activities

A:Reference number: A49823; PMID:84298179; PMID:6591205

A:Accession: B49823

A:Molecule type: protein

A:Residues: 1-8 <SCA>

A:Cross-references: UNIPROT:P04549

R:Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.

Biochem. Biophys. Res. Commun. 124, 350-358, 1984

A:Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry

A:Reference number: A90118; PMID:85046530; PMID:6548628

A:Accession: A05170

A:Molecule type: protein

A:Residues: 'E', 2-8 <WIT>

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6

DB 4 FFPNW 8

RESULT 25

A43976

hyperrehalosemic hormone - yellow mealworm

C:Species: Tenebrio molitor (yellow mealworm)

C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C;Accession: A43976
R;Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle
A;Reference number: A43976; PMID:90341081; PMID:2381871
A;Accession: A43976
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P25419
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FSPNW 8

RESULT 26
B43976
hypertrehalosemic hormone - beetle (Zophobas rugipes)
C;Species: Zophobas rugipes
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C;Accession: B43976
R;Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle
A;Reference number: A43976; PMID:90341081; PMID:2381871
A;Accession: B43976
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Cross-references: UNIPROT:P25419
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FSPNW 8

RESULT 27
A05169
neuropeptide M-I - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05169
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry
A;Reference number: A90118; PMID:85046530; PMID:6548628
A;Accession: A05169
A;Molecule type: protein
A;Residues: 1-8 <WIT>
A;Cross-references: UNIPROT:P04548
C;Keywords: neuropeptide

Query Match 58.3%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FSPNW 8

Db 4 FSPNW 8

RESULT 28

B33995

hypotrehalosemic hormone - black horse fly

C;Species: Tabanus atratus (black horse fly)

C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-Jul-2004

C;Accession: B33995

R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang,

Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989

A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activities

A;Reference number: A33995; PMID:90046758; PMID:2813385

A;Accession: B33995

A;Molecule type: protein

A;Residues: 1-10 <JAF>

A;Cross-references: UNIPROT:P14596

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid (Gln) #status predicted

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F;10/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match 58.3%; Score 14; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 2e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

| |

Db 4 FTPGW 8

RESULT 29

S08997

hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)

C;Species: Gromphadorina portentosa

C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004

C;Accession: S08997

R;Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora cardiaca and of the stick insect *Exatoma tatarum* assigned by tandem fast atom bombardment mass spectrometry

A;Reference number: S08995; PMID:90253659; PMID:2340112

A;Accession: S08997

A;Molecule type: protein

A;Residues: 1-10 <GAE>

A;Cross-references: UNIPROT:P10939

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid (Gln) #status experimental

F;1/Modified site: pyrrolidone carboxylic acid (Thr) #status experimental

F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 2e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

| |

Db 4 FSPGW 8

RESULT 30

A60421

hypertrehalosemic hormone - German cockroach

N;Alternate names: Bld-HrTH

C;Species: Blattella germanica (German cockroach)

C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004

C;Accession: A60421; S09137

R;Veenstra, J.A.; Camps, F.

Neuropeptides 15, 107-109, 1990

A;Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, *Blattella germanica*

A;Reference number: A60421; PMID:91179584; PMID:2080017

A;Accession: A60421

A;Molecule type: protein
A;Residues: 1-10 <VE>
A;Cross-references: UNIPROT:P10939
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S09137
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyroglutamic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FSPGW 8

RESULT 31

S08998
hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C;Accession: S08998
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08998
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Cross-references: UNIPROT:P10939
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyroglutamic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FSPGW 8

RESULT 32

A26381
hypertrehalosemic hormone - gray cockroach
C;Species: Nauphoeta cinerea (gray cockroach)
C;Date: 31-Mar-1988 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: A26381
R;Gaede, G.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 141, 774-781, 1986
A;Title: Amino acid sequence of a hypertrehalosemic neuropeptide from the corpus cardiacum
A;Reference number: A26381; MUID:87100208; PMID:3801028
A;Accession: A26381
A;Molecule type: protein
A;Residues: 1-10 <GAD>
A;Cross-references: UNIPROT:P10939
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyroglutamic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FSPGW 8

RESULT 33

JC1416
hypertrehalosemic hormone I - stick insect (Carausius morosus)
N;Alternate names: neuropeptide Cam-HrTH-I
N;Contains: hypertrehalosemic factor II
C;Species: Carausius morosus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1416; S07157
R;Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992
A;Title: A tryptophan-substituted member of the AXH/RPCH family isolated from a stick insect
A;Reference number: JC1416; MUID:93129188; PMID:1482345
A;Accession: JC1416
A;Molecule type: protein
A;Residues: 1-10 <GAE1>
A;Cross-references: UNIPROT:P11385
R;Gaede, G.; Rinehart Jr., K.L.
Biol. Chem. Hoppe-Seyler 368, 67-75, 1987
A;Title: Primary structure of the hypertrehalosemic factor II from the corpus cardiacum
A;Reference number: S07157; MUID:87157103; PMID:3828078
A;Accession: S07157
A;Molecule type: protein
A;Residues: 2', 2'-10 <GAE2>
C;Comment: Hypertrehalosemic factor II lacks the tryptophan modification.
C;Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplaneta
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Binding site: carbohydrate (Trp) (covalent) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 4 FTPNW 8

RESULT 34

S09138
hypertrehalosemic hormone II - stick insect (Extatosoma tiaratum)
N;Alternate names: Cam-HrTH-II
C;Species: Extatosoma tiaratum
C;Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S09138
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S09138
A;Molecule type: protein
A;Residues: 1-10 <GAE>
A;Cross-references: UNIPROT:P11385
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 2e+03; Mismatches 0; Indels 3; Gaps 0;
Matches 2; Conservative 0

Qy 2 FXXW 6
|
Db 4 FPNW 8

RESULT 35
C3191
hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis
C:Species: Bacteroides fragilis
C>Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993
C:Accession: C3191
R:Speer, B.S.; Bedzyk, L.; Salyers, A.A.
J. Bacteriol. 173, 176-183, 1991
A:Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tra
A:Reference number: A39191; MUID:91100280; PMID:1846135
A:Accession: C3191
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-10 <SPE>
A:Cross-references: GB:M37699

Query Match 58.3%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 3 FSPW 7

RESULT 36
PT0322
Ig heavy chain CRD3 region (clone J2-106A) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0322
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0322
A:Molecule type: DNA
A:Residues: 1-10 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 58.3%; Score 14; DB 2; Length 10;
Best Local Similarity 20.0%; Pred. No. 2e+03;
Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 3 YSSW 7

RESULT 37
T17066
Cytochrome-c oxidase (EC 1.9.3.1) chain I - Oplurus cuvieri mitochondrion (fragment)
C:Species: mitochondrion Oplurus cuvieri
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17066
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A:Title: Evolutionary shifts in three major structural features of the mitochondrial gen
A:Reference number: Z18674; MUID:97315309; PMID:9169559
A:Accession: T17066
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <MAC>
A:Cross-references: UNIPROT:O79903; EMBL:U82685; NID:G3603136; PID:G3603139; PIDN:AAC622

C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 58.3%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 2 FINRW 6

RESULT 38
T17069
cytochrome-c oxidase (EC 1.9.3.1) chain I - Phrynosoma douglassii mitochondrion (fragmen
C:Species: mitochondrion Phrynosoma douglassii
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17069
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A:Title: Evolutionary shifts in three major structural features of the mitochondrial gen
A:Reference number: Z18674; MUID:97315309; PMID:9169559
A:Accession: T17069
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <MAC>
A:Cross-references: UNIPROT:O79906; EMBL:U82686; NID:G3603144; PID:G3603147; PIDN:AAC622

C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 58.3%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 2 FINRW 6

RESULT 39
T12329
cytochrome-c oxidase (EC 1.9.3.1) chain I - Stenocercus crasicaudatus mitochondrion (fra
C:Species: mitochondrion Stenocercus crasicaudatus
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12329
R:Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A:Title: Molecular tests of phylogenetic taxonomies: A general procedure and example usi
A:Reference number: Z17488; MUID:99162288; PMID:10051389
A:Accession: T12329
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <SCH>
A:Cross-references: UNIPROT:Q9ZVS6; EMBL:AF049866; NID:G4105762; PID:G4105765; PIDN:AAD0

C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 58.3%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
Db 2 FINRW 6

RESULT 40

```

PT0274
IG heavy chain CRD3 region (clone 3-109B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0274
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0274
A;Molecule type: DNA
A;Residues: 1-12 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match      58.3%; Score 14; DB 2; Length 12;
Best Local Similarity 20.0%; Pred. No. 2.3e+03;
Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
      : |
Db      3 YSSW 7

Search completed: October 18, 2005, 15:59:23
Job time : 26.3529 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:32:19 ; Search time 117.529 Seconds
(without alignments)
39.213 Million cell updates/sec

Title: US-09-214-371-11

Perfect score: 24

Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 12050

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_03.*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	17	70.8	9	1 AKH_HELZE	P67787 heliothis z
2	17	70.8	13	2 Q9XL12	Q9XL12 bemisia tab
3	16	66.7	8	1 AKHG_GRYBI	P67785 gryllus bim
4	16	66.7	8	1 AKH_ROMMI	P67786 romalea mic
5	16	66.7	10	1 HTF_HELZE	P16353 heliothis z
6	16	66.7	11	2 Q6E5H4	Q6E5H4 mantheyus p
7	16	66.7	11	2 Q9G649	Q9G649 otocryptis
8	16	66.7	17	2 O15276	O15276 homo sapien
9	16	66.7	17	2 Q7Y1X8	Q7Y1X8 lilium long
10	16	66.7	19	2 O91329	O91329 human immun
11	16	66.7	19	2 Q9WJ31	Q9WJ31 human immun
12	16	66.7	20	2 Q6LD18	Q6LD18 mus musculu
13	15	62.5	8	1 AKH_LI8AU	P25418 libellula a
14	15	62.5	9	2 Q7M3N6	Q7M3N6 gryllus bim
15	15	62.5	9	2 Q8WG56	Q8WG56 procambarus
16	15	62.5	10	1 AKHX_LOCM1	P81626 locusta mig
17	15	62.5	10	2 Q7M455	Q7M455 platyleura
18	15	62.5	10	2 Q70F01	Q70F01 sus scrofa
19	15	62.5	10	2 Q79897	Q79897 hoplocercus
20	15	62.5	10	2 Q92707	Q92707 platysaurus
21	15	62.5	10	2 Q6UJL5	Q6UJL5 strophurus
22	15	62.5	10	2 Q6WBU4	Q6WBU4 scelopor
23	15	62.5	10	2 Q6WBU4	Q6WBU4 scelopor
24	15	62.5	10	2 Q6X0E7	Q6X0E7 anolis marc
25	15	62.5	10	2 Q71DW3	Q71DW3 polychrus m
26	15	62.5	10	2 Q71DW6	Q71DW6 polychrus a
27	15	62.5	10	2 Q71E17	Q71E17 morunasauru
28	15	62.5	10	2 Q71E20	Q71E20 enyalioides
29	15	62.5	10	2 Q9ZY72	Q9ZY72 leiocephalu
30	15	62.5	11	2 Q6WES0	Q6WES0 ceratophora
31	15	62.5	11	2 Q9G365	Q9G365 calotes emm

32	15	62.5	11	2 Q9G368	Q9G368 draco blanf
33	15	62.5	11	2 Q9G5Y9	Q9G5Y9 pseudocalot
34	15	62.5	11	2 Q9G5Z2	Q9G5Z2 pseudocalot
35	15	62.5	11	2 Q9G601	Q9G601 bronchocele
36	15	62.5	11	2 Q9G625	Q9G625 calotes ver
37	15	62.5	11	2 Q9G628	Q9G628 calotes mys
38	15	62.5	11	2 Q9G631	Q9G631 calotes nig
39	15	62.5	11	2 Q9G634	Q9G634 calotes lio
40	15	62.5	11	2 Q9G640	Q9G640 calotes cey
41	15	62.5	11	2 Q9G643	Q9G643 calotes cal
42	15	62.5	11	2 Q9G646	Q9G646 sitana pont
43	15	62.5	11	2 Q6WR31	Q6WR31 mycteria am
44	15	62.5	12	2 Q6WR52	Q6WR52 asio otus (
45	15	62.5	12	2 Q6WR67	Q6WR67 neomorphus
46	15	62.5	12	2 Q6WR73	Q6WR73 coccyzus er
47	15	62.5	12	2 Q6WR79	Q6WR79 cuculus can
48	15	62.5	14	2 Q71H30	Q71H30 andrena bra
49	15	62.5	16	2 Q76019	Q76019 aspergillus
50	15	62.5	19	2 Q7S645	Q7S645 neurospora
51	15	62.5	20	1 COXA_THUOB	P80972 thunnus obe
52	15	62.5	20	2 Q95MK5	Q95MK5 varecia var
53	15	62.5	20	2 Q673D5	Q673D5 dehalococco
54	15	62.5	20	2 Q9R5E8	Q9R5E8 bacillus sp
55	14	58.3	8	1 AKH_PROTE	P81856 protophormi
56	14	58.3	8	1 AKH_TABAT	P14595 tabanus atr
57	14	58.3	8	1 HTF1_PERAM	P04548 periplaneta
58	14	58.3	8	1 HTF2_PERAM	P04549 periplaneta
59	14	58.3	8	1 HTF_TENMO	P67789 tenebrio mo
60	14	58.3	8	1 HTF_ZOPRU	P67790 zophobas ru
61	14	58.3	8	1 RPCH_PANBO	P08939 pandalus bo
62	14	58.3	8	2 Q7M4H6	Q7M4H6 ischnura se
63	14	58.3	8	2 Q7M4H7	Q7M4H7 pseudagrion
64	14	58.3	10	1 HTF1_ROMMI	P18110 romalea mic
65	14	58.3	10	1 HTF2_CARMO	P62542 carausius m
66	14	58.3	10	1 HTF2_EXTTI	P62543 extatosoma
67	14	58.3	10	1 HTF_ELAGO	P84220 blattella g
68	14	58.3	10	1 HTF_GROPO	P84221 gromphadori
69	14	58.3	10	1 HTF_LEUMA	P84219 leucophaea
70	14	58.3	10	1 HTF_NAUCI	P84218 nauphoeta c
71	14	58.3	10	1 HTF_TABAT	P14596 tabanus atr
72	14	58.3	10	2 Q79885	Q79885 anolis pate
73	14	58.3	10	2 Q79903	Q79903 oplurus cuv
74	14	58.3	10	2 Q79906	Q79906 phrynosoma
75	14	58.3	10	2 Q8W7U4	Q8W7U4 anolis nite
76	14	58.3	10	2 Q8W8Q2	Q8W8Q2 anolis punc
77	14	58.3	10	2 Q8W8Q3	Q8W8Q3 anolis nite
78	14	58.3	10	2 Q8W8Q4	Q8W8Q4 anolis punc
79	14	58.3	10	2 Q8W969	Q8W969 anolis orto
80	14	58.3	10	2 Q8W970	Q8W970 anolis nite
81	14	58.3	10	2 Q8W971	Q8W971 anolis fusc
82	14	58.3	10	2 Q8WDG6	Q8WDG6 anolis trac
83	14	58.3	10	2 Q8WDH0	Q8WDH0 anolis limi
84	14	58.3	10	2 Q8WDH2	Q8WDH2 anolis lemu
85	14	58.3	10	2 Q8WDH4	Q8WDH4 anolis carp
86	14	58.3	10	2 Q8WDH6	Q8WDH6 anolis wood
87	14	58.3	10	2 Q8WDH8	Q8WDH8 anolis mest
88	14	58.3	10	2 Q8WDI8	Q8WDI8 anolis tran
89	14	58.3	10	2 Q6WBN7	Q6WBN7 scelopor
90	14	58.3	10	2 Q6WBR1	Q6WBR1 scelopor
91	14	58.3	10	2 Q6WBR4	Q6WBR4 scelopor
92	14	58.3	10	2 Q6WBS3	Q6WBS3 scelopor
93	14	58.3	10	2 Q6WBT8	Q6WBT8 scelopor
94	14	58.3	10	2 Q6WBU1	Q6WBU1 scelopor
95	14	58.3	10	2 Q6WBM2	Q6WBM2 phrynosoma
96	14	58.3	10	2 Q6WBW5	Q6WBW5 phrynosoma
97	14	58.3	10	2 Q6WBW8	Q6WBW8 phrynosoma
98	14	58.3	10	2 Q6WBX1	Q6WBX1 phrynosoma
99	14	58.3	10	2 Q6WBX4	Q6WBX4 phrynosoma
100	14	58.3	10	2 Q6WZN6	Q6WZN6 anolis cybo
101	14	58.3	10	2 Q6X061	Q6X061 anolis haet
102	14	58.3	10	2 Q6X071	Q6X071 anolis shre
103	14	58.3	10	2 Q6X0C3	Q6X0C3 anolis whit
104	14	58.3	10	2 Q6X0D2	Q6X0D2 anolis armo

105	14	58.3	10	2	Q6X0D8	Q6x0d8 anolis long	178	14	58.3	19	2	Q44506	Q44506 anabaena va
106	14	58.3	10	2	Q71DR5	Q71dr5 leiocephalu	179	14	58.3	19	2	Q60LM2	Q60lm2 influenza a
107	14	58.3	10	2	Q71DR8	Q71dr8 leiocephalu	180	14	58.3	20	1	CRFC_SPIOL	P30806 spinacia ol
108	14	58.3	10	2	Q71DS4	Q71ds4 tropidurus	181	14	58.3	20	1	GBB4_RAT	O35353 rattus norv
109	14	58.3	10	2	Q71DS7	Q71ds7 tropidurus	182	14	58.3	20	2	Q95MJ7	Q95mj7 tarsius syr
110	14	58.3	10	2	Q71DT0	Q71dt0 uranoscodon	183	14	58.3	20	2	Q95MJ8	Q95mj8 galago moho
111	14	58.3	10	2	Q71DT3	Q71dt3 tropidurus	184	14	58.3	20	2	Q95MJ9	Q95mj9 pan troglod
112	14	58.3	10	2	Q71DT6	Q71dt6 uracentron	185	14	58.3	20	2	Q95MK0	Q95mk0 pongo pygma
113	14	58.3	10	2	Q71DT9	Q71dt9 stenocercus	186	14	58.3	20	2	Q95MK1	Q95mk1 colobus ang
114	14	58.3	10	2	Q71DU2	Q71du2 stenocercus	187	14	58.3	20	2	Q95MK2	Q95mk2 papio cynoc
115	14	58.3	10	2	Q71DU5	Q71du5 stenocercus	188	14	58.3	20	2	Q95MK3	Q95mk3 ateles belz
116	14	58.3	10	2	Q71DU8	Q71du8 sceloporos	189	14	58.3	20	2	Q95MK4	Q95mk4 cheirogaleu
117	14	58.3	10	2	Q71DM0	Q71dm0 phrynosoma	190	14	58.3	20	2	Q95MK6	Q95mk6 eulemur cor
118	14	58.3	10	2	Q71DX5	Q71dx5 urostephous	191	14	58.3	20	2	Q9TRA4	Q9tra4 sus scrofa
119	14	58.3	10	2	Q71DX8	Q71dx8 enyalius le	192	14	58.3	20	2	Q66548	Q66548 human herpe
120	14	58.3	10	2	Q71DY1	Q71dy1 pristiadacty	193	13	54.2	6	1	E101_LITRU	P82096 litoria rub
121	14	58.3	10	2	Q71DY4	Q71dy4 leiosaurus	194	13	54.2	9	2	Q28121	Q28121 bos taurus
122	14	58.3	10	2	Q71DY7	Q71dy7 leiosaurus	195	13	54.2	15	2	Q6JQC4	Q6jcg4 tetraleurod
123	14	58.3	10	2	Q71DZ0	Q71dz0 diplolaemus	196	13	54.2	15	2	Q6JCS2	Q6jcs2 aleuroplatu
124	14	58.3	10	2	Q71DZ3	Q71dz3 diplolaemus	197	13	54.2	16	2	Q697F2	Q697f2 bemisia sp.
125	14	58.3	10	2	Q71E08	Q71e08 anolis cybo	198	13	54.2	16	2	Q9XNP6	Q9xnp6 boophilus m
126	14	58.3	10	2	Q71E11	Q71e11 chalarodon	199	13	54.2	18	2	Q7S173	Q7s173 neurospora
127	14	58.3	10	2	Q71E23	Q71e23 corycophane	200	13	54.2	18	2	Q8RU82	Q8ru82 zea mays (m
128	14	58.3	10	2	Q71E35	Q71e35 basiliscus	201	13	54.2	19	2	Q9TU41	Q9tu41 loxodonta a
129	14	58.3	10	2	Q71SD0	Q71sd0 liolaemus w	202	13	54.2	19	2	Q9TU42	Q9tu42 mammutus p
130	14	58.3	10	2	Q9T8U8	Q9t8u8 liolaemus p	203	13	54.2	19	2	Q99722	Q99722 lampyrotorn
131	14	58.3	10	2	Q9T8X1	Q9t8x1 liolaemus a	204	13	54.2	20	2	Q90X92	Q90x92 gallus gall
132	14	58.3	10	2	Q9ZY56	Q9zy56 stenocercus	205	12	50.0	8	2	Q7GEM6	Q7gem6 branchiosto
133	14	58.3	12	2	Q6WR34	Q6wr34 phoenicopte	206	12	50.0	10	1	GONI_PETMA	P04378 petromyzon
134	14	58.3	12	2	Q6WR37	Q6wr37 buteo jamai	207	12	50.0	10	2	Q6UJL2	Q6ujl2 strophurus
135	14	58.3	12	2	Q6WR43	Q6wr43 scolopax mi	208	12	50.0	11	1	CA31_LITCI	P82089 litoria cit
136	14	58.3	12	2	Q6WR55	Q6wr55 crinifer pi	209	12	50.0	11	1	CA32_LITCI	P82090 litoria cit
137	14	58.3	12	2	Q6WR58	Q6wr58 musophaga v	210	12	50.0	11	1	CORZ_PERAM	P11496 periplaneta
138	14	58.3	12	2	Q6WR82	Q6wr82 urocolius m	211	12	50.0	11	2	Q6S5M8	Q6esm8 pycoltaemu
139	14	58.3	12	2	Q6WR88	Q6wr88 coracias sp	212	12	50.0	11	2	Q9G359	Q9g359 papalura fl
140	14	58.3	12	2	Q6WR91	Q6wr91 trogon curu	213	12	50.0	11	2	Q9G607	Q9g607 aphanictis
141	14	58.3	12	2	Q6WR94	Q6wr94 tockus eryt	214	12	50.0	12	2	P92680	P92680 trimeresuru
142	14	58.3	12	2	Q6WR97	Q6wr97 anseranas a	215	12	50.0	16	2	Q9M237	Q9m237 pan troglod
143	14	58.3	12	2	Q6WRA0	Q6wra0 chauna torq	216	12	50.0	17	2	Q8MJ33	Q8mj33 sus scrofa
144	14	58.3	12	2	Q6WRA3	Q6wra3 megapodius	217	12	50.0	17	2	Q9TR22	Q9tr22 bos taurus
145	14	58.3	12	2	Q6WRA6	Q6wra6 alectura la	218	12	50.0	18	2	Q9QW51	Q9qw51 mus sp. . a
146	14	58.3	12	2	Q6WRA9	Q6wra9 crax rubra	219	12	50.0	19	2	Q7REE1	Q7ree1 plasmodium
147	14	58.3	12	2	Q8HMG3	Q8hn63 sayornis ph	220	11	45.8	2	1	GWA_SEPOF	P58649 octopus min
148	14	58.3	12	2	Q8HMG6	Q8hn66 acryllium v	221	11	45.8	4	1	OCPI_OCTMI	P30425 bothrops in
149	14	58.3	12	2	Q53579	Q53579 rhodobacter	222	11	45.8	5	1	BPPT_BOTIN	P38639 mus musculu
150	14	58.3	13	1	BML2_BOMVA	P84211 bombina var	223	11	45.8	5	1	UF01_MOUSE	P41491 locustia mig
151	14	58.3	13	1	YPNP_PHOLU	P41122 photorhabdu	224	11	45.8	6	1	LOKI_LOCOM	P58803 conus imper
152	14	58.3	13	2	Q7MIF5	Q7mif5 freesia ref	225	11	45.8	7	1	BRHP_CONIM	P83455 pachymedusa
153	14	58.3	13	2	Q66NE7	Q66ne7 borrelia bu	226	11	45.8	7	1	TPFY_PACDA	P82065 litoria rub
154	14	58.3	13	2	Q66NE7	Q66ne7 newcastle d	227	11	45.8	7	1	TY51_LITRU	P35919 achatina fu
155	14	58.3	15	2	Q6LC27	Q6lc27 homo sapien	228	11	45.8	7	1	WWA1_ACHFU	P35940 achatina fu
156	14	58.3	15	2	Q9UC22	Q9uc22 homo sapien	229	11	45.8	7	1	WWA2_ACHFU	P35921 achatina fu
157	14	58.3	15	2	Q53580	Q53580 rhodobacter	230	11	45.8	7	1	WBA3_ACHFU	Q9brv4 homo sapien
158	14	58.3	15	2	Q9R5D6	Q9r5d6 chromatium	231	11	45.8	7	2	Q9BRV4	Q9brv4 homo sapien
159	14	58.3	16	2	Q79B06	Q79b06 helicobacte	232	11	45.8	7	2	Q9S945	Q9s945 saccharomyc
160	14	58.3	16	2	Q9R4E2	Q9r4f2 streptomyce	233	11	45.8	7	2	Q49223	Q49223 glycine max
161	14	58.3	16	2	Q9QW76	Q9qw76 mus sp. hom	234	11	45.8	7	2	Q8KMS9	Q8kms9 enterobacte
162	14	58.3	16	2	Q8QGA1	Q8qga1 brachydanio	235	11	45.8	7	2	Q8GL00	Q8gl00 borrelia bu
163	14	58.3	17	2	Q8MIG9	Q8mig9 cynopterus	236	11	45.8	7	2	Q8GL04	Q8je1 human immun
164	14	58.3	17	2	Q9QUJ4	Q9quj4 mus sp. mep	237	11	45.8	7	2	Q8JEB1	P18691 thunnus alb
165	14	58.3	17	2	Q6QLL7	Q6ql17 influenza a	238	11	45.8	8	1	ACI_THUAL	P84241 geotrupes s
166	14	58.3	17	2	Q6QLL9	Q6ql19 influenza a	239	11	45.8	8	1	AKH_GEOST	P84240 melolontha
167	14	58.3	17	2	Q6QLM0	Q6qlm0 influenza a	240	11	45.8	8	1	AKH_MEML	P84242 pachnoda ma
168	14	58.3	17	2	Q6QLM1	Q6qlm1 influenza a	241	11	45.8	8	1	AKH_PACNA	P83661 cyphononyx
169	14	58.3	18	2	Q8N0X8	Q8n0x8 homo sapien	242	11	45.8	8	1	C125_CYPDO	P68125 dasyurus vi
170	14	58.3	18	2	Q71U72	Q71u72 homo sapien	243	11	45.8	8	1	CKKN_DASVI	P68126 macropus eu
171	14	58.3	18	2	Q9ZYW4	Q9zyw4 habrobracon	244	11	45.8	8	1	CKKN_MACEU	P58785 conus purpu
172	14	58.3	18	2	Q9ZYX7	Q9zyx7 perga conde	245	11	45.8	8	1	COM2_CONPU	P21140 leucophaea
173	14	58.3	19	2	P83003	P83003 entamoeba h	246	11	45.8	8	1	LCK1_LEUMA	P21141 leucophaea
174	14	58.3	19	2	Q9T1W2	Q9t1w2 equus cabal	247	11	45.8	8	1	LCK2_LEUMA	P21142 leucophaea
175	14	58.3	19	2	Q9T2V5	Q9t2v5 crithidia f	248	11	45.8	8	1	LCK3_LEUMA	P21143 leucophaea
176	14	58.3	19	2	Q9ZYW7	Q9zyw7 aphidius ro	249	11	45.8	8	1	LCK4_LEUMA	P19987 leucophaea
177	14	58.3	19	2	Q9ZYW8	Q9zyw8 ichneutes b	250	11	45.8	8	1	LCK5_LEUMA	

251	11	45.8	8	1	LCK6_LEUMA	P19988 leucophaea	324	11	45.8	9	1	LITR_PHYRO	P08946 phyllomedus
252	11	45.8	8	1	LCK7_LEUMA	P19989 leucophaea	325	11	45.8	9	1	LIMP_LOCHI	P31799 locusta mig
253	11	45.8	8	1	LCK8_LEUMA	P19990 leucophaea	326	11	45.8	9	1	NEF_HV128	P12481 human immun
254	11	45.8	8	1	NGIF_RAT	P82598 rattus norv	327	11	45.8	9	1	PTSP_BOMMO	P82003 bombyx mori
255	11	45.8	8	1	PK1_PERAM	P82685 periplaneta	328	11	45.8	9	2	O95953	O95953 homo sapien
256	11	45.8	8	1	PK2_PERAM	P82686 periplaneta	329	11	45.8	9	2	Q16386	Q16386 homo sapien
257	11	45.8	8	1	PK3_PERAM	P82687 periplaneta	330	11	45.8	9	2	Q6LDB5	Q6LDB5 homo sapien
258	11	45.8	8	1	PK4_PERAM	P82688 periplaneta	331	11	45.8	9	2	Q6QF45	Q6QF45 homo sapien
259	11	45.8	8	1	PK5_PERAM	P82689 periplaneta	332	11	45.8	9	2	Q71EB9	Q71EB9 homo sapien
260	11	45.8	8	1	PLP_BRANA	P81707 brassica na	333	11	45.8	9	2	Q7M4S2	Q7M4S2 homo sapien
261	11	45.8	8	1	RTJ3_BOVIN	P82929 bos taurus	334	11	45.8	9	2	O9H326	O9H326 homo sapien
262	11	45.8	8	1	VAM6_MOUSE	P83853 mus musculus	335	11	45.8	9	2	O9H3Y3	O9H3Y3 homo sapien
263	11	45.8	8	2	Q15888	Q15888 homo sapien	336	11	45.8	9	2	Q9UC36	Q9UC36 homo sapien
264	11	45.8	8	2	Q15890	Q15890 homo sapien	337	11	45.8	9	2	Q9UCQ9	Q9UCQ9 homo sapien
265	11	45.8	8	2	Q8IVK3	Q8IVK3 homo sapien	338	11	45.8	9	2	Q9UK44	Q9UK44 homo sapien
266	11	45.8	8	2	Q86SL0	Q86SL0 homo sapien	339	11	45.8	9	2	Q9UMA0	Q9UMA0 homo sapien
267	11	45.8	8	2	Q7M3S2	Q7M3S2 trypanosoma	340	11	45.8	9	2	O9UMF3	O9UMF3 homo sapien
268	11	45.8	8	2	Q7M3S3	Q7M3S3 trypanosoma	341	11	45.8	9	2	O9UQW0	O9UQW0 homo sapien
269	11	45.8	8	2	Q02831	Q02831 oryctolagus	342	11	45.8	9	2	Q7M3N7	Q7M3N7 gryllus bim
270	11	45.8	8	2	Q95M23	Q95M23 sus scrofa	343	11	45.8	9	2	Q7M3N8	Q7M3N8 gryllus bim
271	11	45.8	8	2	Q9TRY3	Q9TRY3 sus sp. ins	344	11	45.8	9	2	Q7M3N9	Q7M3N9 gryllus bim
272	11	45.8	8	2	Q8W8G2	Q8W8G2 diadema sav	345	11	45.8	9	2	Q7M4D5	Q7M4D5 diadema set
273	11	45.8	8	2	Q8W8G3	Q8W8G3 diadema pau	346	11	45.8	9	2	Q9MW43	Q9MW43 homo sapien
274	11	45.8	8	2	Q8W8G4	Q8W8G4 diadema mex	347	11	45.8	9	2	Q8SHF0	Q8SHF0 chamaeleo n
275	11	45.8	8	2	Q8W8G5	Q8W8G5 diadema ant	348	11	45.8	9	2	Q8W8W5	Q8W8W5 diadema set
276	11	45.8	8	2	Q8W8G6	Q8W8G6 diadema mex	349	11	45.8	9	2	Q8W8X4	Q8W8X4 diadema ant
277	11	45.8	8	2	Q8W8G7	Q8W8G7 lomix hirta	350	11	45.8	9	2	Q8W8X4	Q8W8X4 diadema mex
278	11	45.8	8	2	Q94PX5	Q94PX5 felis silve	351	11	45.8	9	2	Q8WFS4	Q8WFS4 diadema mex
279	11	45.8	8	2	Q94PX6	Q94PX6 felis libyc	352	11	45.8	9	2	Q94NA9	Q94NA9 daubentonia
280	11	45.8	8	2	Q94PX7	Q94PX7 felis silve	353	11	45.8	9	2	Q94NB0	Q94NB0 microcebus
281	11	45.8	8	2	Q94V82	Q94V82 varanus yuw	354	11	45.8	9	2	Q94NB1	Q94NB1 microcebus
282	11	45.8	8	2	Q94V88	Q94V88 varanus tri	355	11	45.8	9	2	Q94NB2	Q94NB2 microcebus
283	11	45.8	8	2	Q94V91	Q94V91 varanus tim	356	11	45.8	9	2	Q94VC6	Q94VC6 varanus pil
284	11	45.8	8	2	Q94VA7	Q94VA7 varanus sal	357	11	45.8	9	2	Q94VD8	Q94VD8 varanus nil
285	11	45.8	8	2	Q94VB2	Q94VB2 varanus sal	358	11	45.8	9	2	Q94VE1	Q94VE1 varanus mer
286	11	45.8	8	2	Q94VB5	Q94VB5 varanus sal	359	11	45.8	9	2	Q94VG2	Q94VG2 varanus ind
287	11	45.8	8	2	Q94VCL	Q94VCL varanus rud	360	11	45.8	9	2	Q94VH4	Q94VH4 varanus gla
288	11	45.8	8	2	Q94VE4	Q94VE4 varanus mel	361	11	45.8	9	2	Q94VIO	Q94VIO varanus gig
289	11	45.8	8	2	Q94VF6	Q94VF6 varanus job	362	11	45.8	9	2	Q94V18	Q94V18 varanus ere
290	11	45.8	8	2	Q94VF9	Q94VF9 varanus ind	363	11	45.8	9	2	Q94VJ1	Q94VJ1 varanus dor
291	11	45.8	8	2	Q94VJ4	Q94VJ4 varanus ben	364	11	45.8	9	2	Q94XE6	Q94XE6 tectocoris
292	11	45.8	8	2	Q70Y57	Q70Y57 fuerstia af	365	11	45.8	9	2	Q691D6	Q691D6 anolis sagr
293	11	45.8	8	2	Q70Y84	Q70Y84 plectranth	366	11	45.8	9	2	Q71DX2	Q71DX2 urostrophus
294	11	45.8	8	2	Q715L5	Q715L5 varanus dum	367	11	45.8	9	2	Q85DB0	Q85DB0 lepitemur s
295	11	45.8	8	2	Q9TD02	Q9TD02 asterina pe	368	11	45.8	9	2	Q85DB8	Q85DB8 lepitemur e
296	11	45.8	8	2	Q9TD02	Q9TD02 terranatos	369	11	45.8	9	2	Q9T688	Q9T688 gekko gekko
297	11	45.8	8	2	Q6ZZ01	Q6ZZ01 silene con	370	11	45.8	9	2	Q38366	Q38366 bacterioph
298	11	45.8	8	2	Q8ZZ02	Q8ZZ02 lychnis cor	371	11	45.8	9	2	Q6A1H7	Q6A1H7 hordeum vul
299	11	45.8	8	2	Q85406	Q85406 coxiella bu	372	11	45.8	9	2	Q6ZZ00	Q6ZZ00 silene rotu
300	11	45.8	8	2	Q6LDP8	Q6LDP8 pseudomonas	373	11	45.8	9	2	Q47410	Q47410 escherichia
301	11	45.8	8	2	Q7M0L0	Q7M0L0 clostridium	374	11	45.8	9	2	Q6VCX0	Q6VCX0 streptomyce
302	11	45.8	8	2	Q7M124	Q7M124 kluyvera ci	375	11	45.8	9	2	Q8GL26	Q8GL26 borrelia bu
303	11	45.8	8	2	Q8G9A0	Q8G9A0 borrelia bu	376	11	45.8	9	2	Q8GLJ1	Q8GLJ1 borrelia bu
304	11	45.8	8	2	Q8GL21	Q8GL21 borrelia bu	377	11	45.8	9	2	Q9R5M1	Q9R5M1 staphylococ
305	11	45.8	8	2	Q35835	Q35835 rattus sp.	378	11	45.8	9	2	Q9R635	Q9R635 chlamydia t
306	11	45.8	8	2	P70243	P70243 mus musculu	379	11	45.8	9	2	Q9R9C4	Q9R9C4 borrelia bu
307	11	45.8	8	2	Q99MNO	Q99MNO mus musculu	380	11	45.8	9	2	Q6LA01	Q6LA01 rattus norv
308	11	45.8	8	2	Q62721	Q62721 rattus norv	381	11	45.8	9	2	Q7M078	Q7M078 rattus norv
309	11	45.8	8	2	Q9ET16	Q9ET16 mesocricetu	382	11	45.8	9	2	Q80X07	Q80X07 mus. sp. thr
310	11	45.8	8	2	Q9ET17	Q9ET17 mus caroli	383	11	45.8	9	2	Q90350	Q90350 gb virus c/
311	11	45.8	8	2	Q9ET18	Q9ET18 mus spretus	384	11	45.8	9	2	Q65711	Q65711 berne virus
312	11	45.8	8	2	Q64971	Q64971 alfalfa mos	385	11	45.8	9	2	Q69100	Q69100 human herpe
313	11	45.8	8	2	P79940	P79940 xenopus lae	386	11	45.8	9	2	Q89491	Q89491 murine minu
314	11	45.8	8	2	Q98TU5	Q98TU5 xenopus lae	387	11	45.8	9	2	Q673W5	Q673W5 tyrannus me
315	11	45.8	8	2	Q88LFI	Q88LFI myrmotherul	388	11	45.8	9	2	Q673W6	Q673W6 terpsiphon
316	11	45.8	8	2	Q68LG3	Q68LG3 sakesphorus	389	11	45.8	9	2	Q673W7	Q673W7 telophorus
317	11	45.8	8	2	Q6R7U6	Q6R7U6 gnyptescin	390	11	45.8	9	2	Q673W9	Q673W9 tchagra sen
318	11	45.8	8	2	Q7LZ27	Q7LZ27 naja oxiana	391	11	45.8	9	2	Q673X0	Q673X0 rhodophoneu
319	11	45.8	9	1	CAER_PHYSA	Q7LZC4 phyllomedus	392	11	45.8	9	2	Q673X1	Q673X1 rhipidura a
320	11	45.8	9	1	CONV_CONVE	P83047 conus ventr	393	11	45.8	9	2	Q673X2	Q673X2 pseudobias
321	11	45.8	9	1	DI_NEPNO	P24816 nephrops no	394	11	45.8	9	2	Q673X3	Q673X3 prionops sc
322	11	45.8	9	1	DSIP_RABIT	P01158 oryctolagus	395	11	45.8	9	2	Q673X4	Q673X4 prionops re
323	11	45.8	9	1	LITO_LITAU	P08945 litoria aur	396	11	45.8	9	2	Q673X4	Q673X4 prionops re

397	11	45.8	9	2	Q673X5	Q673x5 platysteira	470	11	45.8	10	2	Q9TR47	Q9tr47 bos taurus
398	11	45.8	9	2	Q673X6	Q673x6 oriolus xan	471	11	45.8	10	2	Q9TS43	Q9ts43 sus scrofa
399	11	45.8	9	2	Q673X7	Q673x7 nilaus afer	472	11	45.8	10	2	Q9TU33	Q9tu33 canis famul
400	11	45.8	9	2	Q673X8	Q673x8 bias flammu	473	11	45.8	10	2	Q9U888	Q9u888 basiliscus
401	11	45.8	9	2	Q673X9	Q673x9 malacotus	474	11	45.8	10	2	Q9U888	Q9u888 basiliscus
402	11	45.8	9	2	Q673Y0	Q673y0 lanius coll	475	11	45.8	10	2	Q79891	Q79891 crotophytus
403	11	45.8	9	2	Q673Y1	Q673y1 lanioturdus	476	11	45.8	10	2	Q79894	Q79894 gambelia wi
404	11	45.8	9	2	Q673Y2	Q673y2 lanioturdus	477	11	45.8	10	2	Q79900	Q79900 liolaemus p
405	11	45.8	9	2	Q673Y3	Q673y3 laniarius f	478	11	45.8	10	2	Q79909	Q79909 sauromalus
406	11	45.8	9	2	Q673Y4	Q673y4 laniarius b	479	11	45.8	10	2	Q79912	Q79912 chamaeleo f
407	11	45.8	9	2	Q673Y5	Q673y5 laniarius a	480	11	45.8	10	2	Q79915	Q79915 leioplepis b
408	11	45.8	9	2	Q673Y6	Q673y6 platysteira	481	11	45.8	10	2	Q79924	Q79924 elgaria pan
409	11	45.8	9	2	Q673Y7	Q673y7 dryoscopus	482	11	45.8	10	2	Q92616	Q92616 aspidosceli
410	11	45.8	9	2	Q673Y8	Q673y8 dryoscopus	483	11	45.8	10	2	Q92632	Q92632 eremias gra
411	11	45.8	9	2	Q673Y9	Q673y9 dicrurus pa	484	11	45.8	10	2	Q92648	Q92648 lialis jica
412	11	45.8	9	2	Q673Z0	Q673z0 cyanolanius	485	11	45.8	10	2	Q92654	Q92654 eupropis au
413	11	45.8	9	2	Q673Z1	Q673z1 corvus coro	486	11	45.8	10	2	Q92733	Q92733 fejeriarya
414	11	45.8	9	2	Q673Z2	Q673z2 coracina me	487	11	45.8	10	2	Q92758	Q92758 teratocoscinc
415	11	45.8	9	2	Q673Z3	Q673z3 telophorus	488	11	45.8	10	2	Q92762	Q92762 uromastyx a
416	11	45.8	9	2	Q673Z4	Q673z4 telophorus	489	11	45.8	10	2	Q92766	Q92766 varanus gri
417	11	45.8	9	2	Q673Z5	Q673z5 telophorus	490	11	45.8	10	2	Q92771	Q92771 xonosaustus
418	11	45.8	9	2	Q673Z6	Q673z6 campephaga	491	11	45.8	10	2	Q92774	Q92774 xantusia vi
419	11	45.8	9	2	Q673Z7	Q673z7 tchagra min	492	11	45.8	10	2	Q8SH83	Q8sh83 brookesia t
420	11	45.8	9	2	Q673Z8	Q673z8 bias musicu	493	11	45.8	10	2	Q8SH85	Q8sh85 brookesia t
421	11	45.8	9	2	Q673Z9	Q673z9 bias musicu	494	11	45.8	10	2	Q8SH88	Q8sh88 brookesia t
422	11	45.8	9	2	Q78DU2	Q78du2 gallus gall	495	11	45.8	10	2	Q8SH90	Q8sh90 brookesia s
423	11	45.8	9	2	Q7LZ66	Q7Lz66 meleagris g	496	11	45.8	10	2	Q8SH93	Q8sh93 brookesia p
424	11	45.8	9	2	Q801K0	Q801k0 illicura mil	497	11	45.8	10	2	Q8SH96	Q8sh96 brookesia p
425	11	45.8	9	2	Q801K1	Q801k1 chiroxiphia	498	11	45.8	10	2	Q8SH99	Q8sh99 brookesia n
426	11	45.8	9	2	Q801K2	Q801k2 antilophia	499	11	45.8	10	2	Q8SHA2	Q8sha2 brookesia b
427	11	45.8	9	2	Q9PRJ4	Q9prj4 lepisosteus	500	11	45.8	10	2	Q8SHA5	Q8sha5 brookesia a
428	11	45.8	9	2	Q857J3	Q857j3 simian sarc	501	11	45.8	10	2	Q8SHA8	Q8sha8 rhampoleon
429	11	45.8	10	1	AEGL_AGRAE	P83455 agrocye ae	502	11	45.8	10	2	Q8SHB1	Q8shb1 rhampoleon
430	11	45.8	10	1	APE_CAPGI	P80474 capnocytoph	503	11	45.8	10	2	Q8SHB4	Q8shb4 furcifer ve
431	11	45.8	10	1	BPP2_BOTIN	P30422 bothrops in	504	11	45.8	10	2	Q8SHB7	Q8shb7 furcifer ou
432	11	45.8	10	1	BPP2_BOTJA	P01022 bothrops ja	505	11	45.8	10	2	Q8SHC0	Q8shc0 furcifer la
433	11	45.8	10	1	BPP8_BOTIN	P30426 bothrops in	506	11	45.8	10	2	Q8SHC3	Q8shc3 furcifer be
434	11	45.8	10	1	BPP_VIPAS	P31351 vipera aspi	507	11	45.8	10	2	Q8SHC6	Q8shc6 furcifer ba
435	11	45.8	10	1	BRK_ONCMY	Q9prz1 oncorhynch	508	11	45.8	10	2	Q8SHC9	Q8shc9 furcifer ba
436	11	45.8	10	1	CAL2_LITCI	P62540 litoria cit	509	11	45.8	10	2	Q8SHD2	Q8shd2 chamaelo w
437	11	45.8	10	1	CAL2_LITSP	P62541 litoria spl	510	11	45.8	10	2	Q8SHD5	Q8shd5 chamaelo s
438	11	45.8	10	1	CAER_LITXA	P52641 litoria xan	511	11	45.8	10	2	Q8SHD8	Q8shd8 chamaelo r
439	11	45.8	10	1	GONI_ALLMI	P37041 alligator m	512	11	45.8	10	2	Q8SHE1	Q8she1 chamaelo q
440	11	45.8	10	1	GONI_CHEPR	P80677 chelyosoma	513	11	45.8	10	2	Q8SHE4	Q8she4 chamaelo q
441	11	45.8	10	1	GONI_CLUPA	P81749 clupea pall	514	11	45.8	10	2	Q8SHE7	Q8she7 chamaelo p
442	11	45.8	10	1	GON2_ALLMI	P86073 alligator m	515	11	45.8	10	2	Q8SHF3	Q8shf3 chamaelo m
443	11	45.8	10	1	GON2_CHEPR	P86078 chelyosoma	516	11	45.8	10	2	Q8SHF6	Q8shf6 chamaelo m
444	11	45.8	10	1	GON2_CHICK	P68072 gallus gall	517	11	45.8	10	2	Q8SHF9	Q8shf9 chamaelo j
445	11	45.8	10	1	GON2_CLUPA	P68075 clupea pall	518	11	45.8	10	2	Q8SHG2	Q8shg2 chamaelo j
446	11	45.8	10	1	GON2_HYDCO	P68076 hydrolagus	519	11	45.8	10	2	Q8SHG5	Q8shg5 chamaelo h
447	11	45.8	10	1	GON2_SQUAC	P68074 squalus aca	520	11	45.8	10	2	Q8SHG8	Q8shg8 chamaelo g
448	11	45.8	10	1	GON3_ONCKE	P20367 oncorhynch	521	11	45.8	10	2	Q8SHH1	Q8shh1 chamaelo f
449	11	45.8	10	1	GON3_PETMA	P30948 petromyzon	522	11	45.8	10	2	Q8SHH4	Q8shh4 chamaelo f
450	11	45.8	10	1	GONL_SQUAC	P27429 squalus aca	523	11	45.8	10	2	Q8SHH7	Q8shh7 chamaelo e
451	11	45.8	10	1	GRP_RANRI	P23260 rana ridibu	524	11	45.8	10	2	Q8SHI0	Q8shi0 chamaelo d
452	11	45.8	10	1	LABA_JATMU	P31270 jatropa mu	525	11	45.8	10	2	Q8SHI3	Q8shi3 chamaelo c
453	11	45.8	10	1	MP2_MICOC	P81533 micropitlis	526	11	45.8	10	2	Q8SHI6	Q8shi6 chamaelo c
454	11	45.8	10	1	NO40_TOBAC	P55962 nicotiana t	527	11	45.8	10	2	Q8SHI9	Q8shi9 chamaelo c
455	11	45.8	10	1	PNAL_PRUDU	P81899 prunus dulc	528	11	45.8	10	2	Q8SHJ2	Q8shj2 chamaelo a
456	11	45.8	10	1	TPIS_NICPL	P19118 nicotiana p	529	11	45.8	10	2	Q8SHJ5	Q8shj5 chamaelo par
457	11	45.8	10	2	Q7M5J0	Q7m530 pyrococcus	530	11	45.8	10	2	Q8SHJ8	Q8shj8 calumma osh
458	11	45.8	10	2	Q7MAX1	Q7m4x1 basidiobolu	531	11	45.8	10	2	Q8SHK1	Q8shk1 calumma nas
459	11	45.8	10	2	Q7SA62	Q7sa62 neurospora	532	11	45.8	10	2	Q8SHK4	Q8shk4 calumma hil
460	11	45.8	10	2	Q15342	Q8wt44 homo sapien	533	11	45.8	10	2	Q8SHK7	Q8shk7 calumma glo
461	11	45.8	10	2	Q8WTT4	Q8wt44 homo sapien	534	11	45.8	10	2	Q8SHL0	Q8shl0 calumma gas
462	11	45.8	10	2	Q96QA7	Q96qa7 homo sapien	535	11	45.8	10	2	Q8SHL3	Q8shl3 calumma fur
463	11	45.8	10	2	Q6LA62	Q6la62 homo sapien	536	11	45.8	10	2	Q8SHL6	Q8shl6 calumma cuc
464	11	45.8	10	2	Q25355	Q25355 locusta mig	537	11	45.8	10	2	Q8SHL9	Q8shl9 calumma bre
465	11	45.8	10	2	Q25356	Q25356 locusta mig	538	11	45.8	10	2	Q8SHM2	Q8shm2 calumma boe
466	11	45.8	10	2	Q7RRV6	Q7rrv6 plasmodium	539	11	45.8	10	2	Q8SHM5	Q8shm5 bradypodion
467	11	45.8	10	2	Q7M2Z8	Q7m2z8 bos taurus	540	11	45.8	10	2	Q8SHM8	Q8shm8 bradypodion
468	11	45.8	10	2	Q7M3E8	Q7m3e8 sus scrofa	541	11	45.8	10	2	Q8SHN1	Q8shn1 bradypodion
469	11	45.8	10	2	Q9N1X1	Q9n1x1 equus cabal	542	11	45.8	10	2	Q8SHN7	Q8shn7 bradypodion

543	11	45.8	10	2	Q8SHP0	Q8shp0 bradypodion	616	11	45.8	10	2	Q6WBL6	Q6wb16 sceloporu
544	11	45.8	10	2	Q8SIT8	Q8sit8 xantusia ar	617	11	45.8	10	2	Q6WBL9	Q6wb19 sceloporu
545	11	45.8	10	2	Q8SIU1	Q8siu1 xantusia be	618	11	45.8	10	2	Q6WBM2	Q6wbm2 sceloporu
546	11	45.8	10	2	Q8SIU4	Q8siu4 xantusia he	619	11	45.8	10	2	Q6WBM5	Q6wbm5 sceloporu
547	11	45.8	10	2	Q8W916	Q8w916 liolaemus m	620	11	45.8	10	2	Q6WBM8	Q6wbm8 sceloporu
548	11	45.8	10	2	Q8WDG8	Q8wdg8 anolis line	621	11	45.8	10	2	Q6WBN1	Q6wb11 sceloporu
549	11	45.8	10	2	Q8WDI0	Q8wdi0 anolis sagr	622	11	45.8	10	2	Q6WBN4	Q6wb14 sceloporu
550	11	45.8	10	2	Q8WFT5	Q8wft5 diadema ant	623	11	45.8	10	2	Q6WBP0	Q6wbp0 sceloporu
551	11	45.8	10	2	Q8WFT6	Q8wft6 diadema ant	624	11	45.8	10	2	Q6WBP3	Q6wbp3 sceloporu
552	11	45.8	10	2	Q94NH4	Q94nh4 rana muscos	625	11	45.8	10	2	Q6WBP6	Q6wbp6 sceloporu
553	11	45.8	10	2	Q94PD8	Q94pd8 rana muscos	626	11	45.8	10	2	Q6WBP9	Q6wbp9 sceloporu
554	11	45.8	10	2	Q94V85	Q94v85 varanus sca	627	11	45.8	10	2	Q6WBP9	Q6wbp9 sceloporu
555	11	45.8	10	2	Q94V97	Q94v97 varanus spe	628	11	45.8	10	2	Q6WBP9	Q6wbp9 sceloporu
556	11	45.8	10	2	Q94VC9	Q94vc9 varanus pan	629	11	45.8	10	2	Q6WBP9	Q6wbp9 sceloporu
557	11	45.8	10	2	Q94VD2	Q94vd2 varanus pan	630	11	45.8	10	2	Q6WBP9	Q6wbp9 sceloporu
558	11	45.8	10	2	Q94VD5	Q94vd5 varanus oli	631	11	45.8	10	2	Q6WBP9	Q6wbp9 sceloporu
559	11	45.8	10	2	Q94VF0	Q94vf0 varanus kin	632	11	45.8	10	2	Q6WBP9	Q6wbp9 sceloporu
560	11	45.8	10	2	Q94VG5	Q94vg5 varanus gri	633	11	45.8	10	2	Q6WBP9	Q6wbp9 sceloporu
561	11	45.8	10	2	Q94VH1	Q94vh1 varanus gle	634	11	45.8	10	2	Q6WBP9	Q6wbp9 sceloporu
562	11	45.8	10	2	Q958J8	Q958j8 rana muscos	635	11	45.8	10	2	Q6WBT2	Q6wbt2 sceloporu
563	11	45.8	10	2	Q958K0	Q958k0 rana casc	636	11	45.8	10	2	Q6WBT5	Q6wbt5 sceloporu
564	11	45.8	10	2	Q958K3	Q958k3 rana aurora	637	11	45.8	10	2	Q6WBU7	Q6wb17 sceloporu
565	11	45.8	10	2	Q958K6	Q958k6 rana pretio	638	11	45.8	10	2	Q6WBW0	Q6wbw0 urosaurus o
566	11	45.8	10	2	Q958K9	Q958k9 rana boylii	639	11	45.8	10	2	Q6WBW3	Q6wbw3 holbrookia
567	11	45.8	10	2	Q958L2	Q958l2 rana tempor	640	11	45.8	10	2	Q6WBW6	Q6wbw6 holbrookia
568	11	45.8	10	2	Q958L5	Q958l5 rana sylvat	641	11	45.8	10	2	Q6WBW9	Q6wbw9 holbrookia
569	11	45.8	10	2	Q958L8	Q958l8 rana catesb	642	11	45.8	10	2	Q6X0E4	Q6x0e4 anolis stra
570	11	45.8	10	2	Q6UJG7	Q6ujg7 heteronotia	643	11	45.8	10	2	Q71DV1	Q71dvl microlophus
571	11	45.8	10	2	Q6UJH0	Q6ujh0 gehyra vari	644	11	45.8	10	2	Q71DV4	Q71dvl sceloporu
572	11	45.8	10	2	Q6UJH3	Q6ujh3 liailis jica	645	11	45.8	10	2	Q71DV7	Q71dvl sceloporu
573	11	45.8	10	2	Q6UJH6	Q6ujh6 pseudotheca	646	11	45.8	10	2	Q71E02	Q71e02 anolis dist
574	11	45.8	10	2	Q6UJH9	Q6ujh9 phyllurus c	647	11	45.8	10	2	Q71E05	Q71e05 anolis cris
575	11	45.8	10	2	Q6UJH2	Q6ujh2 nephurus m	648	11	45.8	10	2	Q71E14	Q71e14 brachyloph
576	11	45.8	10	2	Q6UJH5	Q6ujh5 nephurus w	649	11	45.8	10	2	Q71E26	Q71e26 crytophane
577	11	45.8	10	2	Q6UJH8	Q6ujh8 nephurus l	650	11	45.8	10	2	Q71E29	Q71e29 iaemantus
578	11	45.8	10	2	Q6UJH1	Q6ujh1 nephurus v	651	11	45.8	10	2	Q71E32	Q71e32 basilius
579	11	45.8	10	2	Q6UJH4	Q6ujh4 nephurus l	652	11	45.8	10	2	Q71G22	Q71g22 andrena lim
580	11	45.8	10	2	Q6UJH7	Q6ujh7 carhodactyl	653	11	45.8	10	2	Q71S88	Q71sb8 liolaemus f
581	11	45.8	10	2	Q6UJH0	Q6ujh0 crenodactyl	654	11	45.8	10	2	Q71SC1	Q71sc1 liolaemus r
582	11	45.8	10	2	Q6UJH3	Q6ujh3 oedura marm	655	11	45.8	10	2	Q71SC4	Q71sc4 liolaemus a
583	11	45.8	10	2	Q6UJH6	Q6ujh6 rhynchoedur	656	11	45.8	10	2	Q71SC7	Q71sc7 liolaemus s
584	11	45.8	10	2	Q6UJH9	Q6ujh9 dipodactyl	657	11	45.8	10	2	Q71SD6	Q71sd6 liolaemus a
585	11	45.8	10	2	Q6UJH8	Q6ujh8 strophurus	658	11	45.8	10	2	Q71SD9	Q71sd9 liolaemus a
586	11	45.8	10	2	Q6UJH1	Q6ujh1 strophurus	659	11	45.8	10	2	Q71SE2	Q71se2 phymaturus
587	11	45.8	10	2	Q6UJH4	Q6ujh4 dipodactyl	660	11	45.8	10	2	Q71SE5	Q71se5 phymaturus
588	11	45.8	10	2	Q6UJH7	Q6ujh7 strophurus	661	11	45.8	10	2	Q71SE8	Q71se8 ctenoblepha
589	11	45.8	10	2	Q6UJH0	Q6ujh0 dipodactyl	662	11	45.8	10	2	Q76MK5	Q76mk5 eurypharynx
590	11	45.8	10	2	Q6UJH3	Q6ujh3 dipodactyl	663	11	45.8	10	2	Q76ML6	Q76ml6 eurypharynx
591	11	45.8	10	2	Q6UJH6	Q6ujh6 dipodactyl	664	11	45.8	10	2	Q76MM1	Q76mm1 eurypharynx
592	11	45.8	10	2	Q6UJH9	Q6ujh9 dipodactyl	665	11	45.8	10	2	Q7J5U5	Q7j5u5 ovis arie
593	11	45.8	10	2	Q6UJH2	Q6ujh2 dipodactyl	666	11	45.8	10	2	Q8J755	Q8j755 varanus bre
594	11	45.8	10	2	Q6UJH5	Q6ujh5 dipodactyl	667	11	45.8	10	2	Q9B0Z6	Q9b0z6 salamandra
595	11	45.8	10	2	Q6UJH8	Q6ujh8 dipodactyl	668	11	45.8	10	2	Q9B1W9	Q9b1w9 mertensiell
596	11	45.8	10	2	Q6UJH1	Q6ujh1 dipodactyl	669	11	45.8	10	2	Q9B1X0	Q9b1x0 mertensiell
597	11	45.8	10	2	Q6UJH4	Q6ujh4 strophurus	670	11	45.8	10	2	Q9B4S0	Q9b4s0 mertensiell
598	11	45.8	10	2	Q6UJH7	Q6ujh7 strophurus	671	11	45.8	10	2	Q9B4S5	Q9b4s5 mertensiell
599	11	45.8	10	2	Q6UJH0	Q6ujh0 strophurus	672	11	45.8	10	2	Q9B4S8	Q9b4s8 mertensiell
600	11	45.8	10	2	Q6WBG8	Q6wbg8 liolaemus c	673	11	45.8	10	2	Q9B4T1	Q9b4t1 mertensiell
601	11	45.8	10	2	Q6WBH1	Q6wbh1 liolaemus x	674	11	45.8	10	2	Q9B4U2	Q9b4u2 mertensiell
602	11	45.8	10	2	Q6WBH4	Q6wbh4 liolaemus r	675	11	45.8	10	2	Q9B4U5	Q9b4u5 mertensiell
603	11	45.8	10	2	Q6WBH7	Q6wbh7 liolaemus h	676	11	45.8	10	2	Q9B4U8	Q9b4u8 salamandra
604	11	45.8	10	2	Q6WBI0	Q6wb10 liolaemus s	677	11	45.8	10	2	Q9B4V5	Q9b4v5 mertensiell
605	11	45.8	10	2	Q6WBI3	Q6wb13 liolaemus p	678	11	45.8	10	2	Q9B4V8	Q9b4v8 chioglossa
606	11	45.8	10	2	Q6WBI6	Q6wb16 liolaemus k	679	11	45.8	10	2	Q9B4W1	Q9b4w1 triturus vu
607	11	45.8	10	2	Q6WBI9	Q6wb19 liolaemus h	680	11	45.8	10	2	Q9B4W4	Q9b4w4 pachyrriton
608	11	45.8	10	2	Q6WBJ2	Q6wbj2 liolaemus p	681	11	45.8	10	2	Q9B4W7	Q9b4w7 tylootriton
609	11	45.8	10	2	Q6WBJ5	Q6wbj5 liolaemus g	682	11	45.8	10	2	Q9B4X0	Q9b4x0 notophthalm
610	11	45.8	10	2	Q6WBJ8	Q6wbj8 liolaemus n	683	11	45.8	10	2	Q9G362	Q9g362 acanthosaur
611	11	45.8	10	2	Q6WBK1	Q6wbk1 sceloporu	684	11	45.8	10	2	Q9G694	Q9g694 leiolepis g
612	11	45.8	10	2	Q6WBK4	Q6wbk4 sceloporu	685	11	45.8	10	2	Q9G697	Q9g697 chamaeleo d
613	11	45.8	10	2	Q6WBK7	Q6wbk7 sceloporu	686	11	45.8	10	2	Q9MJQ5	Q9mjqs podospora c
614	11	45.8	10	2	Q6WBL0	Q6wb10 sceloporu	687	11	45.8	10	2	Q9T4P9	Q9t4p9 liolaemus d
615	11	45.8	10	2	Q6WBL3	Q6wb13 sceloporu	688	11	45.8	10	2	Q9T8F5	Q9t8f5 liolaemus b

689	11	45.8	10	2	Q9TG00	Q9TG00 liolaemus l	762	11	45.8	10	2	Q9TG74	Q9TG74 wetmorena h
690	11	45.8	10	2	Q9TG05	Q9TG05 liolaemus o	763	11	45.8	10	2	Q9TG77	Q9TG77 sauresia ag
691	11	45.8	10	2	Q9TG08	Q9TG08 liolaemus c	764	11	45.8	10	2	Q9TG80	Q9TG80 ophiodes st
692	11	45.8	10	2	Q9TG11	Q9TG11 liolaemus u	765	11	45.8	10	2	Q9TG83	Q9TG83 diploglossu
693	11	45.8	10	2	Q9TG14	Q9TG14 liolaemus i	766	11	45.8	10	2	Q9TG86	Q9TG86 diploglossu
694	11	45.8	10	2	Q9TG17	Q9TG17 liolaemus a	767	11	45.8	10	2	Q9TG89	Q9TG89 celestus en
695	11	45.8	10	2	Q9TG10	Q9TG10 liolaemus o	768	11	45.8	10	2	Q9TG92	Q9TG92 annietta pu
696	11	45.8	10	2	Q9TG13	Q9TG13 liolaemus q	769	11	45.8	10	2	Q9TG95	Q9TG95 annietta ge
697	11	45.8	10	2	Q9TG16	Q9TG16 liolaemus k	770	11	45.8	10	2	Q9TG98	Q9TG98 shinisaurus
698	11	45.8	10	2	Q9TG19	Q9TG19 liolaemus a	771	11	45.8	10	2	Q9TGA1	Q9TGA1 heloderma s
699	11	45.8	10	2	Q9TG22	Q9TG22 liolaemus r	772	11	45.8	10	2	Q9TGB4	Q9TGB4 aegilops ta
700	11	45.8	10	2	Q9TG25	Q9TG25 liolaemus m	773	11	45.8	10	2	Q9TGS9	Q9TGS9 phymaturus
701	11	45.8	10	2	Q9TG28	Q9TG28 liolaemus w	774	11	45.8	10	2	Q9THT5	Q9THT5 uta stansbu
702	11	45.8	10	2	Q9TG31	Q9TG31 liolaemus s	775	11	45.8	10	2	Q9THT8	Q9THT8 urosaurus g
703	11	45.8	10	2	Q9TG34	Q9TG34 liolaemus s	776	11	45.8	10	2	Q9TYU1	Q9TYU1 uma scopari
704	11	45.8	10	2	Q9TG37	Q9TG37 liolaemus m	777	11	45.8	10	2	Q9TYU4	Q9TYU4 sceloporui
705	11	45.8	10	2	Q9TG40	Q9TG40 liolaemus o	778	11	45.8	10	2	Q9ZYU7	Q9ZYU7 sator angus
706	11	45.8	10	2	Q9TG43	Q9TG43 liolaemus l	779	11	45.8	10	2	Q9ZYU0	Q9ZYU0 petrosaurus
707	11	45.8	10	2	Q9TG46	Q9TG46 liolaemus p	780	11	45.8	10	2	Q9ZYV3	Q9ZYV3 diposaurus
708	11	45.8	10	2	Q9TG49	Q9TG49 liolaemus f	781	11	45.8	10	2	P82443	P82443 nicotiana t
709	11	45.8	10	2	Q9TG52	Q9TG52 liolaemus c	782	11	45.8	10	2	Q99213	Q99213 aegilops ta
710	11	45.8	10	2	Q9TG55	Q9TG55 liolaemus a	783	11	45.8	10	2	Q6TS30	Q6TS30 lycopersico
711	11	45.8	10	2	Q9TG58	Q9TG58 liolaemus m	784	11	45.8	10	2	Q8GZC8	Q8GZC8 hordeum vul
712	11	45.8	10	2	Q9TG61	Q9TG61 liolaemus p	785	11	45.8	10	2	Q8KH9	Q8KH9 clostridium
713	11	45.8	10	2	Q9TG64	Q9TG64 liolaemus d	786	11	45.8	10	2	Q931X4	Q931X4 vibrio chol
714	11	45.8	10	2	Q9TG67	Q9TG67 liolaemus o	787	11	45.8	10	2	Q93T35	Q93T35 acinetobact
715	11	45.8	10	2	Q9TG70	Q9TG70 liolaemus f	788	11	45.8	10	2	Q47561	Q47561 escherichia
716	11	45.8	10	2	Q9TG73	Q9TG73 liolaemus a	789	11	45.8	10	2	Q6JL97	Q6JL97 neisseria g
717	11	45.8	10	2	Q9TG76	Q9TG76 liolaemus r	790	11	45.8	10	2	Q6RI01	Q6RI01 clostridium
718	11	45.8	10	2	Q9TG79	Q9TG79 liolaemus m	791	11	45.8	10	2	Q79AV7	Q79AV7 klebsiella
719	11	45.8	10	2	Q9TG82	Q9TG82 liolaemus s	792	11	45.8	10	2	Q8G8W5	Q8G8W5 borrelia bu
720	11	45.8	10	2	Q9TG85	Q9TG85 liolaemus l	793	11	45.8	10	2	Q9F9H5	Q9F9H5 helicobacte
721	11	45.8	10	2	Q9TG88	Q9TG88 liolaemus e	794	11	45.8	10	2	Q9B5N2	Q9B5N2 clostridm
722	11	45.8	10	2	Q9TG91	Q9TG91 liolaemus a	795	11	45.8	10	2	Q70580	Q70580 mus musculu
723	11	45.8	10	2	Q9TG94	Q9TG94 liolaemus p	796	11	45.8	10	2	Q6LBT3	Q6LBT3 mus musculu
724	11	45.8	10	2	Q9TG97	Q9TG97 liolaemus b	797	11	45.8	10	2	Q8CJE0	Q8CJE0 rattus norv
725	11	45.8	10	2	Q9TG00	Q9TG00 liolaemus c	798	11	45.8	10	2	Q9ESU5	Q9ESU5 mus musculu
726	11	45.8	10	2	Q9TG03	Q9TG03 liolaemus l	799	11	45.8	10	2	Q42355	Q42355 brachydanio
727	11	45.8	10	2	Q9TG06	Q9TG06 liolaemus c	800	11	45.8	10	2	Q8JFE7	Q8JFE7 ficedula al
728	11	45.8	10	2	Q9TG09	Q9TG09 liolaemus n	801	11	45.8	10	2	Q8J333	Q8J333 ficedula hy
729	11	45.8	10	2	Q9TG12	Q9TG12 liolaemus f	802	11	45.8	10	2	Q7LZC5	Q7LZC5 kassina mac
730	11	45.8	10	2	Q9TG15	Q9TG15 liolaemus n	803	11	45.8	10	2	Q9PRU9	Q9PRU9 sparus aura
731	11	45.8	10	2	Q9TG18	Q9TG18 liolaemus m	804	11	45.8	10	2	Q8UT83	Q8UT83 human immun
732	11	45.8	10	2	Q9TG21	Q9TG21 liolaemus l	805	11	45.8	11	1	CEP1_ACHFU	P22790 achaina fu
733	11	45.8	10	2	Q9TG24	Q9TG24 liolaemus t	806	11	45.8	11	1	CX5A_CONAL	P58848 conus aulic
734	11	45.8	10	2	Q9TG27	Q9TG27 liolaemus c	807	11	45.8	11	1	CX5B_CONAL	P58849 conus aulic
735	11	45.8	10	2	Q9TG30	Q9TG30 liolaemus c	808	11	45.8	11	1	LPW_THETH	P05624 thermus the
736	11	45.8	10	2	Q9TG33	Q9TG33 liolaemus b	809	11	45.8	11	1	MLG_THETH	P41989 thermomyzon
737	11	45.8	10	2	Q9TG36	Q9TG36 liolaemus c	810	11	45.8	11	1	OAIF_SARBU	P83518 sarcophaga
738	11	45.8	10	2	Q9TG39	Q9TG39 liolaemus g	811	11	45.8	11	1	RANC_RANPI	P08951 rana pipien
739	11	45.8	10	2	Q9TG42	Q9TG42 liolaemus b	812	11	45.8	11	1	RR2_CONAM	P42341 conopholis
740	11	45.8	10	2	Q9TG45	Q9TG45 liolaemus r	813	11	45.8	11	2	Q9GIR7	Q9GIR7 saccharomyc
741	11	45.8	10	2	Q9TG48	Q9TG48 liolaemus b	814	11	45.8	11	2	Q8TDA8	Q8TDA8 homo sapien
742	11	45.8	10	2	Q9TG51	Q9TG51 liolaemus c	815	11	45.8	11	2	Q9UCR1	Q9UCR1 homo sapien
743	11	45.8	10	2	Q9TG54	Q9TG54 phymaturus	816	11	45.8	11	2	Q9UE69	Q9UE69 homo sapien
744	11	45.8	10	2	Q9TG57	Q9TG57 teratoscinc	817	11	45.8	11	2	Q9UEL0	Q9UEL0 homo sapien
745	11	45.8	10	2	Q9TG60	Q9TG60 teratoscinc	818	11	45.8	11	2	Q6UZ55	Q6UZ55 littorina s
746	11	45.8	10	2	Q9TG63	Q9TG63 eublepharus	819	11	45.8	11	2	Q7RH63	Q7RH63 plasmodium
747	11	45.8	10	2	Q9TG66	Q9TG66 ophisaurus	820	11	45.8	11	2	Q6DW13	Q6DW13 bos taurus
748	11	45.8	10	2	Q9TG69	Q9TG69 ophisaurus	821	11	45.8	11	2	Q9GL48	Q9GL48 sus scrofa
749	11	45.8	10	2	Q9TG72	Q9TG72 ophisaurus	822	11	45.8	11	2	Q77884	Q77884 oreochromis
750	11	45.8	10	2	Q9TG75	Q9TG75 ophisaurus	823	11	45.8	11	2	Q77885	Q77885 oreochromis
751	11	45.8	10	2	Q9TG78	Q9TG78 anguis frag	824	11	45.8	11	2	Q77892	Q77892 oreochromis
752	11	45.8	10	2	Q9TG81	Q9TG81 ophisaurus	825	11	45.8	11	2	Q77893	Q77893 oreochromis
753	11	45.8	10	2	Q9TG84	Q9TG84 ophisaurus	826	11	45.8	11	2	Q77894	Q77894 oreochromis
754	11	45.8	10	2	Q9TG87	Q9TG87 elgaria mul	827	11	45.8	11	2	Q77895	Q77895 oreochromis
755	11	45.8	10	2	Q9TG90	Q9TG90 elgaria kin	828	11	45.8	11	2	Q77896	Q77896 oreochromis
756	11	45.8	10	2	Q9TG93	Q9TG93 elgaria kin	829	11	45.8	11	2	Q77898	Q77898 oreochromis
757	11	45.8	10	2	Q9TG96	Q9TG96 elgaria coe	830	11	45.8	11	2	Q77906	Q77906 oreochromis
758	11	45.8	10	2	Q9TG99	Q9TG99 mesaspis mo	831	11	45.8	11	2	Q77908	Q77908 oreochromis
759	11	45.8	10	2	Q9TG02	Q9TG02 abronia oax	832	11	45.8	11	2	Q77913	Q77913 oreochromis
760	11	45.8	10	2	Q9TG05	Q9TG05 gerthionotus	833	11	45.8	11	2	Q77914	Q77914 oreochromis
761	11	45.8	10	2	Q9TG08	Q9TG08 barisia imb	834	11	45.8	11	2	Q77918	Q77918 pseudotroph

835	11	45.8	11	2	078118	078118 oreochromis	908	11	45.8	11	2	07Y9G4	07Y9G4 hypsilurus
836	11	45.8	11	2	078120	078120 oreochromis	909	11	45.8	11	2	07Y9G7	07Y9G7 hypsilurus
837	11	45.8	11	2	078120	078120 oreochromis	910	11	45.8	11	2	07Y9H0	07Y9H0 hypsilurus
838	11	45.8	11	2	079636	079636 laudakia hi	911	11	45.8	11	2	07Y9H3	07Y9H3 hypsilurus
839	11	45.8	11	2	079639	079639 laudakia le	912	11	45.8	11	2	07Y9H6	07Y9H6 hypsilurus
840	11	45.8	11	2	079642	079642 laudakia mi	913	11	45.8	11	2	07Y9H9	07Y9H9 diporiphora
841	11	45.8	11	2	079918	079918 physignathu	914	11	45.8	11	2	07Y9I2	07Y9I2 diporiphora
842	11	45.8	11	2	079921	079921 phrynoceph	915	11	45.8	11	2	07Y9I5	07Y9I5 diporiphora
843	11	45.8	11	2	079985	079985 laudakia ca	916	11	45.8	11	2	07Y9I8	07Y9I8 diporiphora
844	11	45.8	11	2	079986	079986 laudakia er	917	11	45.8	11	2	07Y9J1	07Y9J1 diporiphora
845	11	45.8	11	2	08MA21	08MA21 maripa pani	918	11	45.8	11	2	07Y9J4	07Y9J4 diporiphora
846	11	45.8	11	2	08MA23	08MA23 maripa repe	919	11	45.8	11	2	07Y9J7	07Y9J7 diporiphora
847	11	45.8	11	2	08MB39	08MB39 wilsonia hu	920	11	45.8	11	2	07Y9K0	07Y9K0 diporiphora
848	11	45.8	11	2	08MB58	08MB58 seddera hir	921	11	45.8	11	2	07Y9K3	07Y9K3 diporiphora
849	11	45.8	11	2	08MB77	08MB77 odonellia h	922	11	45.8	11	2	07Y9K6	07Y9K6 diporiphora
850	11	45.8	11	2	08MB79	08MB79 aniseia arg	923	11	45.8	11	2	07Y9K9	07Y9K9 amphiboluru
851	11	45.8	11	2	08MB97	08MB97 merremia pe	924	11	45.8	11	2	07Y9L3	07Y9L3 amphiboluru
852	11	45.8	11	2	08MBE1	08MBE1 ipomoea alb	925	11	45.8	11	2	07Y9L5	07Y9L5 amphiboluru
853	11	45.8	11	2	08SKN0	08SKN0 ctenophorus	926	11	45.8	11	2	09G2N4	09G2N4 chlamydoeau
854	11	45.8	11	2	08SKN3	08SKN3 ctenophorus	927	11	45.8	11	2	09G3S0	09G3S0 laudakia sa
855	11	45.8	11	2	08SKN6	08SKN6 ctenophorus	928	11	45.8	11	2	09G3S3	09G3S3 trapelus sa
856	11	45.8	11	2	08SKN9	08SKN9 ctenophorus	929	11	45.8	11	2	09G3S6	09G3S6 agama atra
857	11	45.8	11	2	08SKP2	08SKP2 ctenophorus	930	11	45.8	11	2	09G3J1	09G3J1 pogona barb
858	11	45.8	11	2	08SKP5	08SKP5 ctenophorus	931	11	45.8	11	2	09G3J4	09G3J4 moloch horr
859	11	45.8	11	2	08SKP8	08SKP8 ctenophorus	932	11	45.8	11	2	09G3V0	09G3V0 laudakia st
860	11	45.8	11	2	08SKQ1	08SKQ1 ctenophorus	933	11	45.8	11	2	09G5V3	09G5V3 phrynoceph
861	11	45.8	11	2	08SKQ4	08SKQ4 ctenophorus	934	11	45.8	11	2	09G5V6	09G5V6 phrynoceph
862	11	45.8	11	2	08SKO7	08SKO7 ctenophorus	935	11	45.8	11	2	09G5V9	09G5V9 laudakia st
863	11	45.8	11	2	08SKR0	08SKR0 rankinia di	936	11	45.8	11	2	09G5W2	09G5W2 laudakia tu
864	11	45.8	11	2	08WC29	08WC29 ctenophorus	937	11	45.8	11	2	09G5W5	09G5W5 laudakia tu
865	11	45.8	11	2	08WD02	08WD02 ctenophorus	938	11	45.8	11	2	09G5W8	09G5W8 trapelus sa
866	11	45.8	11	2	08WD05	08WD05 ctenophorus	939	11	45.8	11	2	09G5X1	09G5X1 trapelus pe
867	11	45.8	11	2	08WD08	08WD08 ctenophorus	940	11	45.8	11	2	09G5X4	09G5X4 trapelus ag
868	11	45.8	11	2	08WD11	08WD11 ctenophorus	941	11	45.8	11	2	09G5X7	09G5X7 trapelus ru
869	11	45.8	11	2	08WD14	08WD14 ctenophorus	942	11	45.8	11	2	09G5Y0	09G5Y0 pseudotrapp
870	11	45.8	11	2	08WD17	08WD17 ctenophorus	943	11	45.8	11	2	09G5Y3	09G5Y3 agama impal
871	11	45.8	11	2	08WD20	08WD20 ctenophorus	944	11	45.8	11	2	09G5Y6	09G5Y6 agama agama
872	11	45.8	11	2	08WD23	08WD23 ctenophorus	945	11	45.8	11	2	09G5Z5	09G5Z5 japalura sp
873	11	45.8	11	2	08WD26	08WD26 ctenophorus	946	11	45.8	11	2	09G5Z8	09G5Z8 acanthosaur
874	11	45.8	11	2	08WD29	08WD29 ctenophorus	947	11	45.8	11	2	09G604	09G604 gonoccephalu
875	11	45.8	11	2	08WD50	08WD50 ceratophora	948	11	45.8	11	2	09G610	09G610 lyriocephal
876	11	45.8	11	2	08WER4	08WER4 ceratophora	949	11	45.8	11	2	09G613	09G613 cophotis ce
877	11	45.8	11	2	08WER7	08WER7 ceratophora	950	11	45.8	11	2	09G616	09G616 ceratophora
878	11	45.8	11	2	094V74	094V74 lathanotus	951	11	45.8	11	2	09G619	09G619 ceratophora
879	11	45.8	11	2	094V77	094V77 heloderma s	952	11	45.8	11	2	09G622	09G622 salea horsf
880	11	45.8	11	2	094V94	094V94 varanus sto	953	11	45.8	11	2	09G637	09G637 calotes lio
881	11	45.8	11	2	094VB8	094VB8 varanus sal	954	11	45.8	11	2	09G652	09G652 japalura va
882	11	45.8	11	2	094VE7	094VE7 varanus kom	955	11	45.8	11	2	09G655	09G655 japalura tr
883	11	45.8	11	2	094VG8	094VG8 varanus gou	956	11	45.8	11	2	09G658	09G658 hydrosaurus
884	11	45.8	11	2	094VH7	094VH7 varanus gil	957	11	45.8	11	2	09G661	09G661 tympanocryp
885	11	45.8	11	2	094VH7	094VH7 varanus gil	958	11	45.8	11	2	09G664	09G664 diporiphora
886	11	45.8	11	2	094VK1	094VK1 varanus aca	959	11	45.8	11	2	09G667	09G667 calmanops a
887	11	45.8	11	2	09ESN1	09ESN1 ptycolaeu	960	11	45.8	11	2	09G670	09G670 rankinia ad
888	11	45.8	11	2	06WR61	06WR61 nandayus ne	961	11	45.8	11	2	09G673	09G673 ctenophorus
889	11	45.8	11	2	06WR64	06WR64 neophema el	962	11	45.8	11	2	09G676	09G676 amphiboluru
890	11	45.8	11	2	07M2E6	07M2E6 solanum tub	963	11	45.8	11	2	09G679	09G679 hypsilurus
891	11	45.8	11	2	07M2P2	07M2P2 lycopersico	964	11	45.8	11	2	09G682	09G682 chelosania
892	11	45.8	11	2	07Y9B6	07Y9B6 amphiboluru	965	11	45.8	11	2	09G685	09G685 arua modest
893	11	45.8	11	2	07Y9B9	07Y9B9 tympanocryp	966	11	45.8	11	2	09G688	09G688 physignathu
894	11	45.8	11	2	07Y9C2	07Y9C2 tympanocryp	967	11	45.8	11	2	09G691	09G691 lophognathu
895	11	45.8	11	2	07Y9C5	07Y9C5 tympanocryp	968	11	45.8	11	2	09G698	09G698 elaeis guin
896	11	45.8	11	2	07Y9C8	07Y9C8 tympanocryp	969	11	45.8	11	2	094IR5	094IR5 pinus radia
897	11	45.8	11	2	07Y9D1	07Y9D1 tympanocryp	970	11	45.8	11	2	06T302	06T302 chlamydomon
898	11	45.8	11	2	07Y9D4	07Y9D4 tympanocryp	971	11	45.8	11	2	07M102	07M102 cryza sativ
899	11	45.8	11	2	07Y9D7	07Y9D7 pogona vitt	972	11	45.8	11	2	07M1W2	07M1W2 canavalia e
900	11	45.8	11	2	07Y9E0	07Y9E0 pogona null	973	11	45.8	11	2	047602	047602 escherichia
901	11	45.8	11	2	07Y9E3	07Y9E3 pogona mitc	974	11	45.8	11	2	056413	056413 escherichia
902	11	45.8	11	2	07Y9E6	07Y9E6 pogona mino	975	11	45.8	11	2	0700S6	0700S6 mycoplasma
903	11	45.8	11	2	07Y9E9	07Y9E9 pogona mini	976	11	45.8	11	2	0798K4	0798K4 bacillus su
904	11	45.8	11	2	07Y9F2	07Y9F2 pogona henr	977	11	45.8	11	2	08GLJ9	08GLJ9 borrelia bu
905	11	45.8	11	2	07Y9F5	07Y9F5 pogona brev	978	11	45.8	11	2	08GLJ24	08GLJ24 borrelia bu
906	11	45.8	11	2	07Y9F8	07Y9F8 lophognathu	979	11	45.8	11	2	08K432	08K432 spalax juda
907	11	45.8	11	2	07Y9G1	07Y9G1 hypsilurus	980	11	45.8	11	2	08K433	08K433 spalax gali

981 11 45.8 11 2 Q99JC3
 982 11 45.8 11 2 Q6LD68
 983 11 45.8 11 2 Q80W11
 984 11 45.8 11 2 Q80W11
 985 11 45.8 11 2 Q80W11
 986 11 45.8 11 2 Q80W11
 987 11 45.8 11 2 Q80W11
 988 11 45.8 11 2 Q80W11
 989 11 45.8 11 2 Q80W11
 990 11 45.8 11 2 Q80W11
 991 11 45.8 11 2 Q80W11
 992 11 45.8 11 2 Q80W11
 993 11 45.8 11 2 Q80W11
 994 11 45.8 11 2 Q80W11
 995 11 45.8 11 2 Q80W11
 996 11 45.8 11 2 Q80W11
 997 11 45.8 11 2 Q80W11
 998 11 45.8 11 2 Q80W11
 999 11 45.8 11 2 Q80W11
 1000 11 45.8 11 2 Q80W11

ALIGNMENTS

RESULT 1
 AKH HELZE STANDARD; PRT; 9 AA.
 AC P67787; P08901;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Adipokinetic hormone (Hes-AKH)
 OS Heliothis zea (Corn earworm) (Bollworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 OC Noctuidae; Heliothinae; Helicoverpa.
 OX NCBI_TaxID=7113;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86186794; PubMed=3964263;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Holman G.M.,
 Wagner R.M., Ridgway R.L., Hayes D.K.,
 RT "Isolation and primary structure of a peptide from the corpora
 cardiaca of Heliothis zea with adipokinetic activity."
 RL Biochem. Biophys. Res. Commun. 135:622-628(1986).
 CC -1- FUNCTION: This hormone, released from cells in the corpora
 cardiaca alter the beginning of flight, causes release of
 diglycerides from the fat body and then stimulates the flight
 muscles to use these diglycerides as an energy source.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC PIR; A24244; A24244.
 DR InterPro: IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Amidation; Direct protein sequencing; Flight; Neuropeptide;
 FT MOD_RES 1 1 Pyrrrolidone carboxylic acid.
 FT MOD_RES 9 9 Glycine amide.
 SQ SEQUENCE 9 AA; 1026 MW; 403665A5A1A9D1A7 CRC64;
 Query Match 70.8%; Score 17; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXW 6
 Db 4 FTSSW 8
 RESULT 2
 Q9XLI2 PRELIMINARY; PRT; 13 AA.
 ID Q9XLI2

AC Q9XLI2;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome oxidase I (Fragment).
 OS Bemisia tabaci (Sweetpotato whitefly).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleyrodiformes;
 OC Aleyrodidae; Aleyrodidae; Aleyrodinae; Bemisia.
 OX NCBI_TaxID=7038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=10583831;
 RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,
 RT "A phylogeographical analysis of the Bemisia tabaci species complex
 based on mitochondrial DNA markers."
 RL Mol. Ecol. 8:1683-1691(1999).
 DR EMBL; AF110703; AAD28415.1; -
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;
 Query Match 70.8%; Score 17; DB 2; Length 13;
 Best Local Similarity 40.0%; Pred. No. 2.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXW 6
 Db 3 FTSSW 7
 RESULT 3
 AKHG GRVBI STANDARD; PRT; 8 AA.
 ID AKHG GRVBI
 AC P67785; P14086;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Adipokinetic hormone G (AKH-G).
 OS Gryllus bimaculatus (Two-spotted cricket).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllinae;
 OC Gryllus.
 OX NCBI_TaxID=6999;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88106533; PubMed=34265616;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary sequence analysis by fast atom bombardment mass spectrometry
 of a peptide with adipokinetic activity from the corpora cardiaca of
 the cricket Gryllus bimaculatus."
 RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
 CC -1- FUNCTION: This hormone, released from cells in the corpora
 cardiaca after the beginning of flight, causes release of
 diglycerides from the fat body and then stimulates the flight
 muscles to use these diglycerides as an energy source.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; A28004; A28004.
 DR InterPro: IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Amidation; Direct protein sequencing; Flight; Neuropeptide;
 FT MOD_RES 1 1 Pyrrrolidone carboxylic acid.
 FT MOD_RES 8 8 Tryptophan amide.
 SQ SEQUENCE 8 AA; 938 MW; 867861B59C452D6 CRC64;
 Query Match 66.7%; Score 16; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 4 FSTGW 8

RESULT 4

AKH_ROMMI STANDARD; PRT; 8 AA.
AC P67786; P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adipokinetic hormone (AKH) (RO II).
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
OX NCBI_TaxID=7007;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948; DOI=10.1016/0196-9781(88)90107-6;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -!- FUNCTION: This hormone, released from cells in the corpora
cardiaca after the beginning of flight, causes release of
diglycerides from the fat body and then stimulates the flight
muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Flight; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 Pyrrolidone carboxylic acid.
FT MOD_RES 8 Tryptophan amide.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 66.7%; Score 16; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 4 FSTGW 8

RESULT 5

HTF_HELZE STANDARD; PRT; 10 AA.
AC P16353;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypertrehalosaemic hormone (He2-HRTH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=7113;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=88326324; PubMed=3415690;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G., Tseng C.M.,
RA Zhang Y.S., Hayes D.K.;
RT "Isolation and primary structure of a neuropeptide hormone from
Heliothis zea with hypertrehalosaemic and adipokinetic activities.";
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).

CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
elevate the level of trehalose in the hemolymph (trehalose is the
major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR: A31571; A31571.

DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 Pyrrolidone carboxylic acid.
FT MOD_RES 10 Asparagine amide.
SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

Query Match 66.7%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 4 FSTGW 8

RESULT 6

Q6ESN4 PRELIMINARY; PRT; 11 AA.
ID AC Q6ESN4
AC Q6ESN4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Mantheyus phuwuanensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Mantheyus.
OX NCBI_TaxID=282162;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Vindum J.V., Win H., Thin T., Lwin K.S., Shein A.K.,
RA Tun H.;
RT "Phylogenetic relationships of the genus Ptyctolaemus (Squamata:
Agamidae), with a description of a new species from the Chin Hills of
Western Myanmar";
RL Proceedings Calif. Acad. Sci. 55:222-247(2004).
DR EMBL: AY555836; AAT74867.1;
DR GO: GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1343 MW; 932D371E336411B1 CRC64;

Query Match 66.7%; Score 16; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 4.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 3 FTTRW 7

RESULT 7

Q9G649 PRELIMINARY; PRT; 11 AA.
ID AC Q9G649
AC Q9G649; 2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Oocryptis wiegmanni.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Ocoeryptis.
 OX NCBI_TaxID=118220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and phylogenetic information content of mitochondrial
 RT genomic structural features illustrated with acrodont lizards";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pachyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating trans-cethys migration: an example using acrodont lizard
 RT phylogenetics";
 RL Syst. Biol. 49:233-256(2000).
 DR ENBL: AF128480; AAC00677.1; -;
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1347 MW; 932D3710D3640DC1 CRC64;
 Query Match 66.7%; Score 16; DB 2; Length 11;
 Best Local Similarity 40.0%; Pred. No. 4.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXXW 6
 Db 3 FTARW 7
 RESULT 8
 O15276 PRELIMINARY; PRT; 17 AA.
 ID O15276
 AC O15276
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mitochondrial translation elongation factor EF-Tu (Fragment).
 GN Name=TUFM;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jacobs H.T., Smurthwaite L., Koeby R.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR ENBL: Y11797; CAA72493.1; -;
 DR GO: GO:0003746; F:translational elongation factor activity; IEA.
 KW Elongation factor.
 FT NON_TER 1
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 2019 MW; BF737D12D2AB0A7E CRC64;
 Query Match 66.7%; Score 16; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 5.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXXW 6
 Db 1 FSLTW 5
 RESULT 9
 Q7Y1X8 PRELIMINARY; PRT; 17 AA.
 ID Q7Y1X8
 AC Q7Y1X8
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Male gametic cell-specific (Fragment).
 GN Name=IGCL;
 OS Lilium longiflorum (Trumpet lily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
 OX NCBI_TaxID=4690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22615576; PubMed=12729896; DOI=10.1016/S0014-5793(03)00335-1;
 RA Singh M., Bhalla P.L., Xu H., Singh M.B.;
 RT "Isolation and characterization of a flowering plant male gametic
 RT cell-specific promoter(1).";
 RL FEBS Lett. 542:47-52(2003).
 DR ENBL: AY207012; AAP37155.1; -;
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1880 MW; 661B6348496979F CRC64;
 Query Match 66.7%; Score 16; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 5.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXXW 6
 Db 11 FSSVW 15
 RESULT 10
 O91329 PRELIMINARY; PRT; 19 AA.
 ID O91329
 AC O91329
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98285741; PubMed=9621043;
 RA Belc L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,
 RA Safar M., Barre-Sinoussi F., Kazatchkine M.D.;
 RT "Genetically related human immunodeficiency virus type 1 in three
 RT adults of a family with no identified risk factor for intrafamilial
 RT transmission.";
 RL J. Virol. 72:5831-5839(1998).
 DR ENBL: U87220; AAC32980.1; -;
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0019028; C:viral capsid; IEA.
 DR GO: GO:0019031; C:viral envelope; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 19 AA; 2324 MW; 379CB149AE073911 CRC64;
 Query Match 66.7%; Score 16; DB 2; Length 19;
 Best Local Similarity 40.0%; Pred. No. 6.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXXW 6
 Db 10 FNSTW 14
 RESULT 11
 Q9WJB1 PRELIMINARY; PRT; 19 AA.
 ID Q9WJB1
 AC Q9WJB1
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)


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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=98285741; PubMed=9621043;
RA Belc L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,
SA Safar M., Barre-Sinoussi F., Kazatchkine M.D.;
RT "Genetically related human immunodeficiency virus type 1 in three
RT adults of a family with no identified risk factor for intrafamilial
RT transmission.";
RL J. Virol. 72:5831-5839(1998).
DR EMBL; U87216; AAC32976.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; C:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
KW NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 2294 MW; 3781714A9E073911 CRC64;

Query Match 66.7%; Score 16; DB 2; Length 19;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 10 FNSTW 14

RESULT 12
Q6LDL8 PRELIMINARY; PRT; 20 AA.
AC Q6LDL8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interferon alpha/beta receptor (Fragment).
GN Name=IFNAR;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=95047447; PubMed=7958966; DOI=10.1016/0378-1119(94)90710-2;
RA Lutfalla G., Uze G.;
RT "Structure of the murine interferon alpha/beta receptor-encoding gene:
RT high-frequency rearrangements in the interferon-resistant L1210 cell
RT line.";
RL Gene 148:343-346(1994).
DR EMBL; U06242; AAA65007.1; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
KW Receptor.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2204 MW; 9B9C1DF0C12EBC43 CRC64;

Query Match 66.7%; Score 16; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 2 FSTIW 6
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RESULT 13
AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
[1]
RN SEQUENCE, AND SYNTHESIS.
RP TISSUE=Corpora cardiaca;
RC MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Flight; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1
FT MOD_RES 8 Pyrrolidone carboxylic acid.
FT MOD_RES 8 Tryptophan amide.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 62.5%; Score 15; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 4 FTPSW 8

RESULT 14
Q7M3N6 PRELIMINARY; PRT; 9 AA.
AC Q7M3N6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Neuropeptide Grb-AST B4.
OS Gryllus bimaculatus (two-spotted cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999;
[1]
RN SEQUENCE.
RX MEDLINE=95403341; PubMed=7673141; DOI=10.1074/jbc.270.36.21103;
RA Lorenz M.W., Kellner R., Hoffmann K.H.;
RT "A family of neuropeptides that inhibit juvenile hormone biosynthesis
RT in the cricket, Gryllus bimaculatus.";
RL J. Biol. Chem. 270:21103-21108(1995).
DR PIR; D57444; D57444.
SQ SEQUENCE 9 AA; 1175 MW; 3860B871E9D40B03 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
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Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

Db 3 FASW 7

RESULT 19

ID O79897 PRELIMINARY; PRT; 10 AA.
AC O79897;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Hoplocercus spinosus (Club-tail iguana).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hoplocercinae;
OC Hoplocercus.
OX NCBI_TaxID=52193;
RN [1]
RP SEQUENCE FROM N.A. PubMed=9169559;
RX MEDLINE=9715309; Ananjeva N.B., Papenfuss T.J.;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Evolutionary shifts in three major structural features of the
mitochondrial genome among iguanian lizards.";
RL J. Mol. Evol. 44:660-674(1997).
DR EMBL; U82683; AAC62284.1; -;
DR PIR; I17063; T17063.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

Db 2 FISRW 6

RESULT 20

ID P92707 PRELIMINARY; PRT; 10 AA.
AC P92707;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Platysaurus capensis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Scincophaga; Scincoidea;
OC Cordylidae; Platysaurus.
OX NCBI_TaxID=52175;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153826; PubMed=9000757;
RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
RT "Two novel gene orders and the role of light-strand replication in
rearrangement of the vertebrate mitochondrial genome.";
RL Mol. Biol. Evol. 14:91-104(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
structures of mitochondrial transfer RNAs.";

RL Mol. Biol. Evol. 14:30-39(1997).

DR EMBL; U71329; AAB48286.1; -;

GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON TER 10

SQ SEQUENCE 10 AA; 1322 MW; 0A3480C9D36415B0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

Db 2 FISRW 6

RESULT 21

ID Q6UJL5 PRELIMINARY; PRT; 10 AA.
AC Q6UJL5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Strophurus pulcher.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Strophurus.
OX NCBI_TaxID=255186;
RN [1]
RP SEQUENCE FROM N.A.
RA Melville J., Schulte J.A. II, Larson A.;
RT "A Molecular Study of Phylogenetic Relationships and Evolution of
Antipredator Strategies in Australian Dipodactylus Geckos, Subgenus
Strophurus.";
RL Biol. J. Linn. Soc. Lond. 82:123-138(2004).
DR EMBL; AY369011; AAR18865.1; -;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

Db 2 FISRW 6

RESULT 22

ID Q6WBU4 PRELIMINARY; PRT; 10 AA.
AC Q6WBU4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Sceloporus siniferus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=59719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=23801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).

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DR EMBL; AY297494; AAP84453.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1303 MW; 933480C733640451 CRC64;
Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
| |
Db 2 FTNRW 6

RESULT 23
Q6X0E7 Q6X0E7 PRELIMINARY; PRT; 10 AA.
AC Q6X0E7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Anolis marcanoi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=75264;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990428; PubMed=14628926;
RA Glor R.E., Kolbe J.J., Powell R., Larson A., Losos J.B.;
RT "Phylogenetic analysis of ecological and morphological diversification
in Hispaniolan trunk-ground anoles (Anolis cybotes group).";
RL Evolution 57:2383-2397(2003).
DR EMBL; AY263006; AAP94301.1; -.
DR EMBL; AY263005; AAP94298.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1370 MW; C93480C9D36411A9 CRC64;
Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
| |
Db 2 FTNRW 6

RESULT 24
Q71DW3 Q71DW3 PRELIMINARY; PRT; 10 AA.
AC Q71DW3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Polychrus marmoratus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Polychrus.
OX NCBI_TaxID=38934;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
and morphological data and a phylogenetic taxonomy of iguanian
lizards.";
RL Herpetologica 59:399-419(2003).
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RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528738; AAQ09176.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;
Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
| |
Db 2 FITRW 6

RESULT 25
Q71DW6 Q71DW6 PRELIMINARY; PRT; 10 AA.
AC Q71DW6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Polychrus acutirostris (Iguanid lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Polychrus.
OX NCBI_TaxID=161137;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
and morphological data and a phylogenetic taxonomy of iguanian
lizards.";
RL Herpetologica 59:399-419(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528737; AAQ09173.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;
Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
| |
Db 2 FITRW 6

RESULT 26
Q71DW9 Q71DW9 PRELIMINARY; PRT; 10 AA.
AC Q71DW9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Anisolepis longicauda.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anisolepis.
OX NCBI_TaxID=161142;
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RN  SEQUENCE FROM N.A.
RP  Schulte J.A. II, Valladares J.P., Larson A.;
RA  "Phylogenetic relationships within Iguanidae inferred using molecular
RT  and morphological data and a phylogenetic taxonomy of iguanian
RL  lizards."; Herpetologica 59:399-419 (2003).
RN  SEQUENCE FROM N.A.
RP  Schulte J.A. II, Valladares J.P., Larson A.;
RA  Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL  EMBL; AF528736; AAQ09170.1; -.
DR  GO; GO:0005739; C:mitochondrion; IEA.
KW  Mitochondrion.
FT  NON TER 10
SQ  SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 2 FISRW 6

RESULT 27
Q71E17 PRELIMINARY; PRT; 10 AA.
AC Q71E17;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Morunasaurus annularis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hopllocercinae;
OC Morunasaurus.
OX NCBI_TaxID=211988;
RN  SEQUENCE FROM N.A.
RP  Schulte J.A. II, Valladares J.P., Larson A.;
RA  "Phylogenetic relationships within Iguanidae inferred using molecular
RT  and morphological data and a phylogenetic taxonomy of iguanian
RL  lizards."; Herpetologica 59:399-419 (2003).
RN  SEQUENCE FROM N.A.
RP  Schulte J.A. II, Valladares J.P., Larson A.;
RA  Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL  EMBL; AF528736; AAQ09170.1; -.
DR  GO; GO:0005739; C:mitochondrion; IEA.
KW  Mitochondrion.
FT  NON TER 10
SQ  SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 2 FISRW 6

RESULT 28
Q71E20 PRELIMINARY; PRT; 10 AA.
AC Q71E20;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Morunasaurus annularis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hopllocercinae;
OC Morunasaurus.
OX NCBI_TaxID=211988;
RN  SEQUENCE FROM N.A.
RP  Schulte J.A. II, Valladares J.P., Larson A.;
RA  Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL  EMBL; AF528736; AAQ09170.1; -.
DR  GO; GO:0005739; C:mitochondrion; IEA.
KW  Mitochondrion.
FT  NON TER 10
SQ  SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 2 FISRW 6

RESULT 29
Q92YT2 PRELIMINARY; PRT; 10 AA.
AC Q92YT2;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Leiocephalus carinatus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae;
OC Leiocephalus.
OX NCBI_TaxID=81825;
RN  SEQUENCE FROM N.A.
RP  MEDLINE=99162288; PubMed=10051389; DOI=10.1006/mpev.1998.0541;
RX Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RA "Molecular tests of phylogenetic taxonomies: a general procedure and
RT example using four subfamilies of the lizard family Iguanidae.";
RL Mol. Phylogenet. Evol. 10:367-376(1998).
RN  SEQUENCE FROM N.A.
RP  Schulte J.A. II, Macey J.R., Larson A., Papenfuss T.J.;
RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF049864; AAQ02535.1; -.
DR PIR; T12325; T12325.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ  SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
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DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Envalloides laticeps (Amazon wood lizard).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hopllocercinae;
OC Envalloides.
OX NCBI_TaxID=51206;
RN  SEQUENCE FROM N.A.
RP  Schulte J.A. II, Valladares J.P., Larson A.;
RA "Phylogenetic relationships within Iguanidae inferred using molecular
RT and morphological data and a phylogenetic taxonomy of iguanian
RL lizards."; Herpetologica 59:399-419 (2003).
RN  SEQUENCE FROM N.A.
RP  Schulte J.A. II, Valladares J.P., Larson A.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF528719; AAQ09119.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ  SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 2 FISRW 6

RESULT 29
Q92YT2 PRELIMINARY; PRT; 10 AA.
AC Q92YT2;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Leiocephalus carinatus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae;
OC Leiocephalus.
OX NCBI_TaxID=81825;
RN  SEQUENCE FROM N.A.
RP  MEDLINE=99162288; PubMed=10051389; DOI=10.1006/mpev.1998.0541;
RX Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RA "Molecular tests of phylogenetic taxonomies: a general procedure and
RT example using four subfamilies of the lizard family Iguanidae.";
RL Mol. Phylogenet. Evol. 10:367-376(1998).
RN  SEQUENCE FROM N.A.
RP  Schulte J.A. II, Macey J.R., Larson A., Papenfuss T.J.;
RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF049864; AAQ02535.1; -.
DR PIR; T12325; T12325.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ  SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
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Qy 2 FXXXW 6
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   |
Db 3 FLSRW 7

RESULT 33
Q9G5Y9 PRELIMINARY; PRT; 11 AA.
AC Q9G5Y9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Pseudocalotes flavivula.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Pseudocalotes.
OC NCBI_TaxID=118227;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128502; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1389 MW; C92D371E336411A9 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
   |
   |
Db 3 FFLRW 7

RESULT 35
Q9G601 PRELIMINARY; PRT; 11 AA.
AC Q9G601;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Bronchocela cristatella (Green crested lizard).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Bronchocela.
OC NCBI_TaxID=118090;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128497; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
   |
   |
Db 3 FLTRW 7

RESULT 36
Q9G625 PRELIMINARY; PRT; 11 AA.
ID Q9G625
AC Q9G625
DT 01-MAR-2001 (TrEMBLrel. 16, Created)

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DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (fragment).
 GN Name=COI;
 OS Calotes versicolor.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Calotes.
 OX NCBI_TaxID=48253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118408; DOI=10.1080/10635159950173843;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pathiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating trans-tethys migration: an example using acrodont lizard
 RL phyllogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128489; C:mitochondrion; IEA.
 KW GO:0005739; C:mitochondrion;
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

 Query Match 62.5%; Score 15; DB 2; Length 11;
 Best Local Similarity 40.0%; Pred. No. 7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 QY 2 FXXXW 6
 DB 3 FLTRW 7

 RESULT 37
 Q9G628
 ID Q9G628 PRELIMINARY; PRT; 11 AA.
 AC Q9G628
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (fragment).
 GN Name=COI;
 OS Calotes mystaceus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Calotes.
 OX NCBI_TaxID=118097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and phylogenetic information content of mitochondrial
 RL genomic structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 DR EMBL; AF128488; AAG00701.1; -;
 KW GO:0005739; C:mitochondrion; IEA.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

 Query Match 62.5%; Score 15; DB 2; Length 11;
 Best Local Similarity 40.0%; Pred. No. 7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 QY 2 FXXXW 6
 DB 3 FLTRW 7

 RESULT 38
 Q9G631
 ID Q9G631 PRELIMINARY; PRT; 11 AA.
 AC Q9G631
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (fragment).
 GN Name=COI;
 OS Calotes nigrilabris.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Calotes.
 OX NCBI_TaxID=118098;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and phylogenetic information content of mitochondrial
 RL genomic structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 DR EMBL; AF128486; AAG00695.1; -;
 KW GO:0005739; C:mitochondrion; IEA.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

 Query Match 62.5%; Score 15; DB 2; Length 11;
 Best Local Similarity 40.0%; Pred. No. 7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 QY 2 FXXXW 6
 DB 3 FLTRW 7

 RESULT 39
 Q9G634
 ID Q9G634 PRELIMINARY; PRT; 11 AA.
 AC Q9G634
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (fragment).
 GN Name=COI;
 OS Calotes liolepis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Calotes.
 OX NCBI_TaxID=118096;
 RN [1]


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RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128485; AAG00692.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 3 FLTRW 7

RESULT 40
Q9G640
ID Q9G640 PRELIMINARY; PRT; 11 AA.
AC Q9G640;
DT 01-MAR-2001 (TRENBLrel 16, Created)
DT 01-MAR-2001 (TRENBLrel 16, Last sequence update)
DT 01-JUN-2003 (TRENBLrel 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Calotes ceylonensis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=118094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128483; AAG00686.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 3 FLTRW 7
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Search completed: October 18, 2005, 15:58:34
Job time : 118.529 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:19:12 ; Search time 32.2941 Seconds
(without alignments)
20.804 Million cell updates/sec

Title: US-09-214-371-11

Perfect score: 24

Sequence: 1 XFFXXWXXX 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	70.8	13	3	US-09-085-072-7
2	17	70.8	15	4	US-09-142-524D-87
3	17	70.8	15	4	US-09-142-524D-88
4	17	70.8	29	4	US-08-469-260A-428
5	17	70.8	29	4	US-08-488-446-428
6	17	70.8	29	4	US-08-467-344A-428
7	17	70.8	29	4	US-08-424-550B-428
8	17	70.8	34	1	US-08-118-270-134
9	17	70.8	34	1	US-08-118-270-172
10	17	70.8	34	5	PCT-US93-08528-134
11	17	70.8	34	5	PCT-US93-08528-172
12	17	70.8	36	3	US-08-467-023-137
13	17	70.8	37	4	US-09-330-914A-10
14	17	70.8	41	3	US-08-467-023-136
15	17	70.8	45	3	US-08-467-023-135
16	17	70.8	45	4	US-09-149-476-475
17	17	70.8	47	4	US-09-369-247-129
18	17	70.8	49	1	US-08-118-270-209
19	17	70.8	49	5	PCT-US93-08528-209
20	17	70.8	54	4	US-09-434-840-73
21	17	70.8	54	4	US-09-733-643B-21
22	17	70.8	56	4	US-09-621-976-6592
23	17	70.8	60	4	US-09-270-767-35869
24	17	70.8	60	4	US-09-270-767-51086
25	17	70.8	61	3	US-09-134-001C-4258
26	17	70.8	62	4	US-09-252-991A-28658
27	17	70.8	62	4	US-09-621-976-5704
28	17	70.8	62	4	US-09-248-796A-26247
29	17	70.8	63	4	US-09-902-540-11838
30	17	70.8	69	4	US-09-621-976-6715
31	17	70.8	69	4	US-09-248-796A-24056
32	17	70.8	80	4	US-09-330-914A-4
33	17	70.8	80	4	US-09-270-767-37303
34	17	70.8	80	4	US-09-270-767-52503
35	17	70.8	80	4	US-09-248-796A-24759
36	17	70.8	82	4	US-09-248-796A-19864
37	17	70.8	84	2	US-08-353-476-78
38	17	70.8	84	3	US-08-679-493A-97
39	17	70.8	85	4	US-09-583-110-3199
40	17	70.8	89	4	US-08-621-976-6168
41	17	70.8	91	2	US-08-598-873-19
42	17	70.8	91	3	US-08-605-430-19
43	17	70.8	91	4	US-09-717-054-19
44	17	70.8	93	4	US-09-621-976-6449
45	17	70.8	93	4	US-09-248-796A-16647
46	17	70.8	95	4	US-09-949-016-9308
47	17	70.8	98	4	US-09-252-991A-22311
48	17	70.8	102	3	US-08-984-295-3
49	17	70.8	102	3	US-08-741-411-12
50	17	70.8	104	6	5210073-1
51	17	70.8	104	6	5210073-1
52	17	70.8	105	2	US-08-826-910-3
53	17	70.8	105	2	US-08-826-910-4
54	17	70.8	105	4	US-09-601-144-68
55	17	70.8	105	4	US-09-513-999C-8037
56	17	70.8	105	4	US-09-107-433-2856
57	17	70.8	109	4	US-09-902-540-13327
58	17	70.8	114	3	US-09-450-520A-9
59	17	70.8	114	3	US-09-450-520A-10
60	17	70.8	114	3	US-09-450-520A-11
61	17	70.8	114	4	US-09-897-425-41
62	17	70.8	116	3	US-09-065-059-9
63	17	70.8	116	3	US-08-545-809A-134
64	17	70.8	116	4	US-09-134-000C-6570
65	17	70.8	116	4	US-09-949-016-10735
66	17	70.8	117	1	US-07-634-278-105
67	17	70.8	117	1	US-08-477-728-105
68	17	70.8	117	1	US-08-474-040-105
69	17	70.8	117	1	US-08-487-200-105
70	17	70.8	117	3	US-08-484-537-105
71	17	70.8	120	3	US-09-065-059-1
72	17	70.8	121	4	US-09-107-532A-5275
73	17	70.8	122	3	US-09-540-014-2
74	17	70.8	122	4	US-09-538-864-25
75	17	70.8	122	4	US-10-091-841A-2
76	17	70.8	125	4	US-09-949-016-9663
77	17	70.8	127	3	US-09-540-014-4
78	17	70.8	127	4	US-09-252-991A-17639
79	17	70.8	127	4	US-09-252-991A-24186
80	17	70.8	127	4	US-10-091-841A-4
81	17	70.8	128	3	US-08-467-023-187
82	17	70.8	130	1	US-08-276-852-69
83	17	70.8	130	1	US-08-276-852-70
84	17	70.8	130	1	US-08-276-852-71
85	17	70.8	130	1	US-08-899-575-69
86	17	70.8	130	1	US-08-899-575-70
87	17	70.8	130	1	US-08-899-575-71
88	17	70.8	130	1	US-08-899-575-69
89	17	70.8	130	1	US-08-899-575-70
90	17	70.8	130	1	US-08-899-575-71
91	17	70.8	130	3	US-09-540-014-6
92	17	70.8	130	4	US-10-091-841A-6
93	17	70.8	130	5	PCT-US95-08743-69
94	17	70.8	130	5	PCT-US95-08743-70
95	17	70.8	130	5	PCT-US95-08743-71
96	17	70.8	131	4	US-09-248-796A-15325
97	17	70.8	132	4	US-09-386-658A-2
98	17	70.8	136	3	US-09-450-520A-4
99	17	70.8	136	3	US-09-450-520A-8
100	17	70.8	138	4	US-09-252-991A-26095

Sequence 26247, A
Sequence 11838, A
Sequence 6715, Ap
Sequence 24056, A
Sequence 4, Appli
Sequence 37303, A
Sequence 52520, A
Sequence 24759, A
Sequence 19864, A
Sequence 78, Appl
Sequence 97, Appl
Sequence 3199, Ap
Sequence 6168, Ap
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 6449, Ap
Sequence 16647, A
Sequence 9308, Ap
Sequence 2311, A
Sequence 3, Appli
Sequence 12, Appl
Patent No. 5210073
Patent No. 5210073
Sequence 3, Appli
Sequence 4, Appli
Sequence 68, Appl
Sequence 8037, Ap
Sequence 2856, Ap
Sequence 13327, A
Sequence 9, Appli
Sequence 134, App
Sequence 6570, Ap
Sequence 10735, A
Sequence 105, App
Sequence 105, App
Sequence 105, App
Sequence 105, App
Sequence 105, App
Sequence 1, Appli
Sequence 5275, Ap
Sequence 2, Appli
Sequence 25, Appl
Sequence 2, Appli
Sequence 9663, Ap
Sequence 4, Appli
Sequence 17639, A
Sequence 24186, A
Sequence 4, Appli
Sequence 187, App
Sequence 69, Appl
Sequence 70, Appl
Sequence 71, Appl
Sequence 69, Appl
Sequence 71, Appl
Sequence 70, Appl
Sequence 69, Appl
Sequence 71, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 69, Appl
Sequence 70, Appl
Sequence 15325, A
Sequence 2, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 26095, A

ALIGNMENTS

RESULT 1

US-09-085-072-7
; Sequence 7, Application US/09085072
; Patent No. 6265150
; GENERAL INFORMATION:
; APPLICANT: L. Terstappen et al.
; TITLE OF INVENTION: PHAGE ANTIBODIES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,072
; FILING DATE: 26-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Felt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: 890-2 FWC/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-085-072-7

Query Match 70.8%; Score 17; DB 3; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
DB 6 FASW 10

RESULT 2

US-09-142-524D-87
; Sequence 87, Application US/09142524D
; Patent No. 6719976
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103
; CURRENT APPLICATION NUMBER: US/09/142,524D
; CURRENT FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87

; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4
US-09-142-524D-87

Query Match 70.8%; Score 17; DB 4; Length 15;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
DB 9 FSTAW 13

RESULT 3

US-09-142-524D-88
; Sequence 88, Application US/09142524D
; Patent No. 6719976
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103
; CURRENT APPLICATION NUMBER: US/09/142,524D
; CURRENT FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5
US-09-142-524D-88

Query Match 70.8%; Score 17; DB 4; Length 15;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
DB 4 FSTAW 8

RESULT 4

US-08-469-260A-428
; Sequence 428, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716

CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 428:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-260A-428

Query Match 70.8%; Score 17; DB 4; Length 29;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 12 PASAW 16

RESULT 5
US-08-488-446-428
Sequence 428, Application US/08488446
Patent No. 655898
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,446
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 428:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-446-428

Query Match 70.8%; Score 17; DB 4; Length 29;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 12 PASAW 16

RESULT 6
US-08-467-344A-428
Sequence 428, Application US/08467344A
Patent No. 6586568
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6165
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 428:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 428:
US-08-467-344A-428

Query Match 70.8%; Score 17; DB 4; Length 29;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 | XXXX 6
Db 12 FASAW 16

RESULT 7

US-08-424-550B-428
Sequence 428, Application US/08424550B
Patent No. 6720166
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSAHAAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 428:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-428

Query Match 70.8%; Score 17; DB 4; Length 29;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 12 FASAW 16

RESULT 8

US-08-118-270-134
Sequence 134, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-134

Query Match 70.8%; Score 17; DB 1; Length 34;
Best Local Similarity 40.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 16 FTSAW 20

RESULT 9

US-08-118-270-172
Sequence 172, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118.270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943.236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-172

Query Match 70.8%; Score 17; DB 1; Length 34;
Best Local Similarity 40.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 16 FTTAW 20

RESULT 10
PCT-US93-08528-134
Sequence 134, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943.236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

TELEX: 248633
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-134

Query Match 70.8%; Score 17; DB 5; Length 34;
Best Local Similarity 40.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 16 FTTAW 20

RESULT 11
PCT-US93-08528-172
Sequence 172, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943.236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-172

Query Match 70.8%; Score 17; DB 5; Length 34;
Best Local Similarity 40.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 16 FTTAW 20

RESULT 12
US-08-467-023-137

; Sequence 137, Application US/08467023
; Patent No. 6090386
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.;
; APPLICANT: Pollock, Joanne;
; APPLICANT: Bond, Julian F.;
; APPLICANT: Garman, Richard D;
; APPLICANT: Kuo, Mei-Chang;
; APPLICANT: Yeung, Siu-mei H.;
; APPLICANT: Brauer, Andrew;
; APPLICANT: Exley, Mark A.;
; APPLICANT: Powers, Steven P.
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; TITLE OF INVENTION: Japanese Cedar Pollen
; NUMBER OF SEQUENCES: 261
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
; STREET: 610 Lincoln St
; CITY: Waltham
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,023
; FILING DATE: June 6, 1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,225
; FILING DATE: December 6, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. Remillard
; REGISTRATION NUMBER: 38, 872
; REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-467-023-137

Query Match 70.8%; Score 17; DB 3; Length 36;
Best Local Similarity 40.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
DB 28 PSTAW 32

RESULT 13
US-09-330-914A-10
; Sequence 10, Application US/09330914A
; Patent No. 6432671
; GENERAL INFORMATION:
; APPLICANT: Flohe, Leopold
; APPLICANT: Kallaz, Henryk
; APPLICANT: Montemartini, Marisa
; TITLE OF INVENTION: TRYPAREDOXIN, EXPRESSION PLASMID, PROCESS OF
; PRODUCTION, METHOD OF USE, TEST KIT, AND
; PHARMACEUTICAL COMPOSITION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Brown
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: Unites States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,914A
; FILING DATE: 11-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/06983
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, James P.
; REGISTRATION NUMBER: 28,491
; REFERENCE/DOCKET NUMBER: 29473/35678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-330-914A-10

Query Match 70.8%; Score 17; DB 4; Length 37;
Best Local Similarity 40.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
DB 11 FSASW 15

RESULT 14
US-08-467-023-136
; Sequence 136, Application US/08467023
; Patent No. 6090386
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.;
; APPLICANT: Pollock, Joanne;
; APPLICANT: Bond, Julian F.;
; APPLICANT: Garman, Richard D;
; APPLICANT: Kuo, Mei-Chang;
; APPLICANT: Yeung, Siu-mei H.;
; APPLICANT: Brauer, Andrew;
; APPLICANT: Exley, Mark A.;
; APPLICANT: Powers, Steven P.
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; TITLE OF INVENTION: Japanese Cedar Pollen
; NUMBER OF SEQUENCES: 261
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
; STREET: 610 Lincoln St
; CITY: Waltham
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 US2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-467-023-136

Query Match 70.8%; Score 17; DB 3; Length 41;
Best Local Similarity, 40.0%; Pred. No. 4.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXYW 6
Db 33 FSTAW 37

RESULT 15
US-08-467-023-135
Sequence 135, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Walcham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872

REFERENCE/DOCKET NUMBER: 025.6 US2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-467-023-135

Query Match 70.8%; Score 17; DB 3; Length 45;
Best Local Similarity 40.0%; Pred. No. 4.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXYW 6
Db 33 FSTAW 37

RESULT 16
US-09-149-476-475
Sequence 475, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500

1	EARLIER FILING DATE: 1997-05-23	1	EARLIER APPLICATION NUMBER: 60/056,899
2	EARLIER APPLICATION NUMBER: 60/047,597	2	EARLIER FILING DATE: 1997-08-22
3	EARLIER FILING DATE: 1997-05-23	3	EARLIER APPLICATION NUMBER: 60/056,911
4	EARLIER APPLICATION NUMBER: 60/047,492	4	EARLIER FILING DATE: 1997-08-22
5	EARLIER FILING DATE: 1997-05-23	5	EARLIER APPLICATION NUMBER: 60/056,636
6	EARLIER APPLICATION NUMBER: 60/047,598	6	EARLIER FILING DATE: 1997-08-22
7	EARLIER FILING DATE: 1997-05-23	7	EARLIER APPLICATION NUMBER: 60/056,874
8	EARLIER APPLICATION NUMBER: 60/047,613	8	EARLIER FILING DATE: 1997-08-22
9	EARLIER FILING DATE: 1997-05-23	9	EARLIER APPLICATION NUMBER: 60/056,910
10	EARLIER APPLICATION NUMBER: 60/047,582	10	EARLIER FILING DATE: 1997-08-22
11	EARLIER FILING DATE: 1997-05-23	11	EARLIER APPLICATION NUMBER: 60/056,864
12	EARLIER APPLICATION NUMBER: 60/047,596	12	EARLIER FILING DATE: 1997-08-22
13	EARLIER FILING DATE: 1997-05-23	13	EARLIER APPLICATION NUMBER: 60/056,631
14	EARLIER APPLICATION NUMBER: 60/047,612	14	EARLIER FILING DATE: 1997-08-22
15	EARLIER FILING DATE: 1997-05-23	15	EARLIER APPLICATION NUMBER: 60/056,845
16	EARLIER APPLICATION NUMBER: 60/047,632	16	EARLIER FILING DATE: 1997-08-22
17	EARLIER FILING DATE: 1997-05-23	17	EARLIER APPLICATION NUMBER: 60/056,892
18	EARLIER APPLICATION NUMBER: 60/047,601	18	EARLIER FILING DATE: 1997-08-22
19	EARLIER FILING DATE: 1997-05-23	19	EARLIER APPLICATION NUMBER: 60/057,761
20	EARLIER APPLICATION NUMBER: 60/043,580	20	EARLIER FILING DATE: 1997-08-22
21	EARLIER FILING DATE: 1997-04-11	21	EARLIER APPLICATION NUMBER: 60/047,595
22	EARLIER APPLICATION NUMBER: 60/043,568	22	EARLIER FILING DATE: 1997-05-23
23	EARLIER FILING DATE: 1997-04-11	23	EARLIER APPLICATION NUMBER: 60/047,599
24	EARLIER APPLICATION NUMBER: 60/043,314	24	EARLIER FILING DATE: 1997-05-23
25	EARLIER FILING DATE: 1997-04-11	25	EARLIER APPLICATION NUMBER: 60/047,588
26	EARLIER APPLICATION NUMBER: 60/043,569	26	EARLIER FILING DATE: 1997-05-23
27	EARLIER FILING DATE: 1997-04-11	27	EARLIER APPLICATION NUMBER: 60/047,585
28	EARLIER APPLICATION NUMBER: 60/043,311	28	EARLIER FILING DATE: 1997-05-23
29	EARLIER FILING DATE: 1997-04-11	29	EARLIER APPLICATION NUMBER: 60/047,586
30	EARLIER APPLICATION NUMBER: 60/043,671	30	EARLIER FILING DATE: 1997-05-23
31	EARLIER FILING DATE: 1997-04-11	31	EARLIER APPLICATION NUMBER: 60/047,590
32	EARLIER APPLICATION NUMBER: 60/043,674	32	EARLIER FILING DATE: 1997-05-23
33	EARLIER FILING DATE: 1997-04-11	33	EARLIER APPLICATION NUMBER: 60/047,594
34	EARLIER APPLICATION NUMBER: 60/043,669	34	EARLIER FILING DATE: 1997-05-23
35	EARLIER FILING DATE: 1997-04-11	35	EARLIER APPLICATION NUMBER: 60/047,589
36	EARLIER APPLICATION NUMBER: 60/043,312	36	EARLIER FILING DATE: 1997-05-23
37	EARLIER FILING DATE: 1997-04-11	37	EARLIER APPLICATION NUMBER: 60/047,593
38	EARLIER APPLICATION NUMBER: 60/043,313	38	EARLIER FILING DATE: 1997-05-23
39	EARLIER FILING DATE: 1997-04-11	39	EARLIER APPLICATION NUMBER: 60/047,614
40	EARLIER APPLICATION NUMBER: 60/043,672	40	EARLIER FILING DATE: 1997-05-23
41	EARLIER FILING DATE: 1997-04-11	41	EARLIER APPLICATION NUMBER: 60/043,578
42	EARLIER APPLICATION NUMBER: 60/043,315	42	EARLIER FILING DATE: 1997-04-11
43	EARLIER FILING DATE: 1997-04-11	43	EARLIER APPLICATION NUMBER: 60/043,576
44	EARLIER APPLICATION NUMBER: 60/048,974	44	EARLIER FILING DATE: 1997-04-11
45	EARLIER FILING DATE: 1997-06-06	45	EARLIER APPLICATION NUMBER: 60/047,501
46	EARLIER APPLICATION NUMBER: 60/056,886	46	EARLIER FILING DATE: 1997-05-23
47	EARLIER FILING DATE: 1997-08-22	47	EARLIER APPLICATION NUMBER: 60/043,670
48	EARLIER APPLICATION NUMBER: 60/056,877	48	EARLIER FILING DATE: 1997-04-11
49	EARLIER FILING DATE: 1997-08-22	49	EARLIER APPLICATION NUMBER: 60/056,632
50	EARLIER APPLICATION NUMBER: 60/056,889	50	EARLIER FILING DATE: 1997-08-22
51	EARLIER FILING DATE: 1997-08-22	51	EARLIER APPLICATION NUMBER: 60/056,664
52	EARLIER APPLICATION NUMBER: 60/056,893	52	EARLIER FILING DATE: 1997-08-22
53	EARLIER FILING DATE: 1997-08-22	53	EARLIER APPLICATION NUMBER: 60/056,876
54	EARLIER APPLICATION NUMBER: 60/056,630	54	EARLIER FILING DATE: 1997-08-22
55	EARLIER FILING DATE: 1997-08-22	55	EARLIER APPLICATION NUMBER: 60/056,881
56	EARLIER APPLICATION NUMBER: 60/056,878	56	EARLIER FILING DATE: 1997-08-22
57	EARLIER FILING DATE: 1997-08-22	57	EARLIER APPLICATION NUMBER: 60/056,909
58	EARLIER APPLICATION NUMBER: 60/056,662	58	EARLIER FILING DATE: 1997-08-22
59	EARLIER FILING DATE: 1997-08-22	59	EARLIER APPLICATION NUMBER: 60/056,875
60	EARLIER APPLICATION NUMBER: 60/056,872	60	EARLIER FILING DATE: 1997-08-22
61	EARLIER FILING DATE: 1997-08-22	61	EARLIER APPLICATION NUMBER: 60/056,862
62	EARLIER APPLICATION NUMBER: 60/056,882	62	EARLIER FILING DATE: 1997-08-22
63	EARLIER FILING DATE: 1997-08-22	63	EARLIER APPLICATION NUMBER: 60/057,650
64	EARLIER APPLICATION NUMBER: 60/056,637	64	EARLIER FILING DATE: 1997-09-05
65	EARLIER FILING DATE: 1997-08-22	65	EARLIER APPLICATION NUMBER: 60/056,884
66	EARLIER APPLICATION NUMBER:		

EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query March 70.8%; Score 17; DB 4; Length 45;
Best Local Similarity 40.0%; Pred. No. 4.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 FXXW 6
Db 31 FSAW 35

RESULT 17

US-09-369-247-129
Sequence 129 Application US/09369247
Patent No. 6569992
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 44 Human Secreted Proteins
FILE REFERENCE: P2024P1
CURRENT APPLICATION NUMBER: US/09/369,247
CURRENT FILING DATE: 1999-08-05
EARLIER APPLICATION NUMBER: 60/074,118
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,157
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,137
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,341
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,141
EARLIER FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 129
LENGTH: 47
TYPE: PRT
ORGANISM: Homo sapiens
US-09-369-247-129

Query Match 70.8%; Score 17; DB 4; Length 47;
Best Local Similarity 40.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 FXXW 6
Db 39 FSSW 43

RESULT 18

US-08-118-270-209
Sequence 209, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-118-270-209

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-209

Query Match 70.8%; Score 17; DB 1; Length 49;
Best Local Similarity 40.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 FXXW 6
Db 36 FTSW 40

RESULT 19

PCT-US93-08528-209
Sequence 209, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US93-08428-209

Query Match 70.8%; Score 17; DB 5; Length 49;
Best Local Similarity 40.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 16 FTAAW 40

RESULT 20

US-09-434-840-73
; Sequence 73, Application US/09434840
; Patent No. 6620985
; GENERAL INFORMATION:
; APPLICANT: Glazebrook, Jane
; APPLICANT: Jitaga, Dayadevi
; APPLICANT: Tootle, Tina L
; APPLICANT: Zhou, Nan
; APPLICANT: Feyn, Bart
; TITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR
; FILE REFERENCE: 043503.0009
; CURRENT APPLICATION NUMBER: US/09/434.840
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 09/490.733
; EARLIER FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Thermomyces lanuginosus
US-09-434-840-73

Query Match 70.8%; Score 17; DB 4; Length 54;
Best Local Similarity 40.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 7 FTSSW 11

RESULT 21

US-09-733-643B-21
; Sequence 21, Application US/09733643B
; Patent No. 6734744
; GENERAL INFORMATION:
; APPLICANT: Laroche, Andre J.
; APPLICANT: Huang, Timothy Y
; APPLICANT: Lu, Zhen-Xiang
; APPLICANT: Frick, Michael M.
; APPLICANT: Huang, Hung Chang
; APPLICANT: Chung, Kuo-Juan
; TITLE OF INVENTION: Coniochryium minitans beta-(1,3) exoglucanase gene
; FILE REFERENCE: 24014US1
; CURRENT APPLICATION NUMBER: US/09/733.643B
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/170,168
; PRIOR FILING DATE: 1999-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Exopg
US-09-733-643B-21

Query Match 70.8%; Score 17; DB 4; Length 54;
Best Local Similarity 40.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 23 FAAA W 27

RESULT 22

US-09-621-976-6592
; Sequence 6592, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6592
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6592

Query Match 70.8%; Score 17; DB 4; Length 56;
Best Local Similarity 40.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 8 FTSSW 12

RESULT 23

US-09-270-767-35869
; Sequence 35869, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35869
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35869

Query Match 70.8%; Score 17; DB 4; Length 60;
Best Local Similarity 40.0%; Pred. No. 5.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 13 FTSSW 17

RESULT 24

US-09-270-767-51086
; Sequence 51086, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270.767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 51086

; LENGTH: 60

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-51086

Query Match 70.8%; Score 17; DB 4; Length 60;

Best Local Similarity 40.0%; Pred. No. 5.3e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

| |

Db 13 FTSSW 17

RESULT 25

US-09-134-001C-4258

; Sequence 4258, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134.001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 4258

; LENGTH: 61

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4258

Query Match 70.8%; Score 17; DB 3; Length 61;

Best Local Similarity 40.0%; Pred. No. 5.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

| |

Db 14 FSTSW 18

RESULT 26

US-09-252-991A-28658

; Sequence 28658, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubinfeld et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 28658

; LENGTH: 62

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-28658

Query Match 70.8%; Score 17; DB 4; Length 62;

Best Local Similarity 40.0%; Pred. No. 5.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

| |

Db 58 FAASW 62

RESULT 27

US-09-621-976-5704

; Sequence 5704, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTS and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 5704

; LENGTH: 62

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: -43...-1

US-09-621-976-5704

Query Match 70.8%; Score 17; DB 4; Length 62;

Best Local Similarity 40.0%; Pred. No. 5.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

| |

Db 35 FTAAM 39

RESULT 28

US-09-248-796A-26247

; Sequence 26247, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 26247

; LENGTH: 62

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-26247

Query Match 70.8%; Score 17; DB 4; Length 62;

Best Local Similarity 40.0%; Pred. No. 5.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

| |

Db 27 FSTSW 31

```
RESULT 29
US-09-902-540-11838
; Sequence 11838, Application US/09902540
; Patent No. 633147
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Miegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16815
; SEQ ID NO 11838
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11838
Query Match 70.8%; Score 17; DB 4; Length 63;
Best Local Similarity 40.0%; Pred. No. 5.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXX 6
DB 27 FATAW 31

RESULT 30
US-09-621-976-6715
; Sequence 6715, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PE2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6715
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6715
Query Match 70.8%; Score 17; DB 4; Length 69;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXX 6
DB 62 FATTW 66

RESULT 31
US-09-248-796A-24056
; Sequence 24056, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
```

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; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24056
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24056
Query Match 70.8%; Score 17; DB 4; Length 69;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXX 6
DB 62 FTTAW 66

RESULT 32
US-09-330-914A-4
; Sequence 4, Application US/09330914A
; Patent No. 6432671
; GENERAL INFORMATION:
; APPLICANT: Flohe, Leopold
; APPLICANT: Kalisz, Henryk
; APPLICANT: Montemartini, Marisa
; TITLE OF INVENTION: TRYPAEDOXIN, EXPRESSION PLASMID, PROCESS OF
; PRODUCTION, METHOD OF USE, TEST KIT, AND
; PHARMACEUTICAL COMPOSITION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Brown
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,914A
; FILING DATE: 11-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/06983
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, James P.
; REGISTRATION NUMBER: 28,491
; REFERENCE/DOCKET NUMBER: 29473/35678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-330-914A-4
Query Match 70.8%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
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Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 FXXXW 6
|
Db 8 FSASW 12

RESULT 33

US-09-270-767-37303
; Sequence 37303, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37303
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-37303

Query Match 70.8%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 41 FTASW 45

RESULT 34

US-09-270-767-52520
; Sequence 52520, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52520
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-52520

Query Match 70.8%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 41 FTASW 45

RESULT 35

US-09-248-796A-24759
; Sequence 24759, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24759
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24759

Query Match 70.8%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 72 FTTAW 76

RESULT 36

US-09-248-796A-19864
; Sequence 19864, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19864
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19864

Query Match 70.8%; Score 17; DB 4; Length 82;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
|
Db 74 FTTAW 78

RESULT 37

US-08-353-476-78
; Sequence 78, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/353,476
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bencen, Gerard H
/ REGISTRATION NUMBER: 35,746
/ REFERENCE/DOCKET NUMBER: GP-100
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (904) 375-8100
/ FAX: 904) 372-5800
/ INFORMATION FOR SEQ ID NO: 78:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 84 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: internal
/
US-08-353-476-78

Query Match 70.8%; Score 17; DB 2; Length 84;
Best Local Similarity 40.0%; Pred. No. 6.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 31 FSTW 35

RESULT 38
US-08-679-493A-97
/ Sequence 97, Application US/08679493A
/ Patent No. 6303295
/ GENERAL INFORMATION:
/ APPLICANT: Taylor, Echan W.
/ TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
/ FILE REFERENCE: 55-95
/ CURRENT APPLICATION NUMBER: US/08/679,493A
/ CURRENT FILING DATE: 1996-07-12
/ PRIOR APPLICATION NUMBER: 60/001203
/ PRIOR FILING DATE: 1995-07-11
/ PRIOR APPLICATION NUMBER: 60/003,112
/ PRIOR FILING DATE: 1995-09-01
/ NUMBER OF SEQ ID NOS: 216
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 97
/ LENGTH: 84
/ TYPE: PRT
/ ORGANISM: bovine papillomavirus type 8
US-08-679-493A-97

Query Match 70.8%; Score 17; DB 3; Length 84;
Best Local Similarity 40.0%; Pred. No. 6.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 11 FSTW 35

RESULT 39
US-09-58-1-10-10:
/ Sequence 109, Application US/09583110
/ Patent No. 6699703
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al.
/ TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
/ TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
```

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/ FILE REFERENCE: PATH00-07A
/ CURRENT APPLICATION NUMBER: US/09/583,110
/ CURRENT FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/107,433
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/085,131
/ PRIOR FILING DATE: 1998-05-12
/ PRIOR APPLICATION NUMBER: US 60/051,553
/ PRIOR FILING DATE: 1997-07-02
/ NUMBER OF SEQ ID NOS: 5322
/ SEQ ID NO 3199
/ LENGTH: 86
/ TYPE: PRT
/ ORGANISM: Streptococcus pneumoniae
US-09-583-110-3199

Query Match 70.8%; Score 17; DB 4; Length 86;
Best Local Similarity 40.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 4 FSSAW 8

RESULT 40
US-09-621-976-6168
/ Sequence 6168, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 6168
/ LENGTH: 89
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-621-976-6168

Query Match 70.8%; Score 17; DB 4; Length 89;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
|
DB 58 FSASW 62

Search completed: October 18, 2005, 15:32:10
Job time : 32.2941 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:14:39 ; Search time 125.471 Seconds
(without alignments)
27.742 Million cell updates/sec

Title: US-09-214-371-11
Perfect score: 24
Sequence: 1 KFXXXWXXX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

- Database : A_Geneseq_16Dec04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	70.8	9	7	Adc07129 Honeybee
2	17	70.8	9	7	Adc07134 Painted 1
3	17	70.8	10	3	Aab10010 H. pylori
4	17	70.8	10	4	Aab86090 H. pylori
5	17	70.8	10	4	Aab86058 H. pylori
6	17	70.8	11	7	Adc07163 Painted 1
7	17	70.8	13	4	Aae05735 Complemen
8	17	70.8	13	6	Aeg75574 CDR3
9	17	70.8	14	4	Aam98088 Human pep
10	17	70.8	15	2	Aar97874 Japan ced
11	17	70.8	15	2	Aar97875 Japan ced
12	17	70.8	15	2	Aaw57758 Residues
13	17	70.8	19	5	Aae23038 Human thi
14	17	70.8	20	2	Aaw42165 T-cell ep
15	17	70.8	20	4	Aag62999 Complemen
16	17	70.8	25	7	Ade25429 Plant gro
17	17	70.8	27	4	Aam18617 Peptide #
18	17	70.8	27	4	Aam31077 Peptide #
19	17	70.8	27	4	Aag52487 Human liv
20	17	70.8	27	5	Aag40522 Human pep
21	17	70.8	29	3	Aab09301 Hepatitis
22	17	70.8	32	4	Aag71365 Human gen
23	17	70.8	33	5	Aap60808 Sus scrof
24	17	70.8	33	8	Aos54713 Human gen
25	17	70.8	34	2	Aar50631 G-protein

Aar50593	G-protein
Aaw02823	G-protein
Aaw02785	G-protein
Aao08042	Human pol
Aar53693	Japanese
Aao08979	Human pol
Aay76339	Fragment
Aag10451	Arabidops
Ade11915	Human sec
Aay41113	TNPR/NGFR
Aag51555	Arabidops
Aam37764	Peptide #
Aab64755	Human sec
Aao06835	Human pol
Aam64830	Human bra
Abg59226	Human liv
Abg46611	Human pep
Aar53692	Japanese
Aao07778	Human pol
Aam15556	Peptide #
Abb34562	Peptide #
Aam28045	Peptide #
Abb29389	Peptide #
Abb19970	Protein #
Aam67745	Human bon
Aao12937	Human pol
Aam55349	Human bra
Abg49383	Human liv
Aar53691	Japanese
Abg95335	Human nov
Abc034529	Region of
Adi21190	Novel hum
Adh74192	Human sec
Aam27852	Peptide #
Abb29210	Peptide #
Abb19786	Protein #
Aam67559	Human bon
Aam55165	Human bra
Aam03130	Peptide #
Aay30880	Human sec
Abp51359	Human MDD
Aar50668	G-protein
Aaw02860	G-protein
Abp05131	Human ORF
Aau58484	Propionib
Aam55003	Propionib
Ab45468	Human sec
Aau56768	Propionib
Abm53287	Propionib
Ab16526	Bacteriop
Aao08445	Human pol
Abj18951	Pachogen
Abm71514	Staphyloc
Aay56440	Helicobac
Adh62390	Thermomyc
Aae01321	Human gen
Ada98194	Human sec
Ada44043	Human sec
Adc20359	Human sec
Adf10696	Human sec
Aab27801	Human sec
Aag41143	Zea mays
Aae05519	Human TNF
Aau64706	Propionib
Abp11292	Human ORF
Abm61225	Propionib
Aao1806	Human pol
Aau46944	Propionib
Abm43463	Propionib
Aam90403	Human imm
Aau64940	Propionib
Abb79236	Human pro
Abm61459	Propionib

99 17 70.8 61 4 AAE04154 Aae04154 Human gen
100 17 70.8 61 4 AAU45906 Aau45906 Propionib

ALIGNMENTS

RESULT 1
ADC07129
ID ADC07129 standard; peptide; 9 AA.
XX
AC ADC07129;
XX
DT 18-DEC-2003 (first entry)
XX
DE Honeybee AKH peptide.
XX
KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;
KW obesity; type II diabetes; cholelithiasis; hypertension;
KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;
KW renal failure; liver; chronic pain; sleep apnea; stroke;
KW urinary incontinence; honeybee.
XX
OS Synthetic.
OS Apis mellifera.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "OTHER = Pyroglutamic acid"
FT Misc-difference 9
FT /note= "Preferably C-terminal amide"
XX
XX WO2003066080-A1.
XX
PN 14-AUG-2003.
XX
PD 07-FEB-2003; 2003WO-US003800.
XX
PF 07-FEB-2002; 2002US-00072419.
XX
PR (BLMB-) BLM GROUP.
XX
PA Schacter BZ, Schacter LP;
XX
PI WPI; 2003-712542/67.
XX
DR Pharmaceutical composition useful for promoting weight loss, comprises an
XX insect adipokinetic hormone, having a pyroglutamate residue at its amino
XX terminus.
XX
PS Claim 29; Page 20; 82pp; English.
XX
CC The invention relates to a novel method of promoting lipid mobilisation
CC in a human which comprises administering an insect adipokinetic hormone
CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,
CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,
CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The
CC method of the invention may be useful for treating obesity, type II
CC diabetes, cholelithiasis, hypertension, coronary heart disease, renal
CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal
CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary
CC incontinence. The current sequence is that of the honeybee AKH peptide of
CC the invention.
XX
SQ Sequence 9 AA;

Query Match 70.8%; Score 17; DB 7; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
DB 4 FTSSW 8
RESULT 2
ADC07134
ID ADC07134 standard; peptide; 9 AA.
XX
AC ADC07134;
XX
DT 18-DEC-2003 (first entry)
XX
DE Painted lady AKH peptide.
XX
KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;
KW obesity; type II diabetes; cholelithiasis; hypertension;
KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;
KW renal failure; liver; chronic pain; sleep apnea; stroke;
KW urinary incontinence; painted lady.
XX
OS Synthetic.
OS Vanessa cardui.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "OTHER = Pyroglutamic acid"
FT Misc-difference 9
FT /note= "Preferably C-terminal amide"
XX
XX WO2003066080-A1.
XX
PN 14-AUG-2003.
XX
PD 07-FEB-2003; 2003WO-US003800.
XX
PF 07-FEB-2002; 2002US-00072419.
XX
PR (BLMB-) BLM GROUP.
XX
PA Schacter BZ, Schacter LP;
XX
PI WPI; 2003-712542/67.
XX
DR Pharmaceutical composition useful for promoting weight loss, comprises an
XX insect adipokinetic hormone, having a pyroglutamate residue at its amino
XX terminus.
XX
PS Claim 29; Page 20; 82pp; English.
XX
CC The invention relates to a novel method of promoting lipid mobilisation
CC in a human which comprises administering an insect adipokinetic hormone
CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,
CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,
CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The
CC method of the invention may be useful for treating obesity, type II
CC diabetes, cholelithiasis, hypertension, coronary heart disease, renal
CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal
CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary
CC incontinence. The current sequence is that of the painted lady AKH
XX peptide of the invention.
XX
SQ Sequence 9 AA;

Query Match 70.8%; Score 17; DB 7; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6

Db 4 FTSW 8

RESULT 3
AAB10010
ID AAB10010 standard; protein; 10 AA.
XX
AC AAB10010;
XX
DT 01-NOV-2000 (first entry)
XX
DE H. pylori beta-urease-binding antibody heavy chain CDR1 protein #2.
XX
KW Acid-resistant microorganism; detection; faecal; intestine; infection;
KW monoclonal antibody; heavy chain; complementarity determining region;
KW CDR; beta-urease.
XX
OS Unidentified.
XX
PN WO200026671-A1.
XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-EP008212.
XX
PR 29-OCT-1998; 98EP-00120517.
PR 06-NOV-1998; 98EP-00120687.
XX
PA (CONN-) CONNEX GMBH.
XX
PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
PI Ringels A;
XX
DR WPI; 2000-365747/31.
DR N-PSDB; AAA40166.
XX
PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
PT pylori, comprises reacting a fecal sample with two binding reagents for
PT antigens that survive intestinal passage.
XX
PS Claim 26; Page 22; 84pp; German.
XX
CC This invention describes a novel method for the detection of a mammalian
CC infection by an acid-resistant microorganism (A) by treating a faecal
CC sample with at least two different monoclonal antibodies (MAb) (or their
CC fragments or derivatives) or aptamers (collectively (I)) and detecting
CC formation of a complex (C) between (I) and the corresponding antigen of
CC (A). The first and second (I) bind to epitopes of different antigens
CC (Ag). These epitopes are present, after passage through the intestines,
CC in at least some mammals, and have either: (i) their native structure; or
CC (ii) a structure against which an antibody is produced by an animal
CC infected or immunized with (A), or its extract, lysate, derived protein
CC or fragment, or with a synthetic peptide. Practically all mammals display
CC at least one of the specified epitopes. The method is used to detect
CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M.
CC tuberculosis, C. jejuni and C. pylori. (I) may also be used
CC therapeutically. The method is direct and non-invasive, and provides an
CC inexpensive and easily standardizable diagnosis, despite possible
CC degradation of antigens during passage through the intestines. This
CC sequence represents a fragment of a H. pylori beta-urease-binding
CC antibody heavy chain complementarity determining region CDR1 which is
CC used to illustrate the method of the invention
XX
SQ Sequence 10 AA;
Query Match 70.8%; Score 17; DB 3; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 FXXW 6
|
Db 4 FTSW 8

RESULT 4
AAB86090
ID AAB86090 standard; peptide; 10 AA.
XX
AC AAB86090;
XX
DT 17-JUL-2001 (first entry)
XX
DE H. pylori beta-urease derived antibody light chain CDR1 #1.
XX
KW Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
KW acid-resistant microorganism; complementarity determining region; CDR;
KW feces; heavy chain; light chain.
XX
OS Unidentified.
XX
PN WO200127612-A2.
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-EP010057.
XX
PR 12-OCT-1999; 99EP-00120351.
PR 16-MAR-2000; 2000EP-00105592.
PR 31-MAR-2000; 2000EP-00107028.
PR 10-MAY-2000; 2000EP-00110110.
XX
PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;
PI WPI; 2001-282086/29.
DR N-PSDB; AAF88117.
XX
PT Detecting infections by acid-resistant microorganisms, particularly for
PT diagnosing Helicobacter pylori, comprises immunochromatographic detection
PT of antigen in feces.
XX
PS Claim 27; Page 27; 90pp; German.
XX
CC This invention describes a novel method for detecting infection by an
CC acid-resistant microorganism (A), in a mammal, using
CC immunochromatography. The method is used to diagnose infection by an acid
CC -resistant microorganism (A), in a mammal, such as Helicobacter,
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,
CC inexpensive and non-invasive, and may indicate the stage of infection. A
CC test strip used in the method may include a filter to eliminate particles
CC present in the sample and only a single receptor provides a reasonably
CC secure diagnosis, with specificity and selectivity improved by detecting
CC several epitopes (of catalase) or different antigens (catalase and beta-
CC urase). The method can be automated. This sequence represents a
CC complementarity determining region (CDR) from an antibody raised against
CC the H. pylori catalase or beta-urease antigen which is used to illustrate
CC the method of the invention
XX
SQ Sequence 10 AA;
Query Match 70.8%; Score 17; DB 4; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 FXXW 6
|
Db 4 FTSW 8

RESULT 5
AAB86058
ID AAB86058 standard; peptide; 10 AA.
XX

AC AAE05735;
 XX DT 24-SEP-2001 (first entry)
 XX DE Complementarity-determining region 3 (CDR3) of MoPhabs #7.
 XX CD CDR3; complementarity-determining region 3; monoclonal phage antibody;
 KW MoPhabs; antigen.
 XX OS Synthetic.
 XX PN US6265150-B1.
 XX PD 24-JUL-2001.
 XX PF 26-MAY-1998; 98US-00085072.
 XX PR 07-JUN-1995; 95US-00483633.
 XX PR 18-SEP-1997; 97US-00932892.
 XX (BECT) BECTON DICKINSON & CO.
 PA (CRUC-) CRUCCELL HOLLAND BV.
 XX PI Terstappen LW, Logtenberg T;
 XX WI WPI; 2001-463929/50.
 XX PT Obtaining a phage particle, useful for obtaining human antibodies against
 PT known and novel surface antigens, by incubating a phage library with
 PT target cells to allow binding of the antibody fragment to the antigen.
 XX Example 6; Col 6; 6pp; English.
 XX The invention relates to a method of obtaining a phage particle which has
 CC an antibody fragment directed against an antigen associated with the
 CC surface of target cells in a heterogeneous cell population. The method
 CC involves incubating a library of phage particles with the target cells to
 CC allow binding of the antibody fragment expressed on the surface of the
 CC phage particles to the antigen associated with the target cells. The
 CC method is useful for obtaining human antibodies against known and novel
 CC surface antigens in their native configuration, expressed on
 CC phenotypically defined subpopulations of cells. The present sequence is
 CC complementarity-determining region 3 (CDR3) of monoclonal phage
 CC antibodies (MoPhabs) used in the exemplification of the invention
 XX SQ Sequence 13 AA;
 Query Match 70.8%; Score 17; DB 4; Length 13;
 Best Local Similarity 40.0%; Pred. No. 4.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 FXXXW 6
 Db 6 PASSW 10
 RESULT 8
 ABG75574
 ID ABG75574 standard; peptide; 13 AA.
 XX AC ABG75574;
 XX DT 22-APR-2003 (first entry)
 XX DE CDR3 peptide sequence, #7, used in phage antibody construction.
 XX Phage; antibody; antigen; target cell; phage particle;
 KW cell-type specific phage antibody library; phage antibody; Phab;
 KW monoclonal phage antibody; MoPhab; blood cell; foetal bone marrow cell;
 KW complementarity determining region 3; CDR3; human.
 XX OS Homo sapiens.
 OS Synthetic.

XX US2002132228-A1.
 XX PD 19-SEP-2002.
 XX PF 24-MAY-2001; 2001US-00865048.
 XX PR 07-JUN-1995; 95US-00483633.
 XX PR 18-SEP-1997; 97US-00932892.
 XX PR 26-MAY-1998; 98US-00085072.
 XX (TERS/) TERSTAPPEN L W M M.
 PA (LOGT/) LOGTENBERG T.
 XX PI Terstappen LMMM, Logtenberg T;
 XX WI WPI; 2003-174076/17.
 XX PT Obtaining phage having antibody specific for cell surface antigen of
 PT target cells in heterogeneous cell population, by incubating phage
 PT antibody library with target cells, and separating phage particles bound
 PT target cells.
 XX Example 6; Page 4; 5pp; English.
 XX The invention discloses a method for obtaining a phage comprising an
 CC antibody, or its fragment, directed against antigens associated with a
 CC target cells surface in a heterogeneous cell population. The method
 CC comprises providing a library of antibodies, or their fragments,
 CC expressed on the surface of phage particles, incubating the phage
 CC antibody library with the target cells, separating the target cells and
 CC phage particles associated with them from the phage particles not
 CC associated with the target cells and then recovering the phage particles.
 CC Also disclosed is a cell-type specific phage antibody library and an
 CC antibody, or antibody fragment, obtained using the method. The method is
 CC useful for obtaining a selection of phage antibodies (Phabs) and
 CC monoclonal phage antibodies (MoPhabs). The method is also useful for
 CC detecting known and novel structures on various populations of blood and
 CC foetal bone marrow cells. The sequence presented is an example of the
 CC partly randomised human complementarity determining region 3 (CDR3) used
 CC in the construction of the antibodies
 XX SQ Sequence 13 AA;
 Query Match 70.8%; Score 17; DB 6; Length 13;
 Best Local Similarity 40.0%; Pred. No. 4.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 FXXXW 6
 Db 6 PASSW 10
 RESULT 9
 AAM98088
 ID AAM98088 standard; peptide; 14 AA.
 XX AC AAM98088;
 XX DT 24-JAN-2002 (first entry)
 XX DE Human peptide #1363 encoded by a SNP oligonucleotide.
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX OS Homo sapiens.

XX WO200147944-A2.
 XX
 XX 05-JUL-2001.
 XX
 XX 28-DEC-2000; 2000WO-US035498.
 XX
 XX 28-DEC-1999; 99US-0173419P.
 XX
 XX 27-DEC-2000; 2000US-00173419.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Shimketa RA, Leach M;
 XX
 XX WPI; 2001-465210/50.
 XX
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.
 XX
 XX Disclosure; Page 3967; 4143pp; English.
 XX
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinases, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 70.8%; Score 17; DB 4; Length 14;
 Best Local Similarity 40.0%; Pred. No. 4.4e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXXX 6
 DB 6 FASTW 10
 RESULT 10
 AAR97874
 ID AAR97874 standard; peptide; 15 AA.
 XX
 XX AAR97874;
 XX
 XX 16-AUG-1996 (first entry)
 XX
 XX Japan cedar pollen mature allergen Cry j II amino acids 16-30.
 DE Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
 XX Sugi pollinosis; diagnosis; treatment.
 XX
 XX Cryptomeria japonica.
 OS
 XX JP08047392-A.
 PN
 XX 20-FEB-1996.
 PD
 XX 07-NOV-1994; 94JP-00297840.
 PF
 XX 05-NOV-1993; 93JP-00276773.
 PR
 XX 26-MAY-1994; 94JP-00134868.
 PR
 XX (MEIP) MEIJI MILK PROD CO LTD.
 PA
 XX WPI; 1996-166249/17.
 DR
 XX Japan cedar pollen allergen Cry j II epitope - comprises at least part of
 PT specified 460 aminoacid protein.
 PT
 XX Claim 8; Fig 3; 17pp; Japanese.
 PS
 XX AAR97871-R97960 are overlapping peptides used for the epitope mapping of
 CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
 CC peptides of it are useful in the diagnosis, prevention and treatment of
 CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant
 CC regions of the allergen were identified using the overlapping peptides of
 CC the full epitope derived from a Cry j II antigen-specific T cell line.
 CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460
 CC amino acid allergen are the most allergenic of the 90 peptides tested
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 70.8%; Score 17; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXXX 6
 DB 9 FSTAW 13
 RESULT 11
 AAR97875
 ID AAR97875 standard; peptide; 15 AA.
 XX
 XX AAR97875;
 AC
 XX 16-AUG-1996 (first entry)
 DT
 XX Japan cedar pollen mature allergen Cry j II amino acids 21-35.
 DE Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
 XX Sugi pollinosis; diagnosis; treatment.
 KW
 XX Cryptomeria japonica.
 OS
 XX JP08047392-A.
 PN
 XX 20-FEB-1996.
 PD
 XX 07-NOV-1994; 94JP-00297840.
 PF
 XX 05-NOV-1993; 93JP-00276773.
 PR
 XX 26-MAY-1994; 94JP-00134868.
 PR
 XX (MEIP) MEIJI MILK PROD CO LTD.
 PA
 XX WPI; 1996-166249/17.
 DR
 XX Japan cedar pollen allergen Cry j II epitope - comprises at least part of
 PT specified 460 aminoacid protein.
 PT
 XX Claim 8; Fig 3; 17pp; Japanese.
 PS
 XX AAR97871-R97960 are overlapping peptides used for the epitope mapping of
 CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
 CC peptides of it are useful in the diagnosis, prevention and treatment of
 CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant
 CC regions of the allergen were identified using the overlapping peptides of
 CC the full epitope derived from a Cry j II antigen-specific T cell line.
 CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460
 CC amino acid allergen are the most allergenic of the 90 peptides tested
 XX
 XX Sequence 15 AA;
 SQ

```

Query Match      70.8%; Score 17; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
Db      4 PSTAW 8

RESULT 12
AAW57758
ID AAW57758 standard; peptide; 15 AA.
XX
XX AAW57758;
XX
XX 17-SEP-1998 (first entry)
XX
XX Residues 16-30 of Cry j 2.
XX
XX Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;
XX HLA class II molecule.
XX
XX Cryptomeria japonica.
XX
XX WO9820902-A1.
XX
XX 22-MAY-1998.
XX
XX 12-NOV-1997; 97WO-JP004129.
XX
XX 13-NOV-1996; 96JP-00302053.
XX (MEIP) MEIJI MILK PROD CO LTD.
XX
XX Sone T, Kume A, Dairiki K, Kino K;
XX
XX WPI; 1998-297617/26.
XX
XX Peptides derived from Japanese cedar pollen antigens are
XX immunotherapeutic agents - useful for allergy treatment and typing HLA
XX class II molecules in allergy sufferers.
XX
XX Claim 12; Page 29; 50pp; Japanese.
XX
XX This sequence represents residues 16-30 of the Cry j 2 protein, and is a
XX peptide of the invention. The peptides are derived from Japanese cedar
XX pollen antigens, and are used as immunotherapeutic agents in the
XX treatment of allergy. The peptides can be used for identification and
XX typing of the particular HLA class II molecules in an allergy sufferer,
XX and also for peptide immunotherapy of an allergy. Using these peptides
XX the immunotherapy can be targeted more specifically to the requirements
XX of the individual patient, allowing more effective treatment of an
XX allergy, including those patients for whom treatment with a conventional
XX immunotherapeutic agent is ineffective
XX
XX Sequence 15 AA;

Query Match      70.8%; Score 17; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
Db      9 PSTAW 13

RESULT 13
AAE23038
ID AAE23038 standard; peptide; 19 AA.
XX
XX AAE23038;
XX

```

```

DT 21-AUG-2002 (first entry)
XX Human thioredoxin, 47916 peptide.
XX
XX Human; thioredoxin; 22108; 47916; haematopoietic disorder; leukaemia;
XX cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;
XX cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;
XX brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;
XX cytostatic; carcinoma; cardiac; neuroprotective; antiinflammatory;
XX gene therapy; nootropic.
XX
XX Homo sapiens.
XX
XX WO200226803-A2.
XX
XX 04-APR-2002.
XX
XX 25-SEP-2001; 2001WO-US029967.
XX
XX 25-SEP-2000; 2000US-0235049P.
XX (MILL-) MILLENIUM PHARM INC.
XX
XX Bandaru R, Kapeller-Libermann R;
XX
XX WPI; 2002-416475/44.
XX
XX New human thioredoxin nucleic acid and polypeptide molecules, designated
XX 22108 and 47916, useful for diagnosing, preventing or treating cancer
XX (e.g. carcinoma), cardiovascular diseases (e.g. heart failure) or brain
XX disorders.
XX
XX Disclosure; Page 11; 124pp; English.
XX
XX The invention relates to human thioredoxin nucleic acid and polypeptide
XX molecules, designated 22108 and 47916. The compound that modulates the
XX activity or expression of 22108 and 47916 nucleic acid is useful for
XX treating or preventing a disorder characterised by aberrant activity of
XX 22108 and 47916-expressing cell, specifically for reducing or inhibiting
XX the aberrant activity of the 22108 and 47916-expressing cancer cell. The
XX 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,
XX preventing or treating cancer in a subject (e.g. carcinoma, sarcoma,
XX metastatic or haematopoietic disorders (e.g. leukaemia), or cancers of the
XX lung, breast, thyroid, head neck, prostate or genito-urinary tract),
XX cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart
XX failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's
XX diseases). The thioredoxin DNA is also useful in gene therapy. The
XX present sequence is human thioredoxin, 47916 peptide
XX
XX Sequence 19 AA;

Query Match      70.8%; Score 17; DB 5; Length 19;
Best Local Similarity 40.0%; Pred. No. 5.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
Db      4 PSATW 8

RESULT 14
AAW42165
ID AAW42165 standard; peptide; 20 AA.
XX
XX AAW42165;
XX
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 16-JUN-1998 (first entry)
XX
XX T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.
XX Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;

```

KW diagnosis; allergy; spring tree pollen disease; pollinosis.
 XX Chamaecyparis obtusa.
 OS WO9747648-A1.
 PN 18-DEC-1997.
 PD
 XX 12-JUN-1997; 97WO-JP002031.
 PF 14-JUN-1996; 96JP-00153527.
 PR (MEIP) MEIJI MILK PROD CO LTD.
 PA
 XX Kuno K, Dairiri K;
 PI WPI; 1998-052242/05.
 XX T-cell epitope peptide portion of Japanese cypress pollen antigens Chao1
 PT and Chao2 - used for diagnosis and treatment of spring tree pollen
 PT disease.
 XX Claim 2; Page 36; 71pp; Japanese.
 PS The present sequence represents a T-cell epitope peptide from Japanese
 CC cypress pollen antigen Chao2. The present invention describes peptides
 CC which correspond to the T-cell epitope sites on Japanese cypress pollen
 CC antigens Chao1 and Chao2. The peptides can be used as a reagent for the
 CC diagnosis of allergy to Japanese cypress pollen, and as an antigen in the
 CC treatment and prevention of spring tree pollen disease in which the
 CC pollinosis involves reactivity to Japanese cypress pollen. (Updated on 25
 CC -MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 20 AA;
 Query Match 70.8%; Score 17; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 5.8e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXXW 6
 DB 8 FATW 12
 RESULT 15
 AAG62999
 ID AAG62999 standard; peptide; 20 AA.
 AC AAG62999;
 XX 01-OCT-2001 (first entry)
 DT
 XX Complementarity determining region 3 (CDR3) of VH chain of clone G101.
 XX Antibody; light chain; VL; amyloid protein; blood brain barrier;
 KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
 KW transferrin receptor; neurological disease; Alzheimer's disease;
 KW prion disease; AIDS-related dementia; epilepsy; brain injury.
 XX Homo sapiens.
 OS
 XX WO200143300-A2.
 PN 21-JUN-2001.
 PD 27-NOV-2000; 2000WO-GB004501.
 PF 13-DEC-1999; 99US-0170599P.
 PR (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA Webster C, Osbourn J, Ward G, Miller K;
 XX
 PI
 KW diagnosis; allergy; spring tree pollen disease; pollinosis.
 XX Chamaecyparis obtusa.
 OS WO9747648-A1.
 PN 18-DEC-1997.
 PD
 XX 12-JUN-1997; 97WO-JP002031.
 PF 14-JUN-1996; 96JP-00153527.
 PR (MEIP) MEIJI MILK PROD CO LTD.
 PA
 XX Kuno K, Dairiri K;
 PI WPI; 1998-052242/05.
 XX T-cell epitope peptide portion of Japanese cypress pollen antigens Chao1
 PT and Chao2 - used for diagnosis and treatment of spring tree pollen
 PT disease.
 XX Claim 2; Page 36; 71pp; Japanese.
 PS The present sequence represents a T-cell epitope peptide from Japanese
 CC cypress pollen antigen Chao2. The present invention describes peptides
 CC which correspond to the T-cell epitope sites on Japanese cypress pollen
 CC antigens Chao1 and Chao2. The peptides can be used as a reagent for the
 CC diagnosis of allergy to Japanese cypress pollen, and as an antigen in the
 CC treatment and prevention of spring tree pollen disease in which the
 CC pollinosis involves reactivity to Japanese cypress pollen. (Updated on 25
 CC -MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 20 AA;
 Query Match 70.8%; Score 17; DB 4; Length 20;
 Best Local Similarity 40.0%; Pred. No. 5.8e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXXW 6
 DB 4 FSSSW 8
 RESULT 16
 ADE25429
 ID ADE25429 standard; peptide; 25 AA.
 AC ADE25429;
 XX 29-JAN-2004 (first entry)
 DT
 XX Plant growth associated peptide #1.
 DE
 XX Plant growth; plant growth trait modulation; Brassicaceae; Arabidopsis;
 KW Brassica; Zea; Oryza; Triticum; Hordeum; Lolium; Sorghum; Glycine;
 KW Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon;
 KW Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Pinus;
 KW Quercus.
 XX Magnoliophyta.
 OS
 XX US2003188343-A1.
 PN 02-OCT-2003.
 PD
 XX 07-JAN-2003; 2003US-00338777.
 PF
 XX 09-JAN-2002; 2002US-0347288P.
 PR (LYNX-) LYNX THERAPEUTICS INC.
 XX Bowen BA, Haudenschild CD, Buckler ES;
 PI WPI; 2003-803305/75.
 XX New isolated or recombinant polypeptide for use in modulating a plant
 PT growth trait in a flowering plant e.g. in Arabidopsis, Brassica, Zea, or
 PT Oryza.

XX Disclosure; Page 16; 81pp; English.

XX The invention describes an isolated or recombinant polypeptide (I) comprising a sequence: (a) comprising 1 of 30 sequences (S1), as given in CC the specification, or a conservative variant; (b) encoded by 1 of 30 CC sequences (S2), as given in the specification, or a conservative variant; CC (c) encoded by a sequence that hybridises under stringent conditions to CC S2; and (d) encoded by a sequence 70 % identical to S2. The expression or CC activity of (I) is modulated to modulate a plant growth trait in a CC flowering plant, of the family Brassicaceae, preferably in a plant that CC is Arabidopsis, Brassica, Zea, Oryza, Triticum, Hordeum, Lolium, Sorghum, CC Glycine, Medicago, Helianthus, Lactuca, Beta, Vitis, Solanum, CC Lycopersicon, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus, CC Pinus, or Quercus. A new method is used to detect genes for a plant CC growth trait. This is the amino acid sequence of region of ADE25056 used CC to demonstrate conservative substitutions occurring in the protein.

XX Sequence 25 AA;

Query Match 70.8%; Score 17; DB 7; Length 25;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
20 FAASW 24

Db

RESULT 17

AA18617
ID AAM18617 standard; protein; 27 AA.
AC AAM18617;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #5051 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000670.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00832366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX
PS Claim 27; SEQ ID NO 23443; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENPs; see AAI10068-AA128459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for

CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 27 AA;

Query Match 70.8%; Score 17; DB 4; Length 27;
Best Local Similarity 40.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
4 FSATW 8

Db

RESULT 18

AAM31077
ID AAM31077 standard; protein; 27 AA.
XX
AC AAM31077;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #5114 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-48897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 31346; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENPs;
CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders

XX Sequence 27 AA;

Query Match 70.8%; Score 17; DB 4; Length 27;
Best Local Similarity 40.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
|
4 FSATW 8

Db 4 FSATW 8

RESULT 19
 ID ABG52487
 AC ABG52487 standard; peptide; 27 AA.
 DT 25-FEB-2003 (first entry)
 DE Human liver peptide, SEQ ID No 31135.
 KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 KW hypercholesterolaemia; coronary heart disease.
 OS Homo sapiens.
 PN WO200157273-A2.
 PD 09-AUG-2001.
 PF 30-JAN-2001; 2001WO-US000664.
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 (MOLE-) MOLECULAR DYNAMICS INC.
 Penn SG, Hanzel DK, Chen W, Rank DR;
 WPI; 2001-488898/53.
 Human genome-derived single exon nucleic acid probes useful for analyzing
 gene expression in human adult liver.
 Claim 27; SEQ ID NO 31135; 658pp; English.
 The invention relates to a single exon nucleic acid probe (SENP) (I) for
 measuring human gene expression in a sample derived from human adult
 liver, comprising one of 13109 defined nucleotide sequences given in the
 specification (or complements/fragments). The probe hybridises at high
 stringency to a nucleic acid molecule expressed in the human adult liver.
 (I) may be used for predicting, measuring and displaying gene expression
 in samples derived from human adult liver. The genes identified may be
 involved in genetic liver diseases such as cirrhosis,
 hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 associated with coronary heart disease. ABG47348-ABG59930 represent human
 liver single exon encoded peptides of the invention. Note: The sequence
 information for this patent does not appear in the printed specification
 but was obtained in electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences

Query Match 70.8%; Score 17; DB 4; Length 27;
 Best Local Similarity 40.0%; Pred. No. 7.4e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXX 6
 | |
 4 FSATW 8

Db

RESULT 20
 ID ABG40522
 AC ABG40522 standard; peptide; 27 AA.
 DT 19-AUG-2002 (first entry)
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 30187.
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 OS Homo sapiens.
 PN WO200186003-A2.
 PD 15-NOV-2001.
 PF 30-JAN-2001; 2001WO-US000665.
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 (MOLE-) MOLECULAR DYNAMICS INC.
 Penn SG, Hanzel DK, Chen W, Rank DR;
 WPI; 2002-114183/15.
 Spatially-addressable set of single exon nucleic acid probes, used to
 measure gene expression in human lung samples.
 Claim 27; SEQ ID NO 30187; 634pp; English.
 The invention relates to a spatially-addressable set of single exon
 nucleic acid probes for measuring gene expression in a sample derived
 from human lung comprising single exon nucleic acid probes having one of
 12614 nucleic acid sequences mentioned in the specification, or their
 complements or the 12387 open reading frames derived from the 12614
 probes. Also included are a microarray comprising the novel set of probes
 ; the novel set of probes which hybridise at high stringency to a nucleic
 acid expressed in the human lung; measuring gene expression in a sample
 derived from human lung, comprising (a) contacting the array with a
 collection of detectably labeled nucleic acids derived from human lung
 mRNA, and (b) measuring the label detectably bound to each probe of the
 array; identifying exons in a eukaryotic genome, comprising (a)
 algorithmically predicting at least one exon from genomic sequences of
 the eukaryote; and (b) detecting specific hybridisation of detectably
 labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 having a fragment identical to the predicted exon, the probe is included
 in the above mentioned microarray; assigning exons to a single gene,
 comprising (a) identifying exons from genomic sequence by the method
 above and (b) measuring the expression of each of the exons in several
 tissues and/or cell types using hybridisation to a single exon
 microarrays having a probe with the exon, where a common pattern of
 expression of the exons in the tissues and/or cell types indicates that
 the exons should be assigned to a single gene; a peptide comprising one
 of 12011 sequences, mentioned in the specification, or encoded by the
 probes/open reading frames (ORF). The probes are used for gene expression
 analysis, and for identifying exons in a gene, particularly using human
 lung derived mRNA and for the study of lung diseases such as asthma, lung
 cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-

CC Puldak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagenen syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX
 SQ Sequence 27 AA;
 Query Match 70.8%; Score 17; DB 5; Length 27;
 Best Local Similarity 40.0%; Pred. No. 7.4e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXW 6
 DB 4 FSATW 8
 RESULT 21
 AAB09301
 ID AAB09301 standard; protein; 29 AA.
 XX
 AC AAB09301;
 XX
 DT 06-AUG-2003 (revised)
 DT 30-AUG-2000 (first entry)
 XX
 DE Hepatitis GB virus protein sequence SEQ ID NO:428.
 XX
 KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
 KW detection; characterisation; hepatitis.
 XX
 OS Hepatitis GB virus.
 XX
 PN US051374-A.
 XX
 PD 18-APR-2000.
 XX
 PF 07-JUN-1995; 95US-00488445.
 XX
 PR 14-FEB-1994; 94US-00196030.
 PR 13-MAY-1994; 94US-00242654.
 PR 29-JUL-1994; 94US-00283314.
 PR 23-NOV-1994; 94US-00344185.
 PR 23-NOV-1994; 94US-00344190.
 PR 30-JAN-1995; 95US-00377557.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
 PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
 XX
 DR WPI; 2000-338307/29.
 XX
 PT Detecting target hepatitis GB virus nucleic acid in a test sample
 PT suspected of containing HGBV comprises reacting the test sample the HGBV
 PT polynucleotide probe and detecting the complex that contains target HGBV.
 XX
 PS Example 18; Col 491-492; 369pp; English.
 XX
 CC The present invention describe a method for detecting target hepatitis GB
 CC virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of
 CC containing HGBV. The method involves reacting (T) with a HGBV
 CC polynucleotide probe (I) containing 15 contiguous nucleotides, and which
 CC selectively hybridises to the HGBV genome or its full complement, and
 CC selecting the complex that contains THN, indicating the presence of
 CC target HGBV. The method is used for detecting target HGBV nucleic acid in
 CC the test sample suspected of containing HGBV and for characterisation of
 CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
 CC -E hepatitis causing agents collectively termed as hepatitis GB virus.
 CC AAA55270 to AAA55489 and AAB09985 to AAB09480 represent nucleotide and

CC protein sequences used in the exemplification of the present invention.
 CC (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 29 AA;
 Query Match 70.8%; Score 17; DB 3; Length 29;
 Best Local Similarity 40.0%; Pred. No. 7.8e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXW 6
 DB 12 PASAW 16
 RESULT 22
 AAG71365
 ID AAG71365 standard; peptide; 32 AA.
 XX
 AC AAG71365;
 XX
 DT 30-JUL-2001 (first entry)
 XX
 DE Human gene 10-encoded secreted protein fragment, SEQ ID NO:216.
 XX
 KW Human; secreted protein; proliferative disorder; cancer; chromosome 1;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angioinfectious disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder; tumour;
 KW endocrine disorder; infection; wound healing; vulnerability; cell culture;
 KW chemotaxis; food additive; binding partner identification.
 XX
 OS Homo sapiens.
 XX
 PN WO200132674-A1.
 XX
 PD 10-MAY-2001.
 XX
 PF 25-OCT-2000; 2000WO-US029360.
 XX
 PR 29-OCT-1999; 99US-0162211P.
 PR 30-JUN-2000; 2000US-0215138P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Komatsoulis GA, Young PE, Moore PA;
 PI WPI; 2001-291051/30.
 XX
 PT New nucleic acid molecule encoding a human secreted protein, useful for
 PT preventing, treating or ameliorating medical conditions such as
 PT rheumatoid arthritis, Alzheimer's disease and microbial infections.
 XX
 PS Disclosure; Page 27; 581pp; English.
 XX
 CC AAH31349-AAH31428 represent cDNAs corresponding to 26 human secreted
 CC protein genes, and AAG71243-AAG71319 represent the proteins they encode.
 CC AAG71320-AAG71403 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 52 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin

CC disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention
 XX
 SQ Sequence 32 AA;

Query Match 70.8%; Score 17; DB 4; Length 32;
 Best Local Similarity 40.0%; Pred. No. 8.5e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
 DB 15 FATTW 19

RESULT 23
 ABP60808
 ID ABP60808 standard; protein; 33 AA.
 XX
 AC ABP60808;
 XX
 DT 06-SEP-2002 (first entry)
 XX
 DE Sus scrofa thiorodoxin SEQ ID NO:157.
 XX
 KW Multimeric protein; redox protein; thiorodoxin; thiorodoxin reductase;
 KW oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
 KW vasotrophic; vulnerary; antibacterial; immunosuppressive; antiulcer;
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;
 KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KW gastro oesophageal reflux disease.
 XX
 OS Sus scrofa.
 XX
 PN WO200250289-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050240.
 XX
 PR 19-DEC-2000; 2000US-00742900.
 PR 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-0006038.
 XX
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 XX
 DR WPI; 2002-508806/54.
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 PS Claim 81; Page 248; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body

CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GSRD
 CC (gastro oesophageal reflux disease). ABN9569 to ABN9593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 33 AA;

Query Match 70.8%; Score 17; DB 5; Length 33;
 Best Local Similarity 40.0%; Pred. No. 8.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
 DB 26 FSATW 30

RESULT 24
 ABO54713
 ID ABO54713 standard; protein; 33 AA.
 XX
 AC ABO54713;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human genome derived single exon protein #947.
 XX
 KW Human; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 XX
 OS Homo sapiens.
 XX
 PN US2003194704-A1.
 XX
 PD 16-OCT-2003.
 XX
 PF 03-APR-2002; 2002US-00029386.
 XX
 PR 03-APR-2002; 2002US-00029386.
 XX
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 XX
 PI Penn SG, Rank DR, Hanzel DK;
 XX
 DR WPI; 2004-119264/12.
 XX
 PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 XX
 PS Claim 45; SEQ ID NO 28347; 80pp; English.
 XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule

expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above). The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterizing alternative splicing events, in detecting and characterizing gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030194704

XX Sequence 33 AA;

Query Match 70.8%; Score 17; DB 8; Length 33;
Best Local Similarity 40.0%; Pred. No. 8.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 14 FSASW 18

RESULT 25

AA050631 ID AAR50631 standard; peptide; 34 AA.

XX AC AAR50631;

XX DT 08-MAY-1996 (first entry)

XX DE G-protein coupled receptor TM3 consensus polypeptide #77.

XX KW G-protein coupled receptor; ligand binding assay; transmembrane domain; psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin; muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine; rhodopsin; opsin; odorant; cytomegalovirus; serotonergic.

XX OS Synthetic.

XX PN WO9405695-A1.

XX PD 17-MAR-1994.

XX PF 09-SEP-1993; 93WO-US008528.

XX PR 10-SEP-1992; 92US-00943236.

XX PA (UUNY) UNIV NEW YORK STATE.

XX PI Murphy RB, Schuster DI;

XX WPI; 1994-101120/12.

PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for binding

PT GPR ligands or modulating GPR binding.

XX Claim 9; Page 28; 160pp; English.

XX CC Polypeptides AAR48768-81 and AAR50569-R50718 are based on the consensus transmembrane domain III sequence from G-protein coupled receptor (GPR) proteins, and can be used in G-protein coupled receptor ligand binding assays. The assay can be used to identify fragments pref. transmembrane fragments, from GPR proteins (see AAR48686-R48758 for examples) which retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia

XX SQ Sequence 34 AA;

Query Match 70.8%; Score 17; DB 2; Length 34;
Best Local Similarity 40.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
| |
Db 16 FTTAW 20

RESULT 26

AA050593 ID AAR50593 standard; peptide; 34 AA.

XX AC AAR50593;

XX DT 03-MAY-1996 (first entry)

XX DE G-protein coupled receptor TM3 consensus polypeptide #39.

XX KW G-protein coupled receptor; ligand binding assay; transmembrane domain; psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin; muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine; rhodopsin; opsin; odorant; cytomegalovirus; serotonergic.

XX OS Synthetic.

XX PN WO9405695-A1.

XX PD 17-MAR-1994.

XX PF 09-SEP-1993; 93WO-US008528.

XX PR 10-SEP-1992; 92US-00943236.

XX PA (UUNY) UNIV NEW YORK STATE.

XX PI Murphy RB, Schuster DI;

XX WPI; 1994-101120/12.

PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for binding
GPR ligands or modulating GPR binding.

XX Claim 9; Page 27; 160pp; English.

XX CC Polypeptides AAR48768-81 and AAR50569-R50718 are based on the consensus transmembrane domain III sequence from G-protein coupled receptor (GPR) proteins, and can be used in G-protein coupled receptor ligand binding assays. The assay can be used to identify fragments pref. transmembrane fragments, from GPR proteins (see AAR48686-R48758 for examples) which retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder

```

CC  such as schizophrenia
XX
SQ  Sequence 34 AA;

Query Match      70.8%; Score 17; DB 2; Length 34;
Best Local Similarity 40.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2 FXXXW 6
Db  16 FTSAW 20

RESULT 27
AAW02823
ID  AAW02823 standard; peptide; 34 AA.
XX
AC  AAW02823;
XX
DT  25-MAR-2003 (revised)
DT  20-SEP-1996 (first entry)
XX
DE  G-protein coupled receptor TM3 consensus polypeptide #78.
XX
KW  G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW  schizophrenia; dopamine; cAMP; adenosine; thrombin; adrennergic; opsin;
KW  muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
KW  odorant; cytomagalovirus; serotonergic.
XX
OS  Synthetic.
XX
PN  US5508384-A.
XX
PD  16-APR-1996.
XX
PF  09-SEP-1993; 93US-00118270.
XX
PR  10-SEP-1992; 92US-00943236.
XX
PA  (UUNY ) UNIV NEW YORK STATE.
XX
PI  Schuster DI, Murphy RB;
XX
DR  WPI; 1996-208785/21.
XX
PT  New dopamine receptor peptide - useful as antipsychotic agent, e.g. for
PT  treating schizophrenia.
XX
PS  Disclosure; Col 227-228; 184pp; English.
XX
CC  Polypeptides AAW02747-W02910 are based on the consensus transmembrane
CC  domain III sequence from G-protein coupled receptor (GPR) proteins and
CC  can be used in GPR ligand binding assays. The assays can be used to
CC  identify fragments, pref. transmembrane fragments, from GPR proteins (see
CC  AAW02657-W02635) which retain biological activity such as binding a GPR
CC  ligand or modulating a GPR ligand binding to a GPR (see W02747-AAW02999
CC  for examples of polypeptide fragments). The polypeptide fragments can be
CC  used in compens. for treating subjects suffering from a pathology related
CC  to a GPR abnormality e.g. schizophrenia. (Updated on 25-MAR-2003 to
CC  correct PF field.)
XX
SQ  Sequence 34 AA;

Query Match      70.8%; Score 17; DB 2; Length 34;
Best Local Similarity 40.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2 FXXXW 6
Db  16 FTSAW 20

RESULT 29
AAO08042
ID  AAO08042 standard; protein; 35 AA.
XX
AC  AAO08042;
XX
DT  06-NOV-2001 (first entry)
XX
DE  Human polypeptide SEQ ID NO 21934.
XX
KW  Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW  vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW  tissue growth factor; immunomodulatory; cancer; leukaemia;
KW  nervous system disorders; arthritis; inflammation.
XX

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OS Homo sapiens.
 XX WO200164835-A2.
 XX 07-SEP-2001.
 XX 26-FEB-2001; 2001WO-US004927.
 XX 28-FEB-2000; 2000US-00515126.
 PR 18-MAY-2000; 2000US-00577409.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-514838/56.
 DR N-PSDB; AAI87973.
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX Claim 20; SEQ ID NO 21934; 1399pp + Sequence Listing; English.
 XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 35 AA;
 Query Match 70.8%; Score 17; DB 4; Length 35;
 Best Local Similarity 40.0%; Pred. No. 9.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 2 FXXXW 6
 DB 3 FAATW 7
 RESULT 30
 AAR53693
 ID AAR53693 standard; protein; 36 AA.
 XX AAR53693;
 XX 25-MAR-2003 (revised)
 DT 01-FEB-1995 (first entry)
 XX Japanese cedar pollen allergen Cry j II fragment.
 XX Cedar pollinosis; diagnostic.
 XX Cryptomeria japonica.
 XX WO9411512-A2.
 XX 26-MAY-1994.
 XX 12-NOV-1993; 93WO-US011000.
 XX 12-NOV-1992; 92US-00975179.
 XX (IMMU-) IMMULOGIC PHARM CORP.
 XX

PI Kuo M, Yeung S, Brauer A, Pollock J;
 XX WPI; 1994-183513/22.
 XX Allergenic Cry j II protein and fragments from Japanese cedar pollen -
 PT used to diagnose, treat and prevent Japanese cedar pollinosis.
 XX Disclosure; Page 47; 89pp; English.
 XX The sequence is of a Japanese cedar pollen allergen Cry j II fragment.
 CC The protein and fragments can be used for diagnosis and treatment of
 CC Japanese cedar pollinosis and to identify similar sequences in other
 CC plants. See also AAR53690-6. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX SQ Sequence 36 AA;
 Query Match 70.8%; Score 17; DB 2; Length 36;
 Best Local Similarity 40.0%; Pred. No. 9.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 2 FXXXW 6
 DB 28 FSTAW 32
 RESULT 31
 AAO08979
 ID AAO08979 standard; protein; 37 AA.
 XX AAO08979;
 AC AAO08979;
 XX 06-NOV-2001 (first entry)
 DT Human polypeptide SEQ ID NO 22871.
 DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX Homo sapiens.
 OS WO200164835-A2.
 XX 07-SEP-2001.
 XX 26-FEB-2001; 2001WO-US004927.
 XX 28-FEB-2000; 2000US-00515126.
 PR 18-MAY-2000; 2000US-00577409.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-514838/56.
 DR N-PSDB; AAI88910.
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX Claim 20; SEQ ID NO 22871; 1399pp + Sequence Listing; English.
 XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 37 AA;
 Query Match 70.8%; Score 17; DB 4; Length 37;
 Best Local Similarity 40.0%; Pred. No. 9.5e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXXW 6
 Db 6 FAATW 10
 RESULT 32
 AAY76339
 ID AAY76339 standard; protein; 38 AA.
 XX
 AC AAY76339;
 XX
 DT 23-MAR-2000 (first entry)
 XX
 DE Fragment of human secreted protein encoded by gene 38.
 XX
 KW Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy.
 KW
 XX Homo sapiens.
 OS
 XX
 PN WO9958660-A1.
 XX
 PD 18-NOV-1999.
 XX
 XX 06-MAY-1999; 99WO-US009847.
 XX
 PR 12-MAY-1998; 98US-0085093P.
 PR 12-MAY-1998; 98US-0085094P.
 PR 12-MAY-1998; 98US-0085105P.
 PR 12-MAY-1998; 98US-0085180P.
 PR 18-MAY-1998; 98US-0085906P.
 PR 18-MAY-1998; 98US-0085920P.
 PR 18-MAY-1998; 98US-0085921P.
 PR 18-MAY-1998; 98US-0085922P.
 PR 18-MAY-1998; 98US-0085923P.
 PR 18-MAY-1998; 98US-0085924P.
 PR 18-MAY-1998; 98US-0085925P.
 PR 18-MAY-1998; 98US-0085927P.
 PR 18-MAY-1998; 98US-0085928P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
 PI Olaen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW;
 PI Endress GA, Ebner R;
 XX
 XX WPI; 2000-062296/05.
 DR
 XX
 XX New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders.
 XX
 XX Diacloneur; Page 450; 475pp; English.
 PS
 XX AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
 CC AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human
 CC genes. This sequence represents a fragment of one of the human secreted
 , CC

CC proteins. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions, e.g.
 CC by protein or gene therapy. Also pathological conditions can be diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new genes. Specific uses are
 CC described for each of the 97 genes, based on which tissues they are most
 CC highly expressed in, and include developing products for the diagnosis or
 CC treatment of cancer, tumours, developmental abnormalities and foetal
 CC deficiencies, blood disorders, diseases of the immune system, autoimmune
 CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
 CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
 CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
 CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
 CC also useful for identifying their binding partners. The sequences shown
 CC in AAY76224 to AAY76424 represent fragments of the secreted proteins
 XX
 SQ Sequence 38 AA;
 Query Match 70.8%; Score 17; DB 3; Length 38;
 Best Local Similarity 40.0%; Pred. No. 9.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FXXXW 6
 Db 19 FAAAW 23
 RESULT 33
 AAG10451
 ID AAG10451 standard; protein; 38 AA.
 XX
 AC AAG10451;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 8778.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 XX 25-FEB-2000; 2000EP-00301439.
 XX
 PR 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127452P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.
 PR 16-APR-1999; 99US-0129845P.
 PR 19-APR-1999; 99US-0130077P.
 PR 21-APR-1999; 99US-0130449P.
 PR 23-APR-1999; 99US-0130510P.
 PR 28-APR-1999; 99US-0130891P.
 PR 30-APR-1999; 99US-0131449P.
 PR 30-APR-1999; 99US-0132048P.
 PR 30-APR-1999; 99US-0132407P.
 PR 04-MAY-1999; 99US-0132484P.
 PR 05-MAY-1999; 99US-0132485P.
 PR 06-MAY-1999; 99US-0132486P.
 PR 06-MAY-1999; 99US-0132487P.
 PR 07-MAY-1999; 99US-0132863P.
 PR 11-MAY-1999; 99US-0134256P.
 PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
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PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142302P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147152P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149358P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.

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PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 26-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 70.8%; Score 17; DB 3; Length 38;
Best Local Similarity 40.0%; Pred. No. 9.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
DB 23 FTTSW 27

RESULT 34
ADE11915
ID ADE11915 standard; protein; 38 AA.
XX AC ADE11915;
XX DT 29-JAN-2004 (first entry)
XX DE Human secreted polypeptide #169.
XX KW Secreted protein; cancer; liver disorder; hepatitis; neural disorder;
XX KW Alzheimer's disease; human.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN US2003100051-A1.
XX PD 29-MAY-2003.
XX PF 10-SEP-2001; 2001US-00948783.
XX PR 12-MAY-1998; 98US-0085093P.
XX PR 12-MAY-1998; 98US-0085094P.
XX PR 12-MAY-1998; 98US-0085105P.
XX PR 12-MAY-1998; 98US-0085180P.
XX PR 18-MAY-1998; 98US-0085906P.
XX PR 18-MAY-1998; 98US-0085920P.
XX PR 18-MAY-1998; 98US-0085921P.
XX PR 18-MAY-1998; 98US-0085922P.
XX PR 18-MAY-1998; 98US-0085923P.
XX PR 18-MAY-1998; 98US-0085924P.
XX PR 18-MAY-1998; 98US-0085925P.
XX PR 18-MAY-1998; 98US-0085927P.
XX PR 18-MAY-1998; 98US-0085928P.
XX PR 06-MAY-1999; 99WO-US009847.
XX PR 10-NOV-1999; 99US-00437658.
XX PR 11-SEP-2000; 2000US-0231846P.
XX PR 28-JUN-2001; 2001US-00892877.
XX PA (RUBE/) RUBEN S M.
XX PA (FLOR/) FLORENCE K A.
XX PA (NIJJ/) NI J.
XX PA (ROSE/) ROSEN C A.
XX PA (CART/) CARTER K C.
XX PA (MOOR/) MOORE P A.
XX PA (OLSE/) OLSEN H S.
XX PA (SHIY/) SHI Y.
XX PA (YOUN/) YOUNG P E.
XX PA (WEIY/) WEI Y.
XX PA (BREW/) BREWER L A.
XX PA (SOPP/) SOPPET D R.
XX PA (LAFLE/) LAFLEUR D W.

```

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PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
XX XX Ruben SM, Florence KA, Ni J, Rosen CA, Carter KC, Moore PA;
PI Olsen HS, Shi Y, Young PE, Wei Y, Brewer LA, Soppet DR, Lafleur DW;
PI Endress GA, Ebner R, Birse CE;
XX DR WPI; 2003-801210/75.
XX PT New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g. cancer,
PT liver disorders or neural disorders.
XX XX Claim 11; SEQ ID NO 287; 453pp; English.
XX CC The invention relates to human secreted polypeptides and the
CC polynucleotides encoding them. The sequences are useful for preparing
CC medicaments for preventing, treating or ameliorating medical conditions
CC e.g., cancer, liver disorders such as hepatitis or neural disorders such
CC as Alzheimer's disease. This sequence represents a human secreted
CC polypeptide of the invention.
XX SQ Sequence 38 AA;

Query Match 70.8%; Score 17; DB 7; Length 38;
Best Local Similarity 40.0%; Pred. No. 9.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
DB 19 FAAA 23

RESULT 35
AAV41113
ID AAV41113 standard; peptide; 40 AA.
XX AC AAV41113;
XX DT 17-JAN-2000 (first entry)
XX DE TNFR/NGFR cysteine-rich domain of T129 polypeptide.
XX KW Tumor necrosis factor receptor; TNF; T129 protein; TANGO 129; human;
XX KW cellular process; immunological disorder; abnormal lymphoid development;
XX KW thymic development; T-cell mediated immune response; humoral B cell;
XX KW skeletal muscle disorder; drug screening.
XX OS Homo sapiens.
XX PN WO9952924-A1.
XX PD 21-OCT-1999.
XX PF 08-APR-1999; 99WO-US007832.
XX PR 09-APR-1998; 98US-00057951.
XX PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX PI Holtzman D;
XX DR WPI; 1999-620368/53.
XX PT New isolated tumor necrosis factor receptor member used to develop
XX PT products for treating, e.g. immunological disorders or disorders of the
XX PT skeletal muscle.
XX PS Example 3; Fig 2; 118pp; English.
XX CC The invention provides an isolated human tumor necrosis factor (TNF)
XX CC receptor member, T129 (also referred as TANGO 129). The T129 polypeptide

```

CC can be expressed by standard recombinant methodology. The T219
 CC polypeptides are useful as modulating agents in regulating a variety of
 CC cellular processes. Agents or modulators which have a stimulatory or
 CC inhibitory effect on T129 activity (e.g. T129 gene expression) as
 CC identified by a screening assay can be administered to individuals to
 CC treat (prophylactically or therapeutically) disorders, e.g. an
 CC immunological disorder associated with aberrant T129 activity, disorders
 CC associated with abnormal lymphoid and/or thymic development, T-cell
 CC mediated immune response, T-cell dependent help for B cells, and abnormal
 CC humoral B cell activity, and possibly disorders of the skeletal muscle.
 CC The products can also be used for detection, diagnosis, drug screening
 CC and production of transgenic animals. The present sequence represents a
 CC TNFR/NGFR cysteine-rich domain of T129 polypeptide
 XX

SQ Sequence 40 AA;

Query Match 70.8%; Score 17; DB 2; Length 40;
 Best Local Similarity 40.0%; Pred. No. 1e+04;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
 | |
 Db 6 FSAW 10

RESULT 36

AAG51555
 ID AAG51555 standard; protein; 40 AA.

AC AAG51555;

XX DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 65445.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; Genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX PD 06-SEP-2000.

XX FF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-011825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.

PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 30-APR-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0132867P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.

PR 21-MAY-1999; 99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.

PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

PR 04-JUN-1999; 99US-0137502P.

PR 07-JUN-1999; 99US-0137724P.

PR 08-JUN-1999; 99US-0138094P.

PR 10-JUN-1999; 99US-0138540P.

PR 14-JUN-1999; 99US-0138847P.

PR 14-JUN-1999; 99US-0139119P.

PR 16-JUN-1999; 99US-0139452P.

PR 17-JUN-1999; 99US-0139453P.

PR 18-JUN-1999; 99US-0139492P.

PR 18-JUN-1999; 99US-0139454P.

PR 18-JUN-1999; 99US-0139455P.

PR 18-JUN-1999; 99US-0139456P.

PR 18-JUN-1999; 99US-0139457P.

PR 18-JUN-1999; 99US-0139458P.

PR 18-JUN-1999; 99US-0139459P.

PR 18-JUN-1999; 99US-0139460P.

PR 18-JUN-1999; 99US-0139461P.

PR 18-JUN-1999; 99US-0139462P.

PR 18-JUN-1999; 99US-0139463P.

PR 18-JUN-1999; 99US-0139750P.

PR 18-JUN-1999; 99US-0139763P.

PR 21-JUN-1999; 99US-0139817P.

PR 21-JUN-1999; 99US-0139899P.

PR 23-JUN-1999; 99US-0140353P.

PR 23-JUN-1999; 99US-0140354P.

PR 24-JUN-1999; 99US-0140695P.

PR 28-JUN-1999; 99US-0140823P.

PR 29-JUN-1999; 99US-0140991P.

PR 30-JUN-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-0141842P.

PR 01-JUL-1999; 99US-0142154P.

PR 02-JUL-1999; 99US-0142055P.

PR 06-JUL-1999; 99US-0142390P.

PR 08-JUL-1999; 99US-0142803P.

PR 09-JUL-1999; 99US-0142920P.

PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.

PR 14-JUL-1999; 99US-0143624P.

PR 15-JUL-1999; 99US-0144005P.

PR 16-JUL-1999; 99US-0144085P.

PR 16-JUL-1999; 99US-0144086P.

PR 19-JUL-1999; 99US-0144325P.

PR 19-JUL-1999; 99US-0144331P.

PR 19-JUL-1999; 99US-0144332P.

PR 19-JUL-1999; 99US-0144333P.

PR 19-JUL-1999; 99US-0144334P.

PR 19-JUL-1999; 99US-0144335P.

PR 20-JUL-1999; 99US-0144352P.

PR 20-JUL-1999; 99US-0144632P.

PR 20-JUL-1999; 99US-0144884P.

PR 21-JUL-1999; 99US-0144814P.

PR 21-JUL-1999; 99US-0145086P.

PR 21-JUL-1999; 99US-0145088P.

PR 22-JUL-1999; 99US-0145085P.

PR 22-JUL-1999; 99US-0145087P.

PR 22-JUL-1999; 99US-0145089P.

PR 22-JUL-1999; 99US-0145192P.

PR 23-JUL-1999; 99US-0145145P.

PR 23-JUL-1999; 99US-0145218P.

PR 23-JUL-1999; 99US-0145224P.

PR 26-JUL-1999; 99US-0145276P.

PR 27-JUL-1999; 99US-0145913P.

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PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 08-AUG-1999; 99US-0147493P.
PR 08-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 13-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 21-SEP-1999; 99US-0155139P.
PR 21-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.

Query Match 70.8%; Score 17; DB 3; Length 40;
Best Local Similarity 40.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 33 FSSAW 37

RESULT 37
AAM37764
ID AAM37764 standard; protein; 40 AA.
XX
AC AAM37764;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #11801 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
(MOLE-) MOLECULAR DYNAMICS INC.
XX
Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488897/53.
XX
Human genome-derived single exon nucleic acid probes useful for analyzing
gene expression in human placenta.
XX
Claim 27; SEQ ID NO 38033; 654bp; English.
XX
The present invention relates to single exon nucleic acid probes (SENP:
see AA131315-AA157546). The present sequence is a peptide encoded by one
such probe. The probes are useful for producing a microarray for
predicting, measuring and displaying gene expression in samples derived
from human placenta. The probes are useful for antenatal diagnosis of
human genetic disorders
XX
Sequence 40 AA;
XX
Query Match 70.8%; Score 17; DB 4; Length 40;
Best Local Similarity 40.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
```

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Db      23 FTSSW 27

RESULT 38
AAB64755
ID   AAB64755 standard; protein; 40 AA.
XX
AC   AAB64755;
XX
DT   23-MAR-2001 (first entry)
XX
DE   Human secreted protein sequence encoded by gene 36 SEQ ID NO:149.
XX
KW   Human; secreted protein; diagnosis; cytostatic; antirheumatic;
KW   antiarthritic; dermatological; cardiant; antiinflammatory; anti-ulcer;
KW   gastrointestinal; solid tumour; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; myocardial angiogenesis; Crohn's disease; ulcer.
XX
OS   Homo sapiens.
XX
PN   WO200077237-A1.
XX
PD   21-DEC-2000.
XX
PF   01-JUN-2000; 2000WO-US014928.
XX
PR   11-JUN-1999; 99US-0138633P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (ROSE/) ROSEN C A.
XX
PI   Rosen CA, Ruben SM, Komatsoulis GA;
XX
WPI; 2001-071280/08.
XX
DR
XX
PT   Nucleic acids encoding 149 human secreted polypeptides, useful for
PT   preventing, diagnosing and/or treating diseases such as tumors,
PT   rheumatoid arthritis, psoriasis and diabetic retinopathy.
XX
PS   Disclosure; Page 510; 520pp; English.
XX
CC   The polynucleotide sequences given in AAF33037 to AAF33085 encode the
CC   human secreted proteins given in AAB64666 to AAB64714. AAB64715 to
CC   AAB64771 represent human secreted polypeptide sequences and proteins
CC   homologous to them, which are given in the exemplification of the present
CC   invention. Human secreted proteins have activities based on the tissues
CC   and cells the genes are expressed in. Examples of activities include:
CC   cytostatic; antirheumatic; antiarthritic; dermatological; cardiant;
CC   antiinflammatory; gastrointestinal; and anti-ulcer. The polynucleotides
CC   and polypeptides can be used in the prevention, treatment and diagnosis
CC   of diseases associated with inappropriate polypeptide expression.
CC   Disorders that may be treated or prevented include solid tumours,
CC   rheumatoid arthritis, psoriasis, diabetic retinopathy, myocardial
CC   angiogenesis, Crohn's disease and ulcers. The polynucleotides and their
CC   complementary sequences may also be used as DNA probes in diagnostic
CC   assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate
CC   the presence of similar nucleic acid sequences in samples, and therefore
CC   which patients may be in need of restorative therapy. The polypeptides
CC   may also be used as antigens in the production of antibodies against the
CC   polypeptide and in assays to identify modulators (agonists and
CC   antagonists) of polypeptide expression and activity. The anti-polypeptide
CC   antibodies and antagonists may also be used to down regulate expression
CC   and activity. AAF33028 to AAF33036 and AAB64665 represent sequences used
CC   in the exemplification of the present invention
XX
SQ   Sequence 40 AA;

Query Match      70.8%; Score 17; DB 4; Length 40;
Best Local Similarity 40.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXXXX 6
Db      20 FAATW 24

RESULT 40
AAM64830
ID   AAM64830 standard; protein; 40 AA.
XX
AC   AAM64830;
XX
DT   05-NOV-2001 (first entry)
XX

```

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Db      8 FAATW 12

RESULT 39
AAO06835
ID   AAO06835 standard; protein; 40 AA.
XX
AC   AAO06835;
XX
DT   06-NOV-2001 (first entry)
XX
DE   Human polypeptide SEQ ID NO 20727.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorders; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200164835-A2.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-US004927.
XX
PR   28-FEB-2000; 2000US-00515126.
PR   18-MAY-2000; 2000US-00577409.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Drmanac RT;
XX
WPI; 2001-514838/56.
XX
DR   N-PSDB; AAI86766.
XX
PT   Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT   and treating e.g. leukemia, inflammation and immune disorders.
XX
PS   Claim 20; SEQ ID NO 20727; 1399pp + Sequence Listing; English.
XX
CC   The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC   the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 40 AA;

Query Match      70.8%; Score 17; DB 4; Length 40;
Best Local Similarity 40.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXXXX 6
Db      20 FAATW 24

RESULT 40
AAM64830
ID   AAM64830 standard; protein; 40 AA.
XX
AC   AAM64830;
XX
DT   05-NOV-2001 (first entry)
XX

```

XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36935.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PP 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-483446/52.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains.
XX PS Example 4; SEQ ID NO 36935; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX CC the probes of the invention
XX SQ Sequence 40 AA;
Query Match 70.8%; Score 17; DB 4; Length 40;
Best Local Similarity 40.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXW 6
Db 23 FTSSW 27
Search completed: October 18, 2005, 15:26:11
Job time : 126.471 secs

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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:44:54 ; Search time 21.6471 Seconds
(without alignments)
35.558 Million cell updates/sec

Title: US-09-214-371-10

Perfect score: 23

Sequence: 1 FXXXWXXX 8

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	73.9	9	2	A24244
2	16	69.6	8	2	A28004
3	16	69.6	10	2	A31571
4	15	65.2	8	2	S10596
5	15	65.2	9	2	D57444
6	15	65.2	10	2	T17063
7	15	65.2	10	2	T12325
8	15	65.2	10	2	S53789
9	15	65.2	15	2	PH1613
10	15	65.2	17	2	A34704
11	15	65.2	20	2	S77981
12	15	65.2	20	2	PN0171
13	15	65.2	20	2	PH1380
14	14	60.9	8	2	A33995
15	14	60.9	8	2	A44960
16	14	60.9	8	2	B44960
17	14	60.9	8	2	A58620
18	14	60.9	8	2	S11545
19	14	60.9	8	2	S55310
20	14	60.9	8	2	A61348
21	14	60.9	8	2	S08995
22	14	60.9	8	2	S08996
23	14	60.9	8	2	A49823
24	14	60.9	8	2	B49823
25	14	60.9	8	2	A43976
26	14	60.9	8	2	B43976
27	14	60.9	8	2	A05169
28	14	60.9	10	2	B33995
29	14	60.9	10	2	S08997

30	14	60.9	10	2	A60421	hypertrehalosemic
31	14	60.9	10	2	S08998	hypertrehalosemic
32	14	60.9	10	2	A26381	hypertrehalosemic
33	14	60.9	10	2	JC1416	hypertrehalosemic
34	14	60.9	10	2	S09138	hypertrehalosemic
35	14	60.9	10	2	C39191	hypothetical prote
36	14	60.9	10	2	PT0322	ig heavy chain CRD
37	14	60.9	10	2	T17066	cytochrome-c oxida
38	14	60.9	10	2	T17069	cytochrome-c oxida
39	14	60.9	10	2	T12329	cytochrome-c oxida
40	14	60.9	12	2	PT0274	ig heavy chain CRD
41	14	60.9	12	2	PH1324	ig heavy chain DJ
42	14	60.9	13	2	PC4391	cysteine proteinas
43	14	60.9	16	2	C37290	homeotic protein G
44	14	60.9	19	2	S37290	nitrogen fixation
45	14	60.9	20	2	PC1240	calcium-binding pr
46	13	56.5	9	2	PT0288	ig heavy chain CRD
47	13	56.5	9	2	I46023	growth hormone rec
48	13	56.5	11	2	C53652	rhIR protein - pse
49	13	56.5	11	2	PT0302	ig heavy chain CRD
50	12	52.2	8	2	T13818	cytochrome oxidase
51	12	52.2	10	1	RHLMGS	gonadoliberin - se
52	12	52.2	11	2	S05002	corazonin - Americ
53	12	52.2	18	2	S39009	oviductin - golden
54	11	47.8	3	3	F37196	bradykinin-potenti
55	11	47.8	4	2	A34626	RPCH-related neuro
56	11	47.8	4	2	B53284	T-cell receptor be
57	11	47.8	4	2	PT0661	T-cell receptor be
58	11	47.8	5	2	A32516	cholecystokinin-5
59	11	47.8	5	2	A60803	neuropeptide - sea
60	11	47.8	5	2	JH0253	gut pentapeptide -
61	11	47.8	5	2	PT0281	ig heavy chain CRD
62	11	47.8	5	2	PT0308	ig heavy chain CRD
63	11	47.8	5	2	PT0729	T-cell receptor be
64	11	47.8	5	2	PT0580	T-cell receptor be
65	11	47.8	5	2	G37196	bradykinin-potenti
66	11	47.8	6	2	S66195	alcohol dehydrogen
67	11	47.8	6	2	B34835	dnaA protein - Pse
68	11	47.8	6	2	A31263	dihydrofolate redu
69	11	47.8	6	2	B31263	dihydrofolate redu
70	11	47.8	6	2	B35640	cerebellar degener
71	11	47.8	6	2	PT0629	T-cell receptor be
72	11	47.8	6	2	PT0532	T-cell receptor be
73	11	47.8	6	2	PT0519	T-cell receptor be
74	11	47.8	6	2	PT0637	T-cell receptor be
75	11	47.8	6	2	PT0641	T-cell receptor be
76	11	47.8	6	2	PT0726	T-cell receptor be
77	11	47.8	6	2	F41946	T-cell receptor ga
78	11	47.8	6	2	PD0028	pev-kinin 2 - pena
79	11	47.8	6	2	A61068	locustakinin - mig
80	11	47.8	6	4	I79564	hypothetical TcL3
81	11	47.8	7	2	S21230	dermorphin (Tirp-4,
82	11	47.8	7	2	S09652	hypothetical prote
83	11	47.8	7	2	PQ0727	H2 class I protein
84	11	47.8	7	2	E48394	glycoprotein compo
85	11	47.8	7	2	PH1602	ig H chain V-D-J r
86	11	47.8	7	2	PT0526	T-cell receptor be
87	11	47.8	7	2	PT0628	T-cell receptor be
88	11	47.8	7	2	PT0642	T-cell receptor be
89	11	47.8	7	2	PT0722	T-cell receptor be
90	11	47.8	7	2	PT0688	T-cell receptor be
91	11	47.8	7	2	PT0586	T-cell receptor be
92	11	47.8	7	2	PT0728	T-cell receptor be
93	11	47.8	7	2	PT0728	glucuronosyltransf
94	11	47.8	7	2	B48394	major fat-globule
95	11	47.8	7	2	PD0029	pev-kinin 1 - pena
96	11	47.8	7	2	PN0649	pullulanase (EC 3.
97	11	47.8	7	2	S57274	triacylglycerol li
98	11	47.8	7	2	S33244	neuromodulatory pe
99	11	47.8	7	2	S33245	neuromodulatory pe
100	11	47.8	7	2	S33246	neuromodulatory pe
101	11	47.8	7	2	S33567	tubulin beta-3 cha
102	11	47.8	7	2	A58512	venom heptapeptide

103	11	47.8	7	2	A61081	tryptophyllin, bas	176	11	47.8	10	2	B38887	T-cell receptor ga
104	11	47.8	7	4	I53382	hypothetical pepti	177	11	47.8	10	2	PH0916	T-cell receptor be
105	11	47.8	7	4	A58725	virotoxin - deatro	178	11	47.8	10	2	PH0923	T-cell receptor be
106	11	47.8	8	2	S15422	adipokinetic hormo	179	11	47.8	10	2	A40753	aldehyde ferredoxi
107	11	47.8	8	2	A58641	adipokinetic hormo	180	11	47.8	10	2	A59272	peptide-N4-(N-acet
108	11	47.8	8	2	PQ0012	cholecystokinin -	181	11	47.8	10	2	S66248	processing enzyme,
109	11	47.8	8	2	A43001	cholecystokinin -	182	11	47.8	10	2	A27617	triose-phosphate i
110	11	47.8	8	2	PT0724	T-cell receptor be	183	11	47.8	10	2	A46030	gonadoliberin I - ch
111	11	47.8	8	2	A38887	T-cell receptor ga	184	11	47.8	10	2	A21114	gonadoliberin I - ch
112	11	47.8	8	2	A59495	Vesicle associated	185	11	47.8	10	2	B37196	bradykinin-potent
113	11	47.8	8	2	S19288	acylase - Kluuvera	186	11	47.8	10	2	H37196	bradykinin-potent
114	11	47.8	8	2	A39108	glycine reductase	187	11	47.8	10	2	F33932	Ig mu chain J regi
115	11	47.8	8	2	C61512	variant surface gl	188	11	47.8	10	2	F33932	cytochrome-c oxida
116	11	47.8	8	2	D61512	variant surface gl	189	11	47.8	10	2	TL7075	cytochrome-c oxida
117	11	47.8	8	2	JS0315	leucokinin V - Mad	190	11	47.8	10	2	TL7075	cytochrome-c oxida
118	11	47.8	8	2	JS0316	leucokinin VI - Ma	191	11	47.8	10	2	TL7075	cytochrome-c oxida
119	11	47.8	8	2	JS0317	leucokinin VII - M	192	11	47.8	10	2	TL7075	cytochrome-c oxida
120	11	47.8	8	2	JS0318	leucokinin VIII -	193	11	47.8	10	2	TL7075	cytochrome-c oxida
121	11	47.8	8	2	S21663	neuropeptide - flo	194	11	47.8	10	2	TL7060	cytochrome-c oxida
122	11	47.8	8	2	A41117	acetylcholinestera	195	11	47.8	10	2	TL7060	cytochrome-c oxida
123	11	47.8	8	2	A31570	angiotensin-conver	196	11	47.8	10	2	TL7060	cytochrome-c oxida
124	11	47.8	9	1	AKLQIM	locustamycininhibi	197	11	47.8	10	2	TL7060	cytochrome-c oxida
125	11	47.8	9	2	S07205	litorin 2-Glu - Au	198	11	47.8	10	2	TL7072	cytochrome-c oxida
126	11	47.8	9	2	S07204	litorin I - Austr	199	11	47.8	10	2	TL7072	cytochrome-c oxida
127	11	47.8	9	2	S07241	litorin - Rohde's	200	11	47.8	10	2	TL7072	cytochrome-c oxida
128	11	47.8	9	2	A61357	phyllacaerulein -	201	11	47.8	10	2	TL7072	cytochrome-c oxida
129	11	47.8	9	2	JS0302	xenopsin-related p	202	11	47.8	10	2	TL7072	cytochrome-c oxida
130	11	47.8	9	2	A60320	xenopsin-related p	203	11	47.8	10	2	TL7072	cytochrome-c oxida
131	11	47.8	9	2	PT0231	Ig heavy chain CDR	204	11	47.8	10	2	TL7072	cytochrome-c oxida
132	11	47.8	9	2	PT0231	Ig heavy chain CDR	205	11	47.8	10	2	TL7072	cytochrome-c oxida
133	11	47.8	9	2	PT0272	Ig heavy chain CDR	206	11	47.8	10	2	TL7072	cytochrome-c oxida
134	11	47.8	9	2	PT0299	Ig heavy chain CDR	207	11	47.8	10	2	TL7072	cytochrome-c oxida
135	11	47.8	9	2	PT0324	Ig heavy chain CDR	208	11	47.8	10	2	TL7072	cytochrome-c oxida
136	11	47.8	9	2	PT0634	T-cell receptor be	209	11	47.8	10	2	TL7072	cytochrome-c oxida
137	11	47.8	9	2	PT0562	T-cell receptor be	210	11	47.8	10	2	TL7072	cytochrome-c oxida
138	11	47.8	9	2	I50350	gene c-mpl protein	211	11	47.8	10	2	TL7072	cytochrome-c oxida
139	11	47.8	9	2	S78426	52.5K protein - sp	212	11	47.8	10	2	TL7072	cytochrome-c oxida
140	11	47.8	9	2	S56004	glucan 1,3-beta-gl	213	11	47.8	10	2	TL7072	cytochrome-c oxida
141	11	47.8	9	2	A45848	cell surface adhes	214	11	47.8	10	2	TL7072	cytochrome-c oxida
142	11	47.8	9	2	A57444	neuropeptide Grb-A	215	11	47.8	10	2	TL7072	cytochrome-c oxida
143	11	47.8	9	2	B57444	neuropeptide Grb-A	216	11	47.8	10	2	TL7072	cytochrome-c oxida
144	11	47.8	9	2	C57444	neuropeptide Grb-A	217	11	47.8	10	2	TL7072	cytochrome-c oxida
145	11	47.8	9	2	A37027	macrophage chemota	218	11	47.8	10	2	TL7072	cytochrome-c oxida
146	11	47.8	9	2	ODR8	delta sleep-induci	219	11	47.8	10	2	TL7072	cytochrome-c oxida
147	11	47.8	9	2	A60522	sperm-activating p	220	11	47.8	10	2	TL7072	cytochrome-c oxida
148	11	47.8	10	1	XASNPC	angiotensin-conver	221	11	47.8	10	2	TL7072	cytochrome-c oxida
149	11	47.8	10	1	XAVI6B	angiotensin-conver	222	11	47.8	10	2	TL7072	cytochrome-c oxida
150	11	47.8	10	1	RHPGG	gonadoliberin - pi	223	11	47.8	10	2	TL7072	cytochrome-c oxida
151	11	47.8	10	1	RHSHG	gonadoliberin - sh	224	11	47.8	10	2	TL7072	cytochrome-c oxida
152	11	47.8	10	1	A61126	gonadoliberin - sp	225	11	47.8	10	2	TL7072	cytochrome-c oxida
153	11	47.8	10	1	RHAQ1	gonadoliberin I -	226	11	47.8	10	2	TL7072	cytochrome-c oxida
154	11	47.8	10	1	RHAQ2	gonadoliberin II -	227	11	47.8	10	2	TL7072	cytochrome-c oxida
155	11	47.8	10	2	S71868	glutathione transf	228	11	47.8	10	2	TL7072	cytochrome-c oxida
156	11	47.8	10	2	B46030	gonadoliberin II -	229	11	47.8	10	2	TL7072	cytochrome-c oxida
157	11	47.8	10	2	JC1367	thyroliberin poten	230	11	47.8	10	2	TL7072	cytochrome-c oxida
158	11	47.8	10	2	A60647	neuromedin C - bov	231	11	47.8	10	2	TL7072	cytochrome-c oxida
159	11	47.8	10	2	PQ0177	neuromedin C - lau	232	11	47.8	10	2	TL7072	cytochrome-c oxida
160	11	47.8	10	2	A61337	caerulein - frog (233	11	47.8	10	2	TL7072	cytochrome-c oxida
161	11	47.8	10	2	A13687	caerulein-like pep	234	11	47.8	10	2	TL7072	cytochrome-c oxida
162	11	47.8	10	2	S59625	beta-galactosidase	235	11	47.8	10	2	TL7072	cytochrome-c oxida
163	11	47.8	10	2	PQ0753	beta-fructofuranos	236	11	47.8	10	2	TL7072	cytochrome-c oxida
164	11	47.8	10	2	S63696	DNA polymerase - Y	237	11	47.8	10	2	TL7072	cytochrome-c oxida
165	11	47.8	10	2	A49187	gonadotropin-relea	238	11	47.8	10	2	TL7072	cytochrome-c oxida
166	11	47.8	10	2	A35556	hypothetical prote	239	11	47.8	10	2	TL7072	cytochrome-c oxida
167	11	47.8	10	2	PT0245	Ig heavy chain CDR	240	11	47.8	10	2	TL7072	cytochrome-c oxida
168	11	47.8	10	2	PT0289	Ig heavy chain CDR	241	11	47.8	10	2	TL7072	cytochrome-c oxida
169	11	47.8	10	2	PT0310	Ig heavy chain CDR	242	11	47.8	10	2	TL7072	cytochrome-c oxida
170	11	47.8	10	2	PH1344	Ig heavy chain DJ	243	11	47.8	10	2	TL7072	cytochrome-c oxida
171	11	47.8	10	2	S23370	T-cell receptor al	244	11	47.8	10	2	TL7072	cytochrome-c oxida
172	11	47.8	10	2	E49033	T-cell receptor ga	245	11	47.8	10	2	TL7072	cytochrome-c oxida
173	11	47.8	10	2	F49033	T-cell receptor ga	246	11	47.8	10	2	TL7072	cytochrome-c oxida
174	11	47.8	10	2	E41946	T-cell receptor ga	247	11	47.8	10	2	TL7072	cytochrome-c oxida
175	11	47.8	10	2	E41946	T-cell receptor ga	248	11	47.8	10	2	TL7072	cytochrome-c oxida

249	11	47.8	12	2	A26093	microbial collagen	322	11	47.8	14	2	S03530	Ig heavy chain J r
250	11	47.8	12	2	G64003	hypothetical prote	323	11	47.8	14	2	I54284	Ci-inhibitor - hum
251	11	47.8	12	2	S69123	proton-translocati	324	11	47.8	14	2	PT0223	Ig heavy chain CDR
252	11	47.8	12	2	A40763	sucrose-6-phosphat	325	11	47.8	14	2	PH1348	Ig heavy chain DJ
253	11	47.8	12	2	PH1368	Ig heavy chain DJ	326	11	47.8	14	2	PH1327	Ig heavy chain DJ
254	11	47.8	12	2	S43957	Ig mu chain V regi	327	11	47.8	14	2	PH1356	Ig heavy chain DJ
255	11	47.8	12	2	A49033	T-cell receptor de	328	11	47.8	14	2	PH1332	Ig heavy chain DJ
256	11	47.8	12	2	S25039	T-cell receptor de	329	11	47.8	14	2	PH1322	Ig heavy chain DJ
257	11	47.8	12	2	H41946	Ig heavy chain V r	330	11	47.8	14	2	PH1757	T cell receptor al
258	11	47.8	12	2	A42324	T-cell receptor ga	331	11	47.8	14	2	PH1758	T cell receptor al
259	11	47.8	12	2	I57678	cytochrome P450c27	332	11	47.8	14	2	PH1759	T cell receptor al
260	11	47.8	12	2	I57678	gene rPLP-A protei	333	11	47.8	14	2	PH1766	T cell receptor al
261	11	47.8	12	2	I41235	glutamine-tRNA lig	334	11	47.8	14	2	PH1767	T cell receptor al
262	11	47.8	12	2	JS0424	urotensin II-B pep	335	11	47.8	14	2	PH1768	T cell receptor al
263	11	47.8	12	2	A49637	MHC class II histo	336	11	47.8	14	2	PH1769	T cell receptor al
264	11	47.8	12	2	I77529	estrogen receptor	337	11	47.8	14	2	S57572	T cell receptor V-
265	11	47.8	12	2	S43170	kinesin light chai	338	11	47.8	14	2	S58426	spermadhesin AWN h
266	11	47.8	12	2	PN0046	ATP synthase D cha	339	11	47.8	14	2	PH1625	Ig H chain V-D-J r
267	11	47.8	12	2	I58273	thyroglobulin - ra	340	11	47.8	14	2	PH1626	Ig H chain V-D-J r
268	11	47.8	12	2	PQ0776	NADH2 dehydrogenas	341	11	47.8	14	2	PH1627	Ig H chain V-D-J r
269	11	47.8	13	1	XAV19B	angiotensin-conver	342	11	47.8	14	2	PH1594	Ig H chain V-D-J r
270	11	47.8	13	1	MTCWAD	melanotropin-conver	343	11	47.8	14	2	PH0801	T-cell receptor al
271	11	47.8	13	1	MTHOND	melanotropin alpha	344	11	47.8	14	2	PH0747	T-cell receptor be
272	11	47.8	13	2	PQ0445	urotensin II - lau	345	11	47.8	14	2	F49037	TcR delta chain V-
273	11	47.8	13	2	PH1676	Ig heavy chain V r	346	11	47.8	14	2	B44854	L-2,4-diaminobutyr
274	11	47.8	13	2	B28810	glutathione transf	347	11	47.8	14	2	PT0026	calotropin DI - mu
275	11	47.8	13	2	PT0293	Ig heavy chain CRD	348	11	47.8	14	2	S33801	chaperone, TCPI-re
276	11	47.8	13	2	PT0304	Ig heavy chain CRD	349	11	47.8	14	2	S33802	chaperone, TCPI-re
277	11	47.8	13	2	S57567	T cell receptor V-	350	11	47.8	14	2	PT0029	mastoparan B - hor
278	11	47.8	13	2	S23372	T-cell receptor al	351	11	47.8	14	2	S14336	leukotriene B-4 12
279	11	47.8	13	2	PH0138	T-cell receptor be	352	11	47.8	14	2	A47421	calcium-binding pr
280	11	47.8	13	2	S61798	T-cell-specific tr	353	11	47.8	14	2	S68095	S-allele-associate
281	11	47.8	13	2	B56864	dipeptidyl-peptida	354	11	47.8	14	2	S39931	Trp EG leader pept
282	11	47.8	13	2	B25448	Ig kappa-1 chain,	355	11	47.8	14	2	A44515	probrusin tetradec
283	11	47.8	13	2	PH1636	Ig H chain V-D-J r	356	11	47.8	14	2	JH0328	unspecific monooxy
284	11	47.8	13	2	PH1620	Ig H chain V-D-J r	357	11	47.8	15	2	B26997	Sfil-glycoprotein
285	11	47.8	13	2	G37266	Ig heavy chain C r	358	11	47.8	15	2	A26997	stylar glycoprotei
286	11	47.8	13	2	D37267	Ig heavy chain C r	359	11	47.8	15	2	PQ0195	glucan 1,4-alpha-g
287	11	47.8	13	2	B26406	Ig kappa chain J r	360	11	47.8	15	2	PQ0174	alpha-glucosidase
288	11	47.8	13	2	PH0928	T-cell receptor be	361	11	47.8	15	2	PQ0175	oligo-1,6-glucosid
289	11	47.8	13	2	A47630	Ig kappa chain J r	362	11	47.8	15	2	S21202	leukocyte elastase
290	11	47.8	13	2	I51905	collecting duct wa	363	11	47.8	15	2	S21240	cystatin Ci-4a - m
291	11	47.8	13	2	S54344	glycerolaldehyde-3-p	364	11	47.8	15	2	S21241	Ig heavy chain V r
292	11	47.8	13	2	A59491	epithelial dog all	365	11	47.8	15	2	S24159	Ig heavy chain J r
293	11	47.8	13	2	I54984	aeg-46.5 protein -	366	11	47.8	15	2	PQ0232	proteinase - Therm
294	11	47.8	13	2	PC2369	unidentified 85K p	367	11	47.8	15	2	PH1319	hypothetical prote
295	11	47.8	13	2	S60046	early nodulin 40	368	11	47.8	15	2	S26791	self-incompatibili
296	11	47.8	13	2	A61514	glutathione transf	369	11	47.8	15	2	PS0382	gamma 2 gliadin -
297	11	47.8	13	2	A60379	factor X activator	370	11	47.8	15	2	S39012	Ig heavy chain J r
298	11	47.8	13	2	S32551	bombesin - fire-be	371	11	47.8	15	2	T46625	Fc gamma receptor
299	11	47.8	13	2	S66558	polistes mastopara	372	11	47.8	15	2	S08209	Ig heavy chain DJ
300	11	47.8	13	2	A86126	trp operon leader	373	11	47.8	15	2	PQ0750	Ig heavy chain DJ
301	11	47.8	13	2	A60409	trp operon leader	374	11	47.8	15	2	B56891	Ig heavy chain DJ
302	11	47.8	13	2	A05174	bombesin-like pept	375	11	47.8	15	2	S10388	gamma 2 gliadin -
303	11	47.8	14	1	BSTD	tryptophyl-in-13 -	376	11	47.8	15	2	S10386	Ig heavy chain J r
304	11	47.8	14	1	QMVHXX	bombesin - fire-be	377	11	47.8	15	2	A47628	Fc gamma receptor
305	11	47.8	14	1	QMWAPP	mastoparan X - hor	378	11	47.8	15	2	PH1365	Ig heavy chain DJ
306	11	47.8	14	1	LFEBWC	polistes mastopara	379	11	47.8	15	2	PH1366	Ig heavy chain DJ
307	11	47.8	14	1	LFEBWT	trp operon leader	380	11	47.8	15	2	PH1342	Ig heavy chain DJ
308	11	47.8	14	1	LFECW	trp operon leader	381	11	47.8	15	2	PH1318	Ig heavy chain DJ
309	11	47.8	14	2	PC2373	probable IMP dehyd	382	11	47.8	15	2	PH1320	Ig heavy chain DJ
310	11	47.8	14	2	A60622	somatostatin - spo	383	11	47.8	15	2	S43956	Ig mu chain V regi
311	11	47.8	14	2	A60840	somatostatin I - E	384	11	47.8	15	2	PH1762	T cell receptor al
312	11	47.8	14	2	C60414	somatostatin - sli	385	11	47.8	15	2	PH1788	T cell receptor al
313	11	47.8	14	2	B60842	somatostatin I - c	386	11	47.8	15	2	G49655	T-cell receptor be
314	11	47.8	14	2	S00172	somatostatin I - s	387	11	47.8	15	2	PQ0073	T-cell receptor be
315	11	47.8	14	2	PH1677	Ig heavy chain V r	388	11	47.8	15	2	A45103	Ig H chain V-D-J r
316	11	47.8	14	2	PH1705	Ig heavy chain V r	389	11	47.8	15	2	PH1616	Ig H chain V-D-J r
317	11	47.8	14	2	PT0077	proteochondroitin c	390	11	47.8	15	2	PH1590	Ig H chain V-D-J r
318	11	47.8	14	2	E90858	trp operon leader	391	11	47.8	15	2	PH1612	Ig H chain V-D-J r
319	11	47.8	14	2	B85761	trp operon leader	392	11	47.8	15	2	PH0782	T-cell receptor al
320	11	47.8	14	2	A35105	hypothetical prote	393	11	47.8	15	2	E49037	TcR delta chain V-
321	11	47.8	14	2	PC1215	homeotic protein E	394	11	47.8	15	2	PL0109	complement factor

395	11	47.8	15	2	S02381	probable membrane	468	11	47.8	17	2	PH1357	Ig heavy chain DJ
396	11	47.8	15	2	PH0216	agarase (EC 3.2.1.1.	469	11	47.8	17	2	PH1630	Ig H chain V-D-J r
397	11	47.8	15	2	S21411	modulation protein	470	11	47.8	17	2	PH0384	Ig heavy chain J r
398	11	47.8	15	2	S33781	acetolactate synth	471	11	47.8	17	2	A46592	lactase-phlorizin
399	11	47.8	15	2	B60763	endo-1,3-beta-gluc	472	11	47.8	17	2	A44560	cytotoxin B - Clos
400	11	47.8	15	2	A48372	benzoyl-CoA ligase	473	11	47.8	17	2	A27636	tachyplesin I - ho
401	11	47.8	15	2	T09463	ribosomal protein	474	11	47.8	17	2	A38824	tachyplesin I - ho
402	11	47.8	15	2	PA0036	glycine cleavage s	475	11	47.8	17	2	JX0125	tachyplesin III -
403	11	47.8	15	2	PA0099	phenotypic variati	476	11	47.8	17	2	PC1318	large granule L6 c
404	11	47.8	15	2	FX0031	mixed lymphocyte r	477	11	47.8	17	2	S10786	enamelin, 26K - bo
405	11	47.8	15	2	C84035	hypothetical prote	478	11	47.8	17	2	I53392	CD33 antigen homol
406	11	47.8	15	4	I38032	hypothetical MNI/T	479	11	47.8	17	2	I67524	CD33 antigen homol
407	11	47.8	16	1	A49761	locustapayrokinin -	480	11	47.8	17	2	I67526	CD33 antigen homol
408	11	47.8	16	1	MTDFBS	melanotropin beta	481	11	47.8	17	2	A61211	anantin - Streptom
409	11	47.8	16	2	E41425	cytochrome P450 1f	482	11	47.8	17	2	B48943	phage antigenic de
410	11	47.8	16	2	S03405	hydrogenase (EC 1.	483	11	47.8	17	2	E59137	protein Pf33 - gol
411	11	47.8	16	2	I57530	gene c-fms protein	484	11	47.8	17	2	A29834	trp leader peptide
412	11	47.8	16	2	A60551	leukocyte elastase	485	11	47.8	17	2	MTDFBC	melanotropin beta
413	11	47.8	16	2	A29541	little gastrin - C	486	11	47.8	18	1	MTDOB	melanotropin beta
414	11	47.8	16	2	S03532	Ig heavy chain J r	487	11	47.8	18	2	S29379	sorbitol dehydroge
415	11	47.8	16	2	D45021	Ig heavy chain J7	488	11	47.8	18	2	S4780	protein-tyrosine k
416	11	47.8	16	2	A36300	T-cell receptor ga	489	11	47.8	18	2	G2018	epoxide hydrolase
417	11	47.8	16	2	PS0383	Ig heavy chain J r	490	11	47.8	18	2	S74195	proteasome chain L
418	11	47.8	16	2	S26746	Ig heavy chain J r	491	11	47.8	18	2	S04229	N4-(beta-N-acetyl)g
419	11	47.8	16	2	S66613	protein p12E - Fx1	492	11	47.8	18	2	D49570	plasma membrane ca
420	11	47.8	16	2	S28213	glutathione transf	493	11	47.8	18	2	S43834	DNA topoisomerase
421	11	47.8	16	2	PT0237	Ig heavy chain CDR	494	11	47.8	18	2	PH1368	Ig heavy chain DJ
422	11	47.8	16	2	PT0282	Ig heavy chain CDR	495	11	47.8	18	2	PH1323	Ig heavy chain DJ
423	11	47.8	16	2	PT0296	Ig heavy chain CDR	496	11	47.8	18	2	S03528	Ig heavy chain J1
424	11	47.8	16	2	PH1346	Ig heavy chain DJ	497	11	47.8	18	2	A32220	T-cell receptor de
425	11	47.8	16	2	S23184	redoxendonuclease	498	11	47.8	18	2	A25941	Ig heavy chain J-H
426	11	47.8	16	2	PH1637	Ig H chain V-D-J r	499	11	47.8	18	2	S29264	ovohemerythrin - d
427	11	47.8	16	2	PH1638	Ig H chain V-D-J r	500	11	47.8	18	2	S55501	thrombospondin pre
428	11	47.8	16	2	PH1604	Ig H chain V-D-J r	501	11	47.8	18	2	S52125	gamma2-gliadin P25
429	11	47.8	16	2	A48839	T-cell receptor al	502	11	47.8	18	2	C56211	progesterone recep
430	11	47.8	16	2	PH0748	T-cell receptor be	503	11	47.8	18	2	S46418	NTU1 protein - cur
431	11	47.8	16	2	D49037	TcR delta chain V-	504	11	47.8	18	2	I40062	shikimate 5-dehydr
432	11	47.8	16	2	A48236	transforming prote	505	11	47.8	18	2	S21669	1H-4-oxoquinoline
433	11	47.8	16	2	S33589	beta-crystallin A4	506	11	47.8	18	2	T03799	leader peptide trp
434	11	47.8	16	2	B44820	7K protein - Esche	507	11	47.8	18	2	S19914	choline O-acetyltr
435	11	47.8	16	2	PC1299	subtilisin (EC 3.4	508	11	47.8	18	2	I52623	hypothetical prote
436	11	47.8	16	2	A24099	crystal protein, 2	509	11	47.8	18	2	PT0239	Ig heavy chain CDR
437	11	47.8	16	2	T44936	calmodulin kinase	510	11	47.8	18	2	PT0286	Ig heavy chain CDR
438	11	47.8	16	2	A20190	hypodermin B - ear	511	11	47.8	18	2	PH1349	Ig heavy chain DJ
439	11	47.8	16	2	A48630	bothrojaracin - ja	512	11	47.8	18	2	PH1350	Ig heavy chain DJ
440	11	47.8	16	2	I37452	protein kinase - h	513	11	47.8	18	2	S43958	Ig mu chain V regi
441	11	47.8	16	2	S13898	alkaline phosphata	514	11	47.8	18	2	A40256	interleukin-7 rece
442	11	47.8	16	2	B23692	transcription fact	515	11	47.8	18	2	I35141	T-cell receptor de
443	11	47.8	16	2	E37290	homeotic protein G	516	11	47.8	18	2	C49254	TcR C gamma 1 chai
444	11	47.8	16	2	S05703	homeotic protein c	517	11	47.8	18	2	G49037	TcR delta chain V-
445	11	47.8	16	4	I79565	hypothetical TcR3/	518	11	47.8	18	2	A61577	24k serine protein
446	11	47.8	17	1	GMSH	gastrin - sheep	519	11	47.8	18	2	S20322	gluten - wheat
447	11	47.8	17	2	S66198	alcohol dehydrogen	520	11	47.8	18	2	S20322	polyphemusin I - A
448	11	47.8	17	2	A60071	gastrin - rhesus m	521	11	47.8	18	2	JU0124	polyphemusin II -
449	11	47.8	17	2	S24570	Ig heavy chain J r	522	11	47.8	18	2	JU0125	hypothetical prote
450	11	47.8	17	2	H45048	T-cell receptor be	523	11	47.8	18	2	A35678	hypothetical prote
451	11	47.8	17	2	I49048	T-cell receptor be	524	11	47.8	18	2	S27141	neuropeptide A - b
452	11	47.8	17	2	S03531	Ig heavy chain J5	525	11	47.8	18	2	A24749	ancovenin - Strept
453	11	47.8	17	2	S26747	Ig heavy chain J r	526	11	47.8	19	1	EWSM02	cytochrome P450-C
454	11	47.8	17	2	S26744	Ig heavy chain J r	527	11	47.8	19	2	I49422	L-lactate dehydrog
455	11	47.8	17	2	B44873	caldesmon - rabbit	528	11	47.8	19	2	S71871	glutathione transf
456	11	47.8	17	2	I57941	beta 3-adrenergic	529	11	47.8	19	2	I45957	protein kinase (BC
457	11	47.8	17	2	I51910	Sp-A2 - human (fra	530	11	47.8	19	2	PC1251	testin II - rat (f
458	11	47.8	17	2	A41053	glutamate receptor	531	11	47.8	19	2	S60633	H+-transporting tw
459	11	47.8	17	2	E40442	integraser homolog	532	11	47.8	19	2	PH1304	Ig heavy chain DJ
460	11	47.8	17	2	S18534	hypothetical prote	533	11	47.8	19	2	PT0244	Ig heavy chain CDR
461	11	47.8	17	2	B44923	carboxypeptidase 3	534	11	47.8	19	2	G49048	T-cell receptor be
462	11	47.8	17	2	S19614	globin - polychaet	535	11	47.8	19	2	PH1307	Ig heavy chain DJ
463	11	47.8	17	2	S03533	Ig heavy chain J r	536	11	47.8	19	2	S43960	Ig mu chain V regi
464	11	47.8	17	2	PT0234	Ig heavy chain CDR	537	11	47.8	19	2	A28814	Ig kappa chain V r
465	11	47.8	17	2	PT0235	Ig heavy chain CRD	538	11	47.8	19	2	I53673	amyloid protein -
466	11	47.8	17	2	PH1367	Ig heavy chain DJ	539	11	47.8	19	2	B61409	genome polyprotein
467	11	47.8	17	2	PH1331	Ig heavy chain DJ	540	11	47.8	19	2	PX0062	beta-galactoside-b

541	11	47.8	19	2	S02269	glycogen(starch) s	614	11	47.8	20	2	PH1358	Ig heavy chain DJ
542	11	47.8	19	2	B56613	virion morphogenes	615	11	47.8	20	2	PH1341	Ig heavy chain DJ
543	11	47.8	19	2	S63489	dissimilatory sulf	616	11	47.8	20	2	PH1326	Ig heavy chain DJ
544	11	47.8	19	2	T50329	wd-repeat protein	617	11	47.8	20	2	PC2248	lambda 112 protein
545	11	47.8	19	2	S60110	hypothetical prote	618	11	47.8	20	2	S60350	kallikrein, pankre
546	11	47.8	19	2	PH1352	Ig heavy chain DJ	619	11	47.8	20	2	S15961	estrogen receptor
547	11	47.8	19	2	PH1353	Ig heavy chain DJ	620	11	47.8	20	2	A36689	1-phosphatidylinos
548	11	47.8	19	2	PH1339	Ig heavy chain DJ	621	11	47.8	20	2	PQ0071	T-cell receptor be
549	11	47.8	19	2	PH1315	Ig heavy chain DJ	622	11	47.8	20	2	S56756	link protein - rat
550	11	47.8	19	2	PH1330	Ig heavy chain DJ	623	11	47.8	20	2	S68341	procathepsin L - g
551	11	47.8	19	2	S57515	T cell receptor be	624	11	47.8	20	2	S66222	defensin AMP2 - Da
552	11	47.8	19	2	S57516	T cell receptor be	625	11	47.8	20	2	C56894	intracrystalline c
553	11	47.8	19	2	S03519	T-cell receptor ga	626	11	47.8	20	2	D84716	hypothetical prote
554	11	47.8	19	2	I46654	T-cell receptor de	627	11	47.8	20	2	T44453	acetyl-CoA synthet
555	11	47.8	19	2	PH1624	Ig H chain V-D-J r	628	11	47.8	20	2	A44927	major outer membra
556	11	47.8	19	2	PH0793	T-cell receptor al	629	11	47.8	20	2	S45637	oxidoreductase - p
557	11	47.8	19	2	I49037	TcR delta chain V-	630	11	47.8	20	2	S63490	dissimilatory sulf
558	11	47.8	19	2	B46592	lactase-phlorizin	631	11	47.8	20	2	A40451	dormancy-related p
559	11	47.8	19	2	A48354	nonstructural prot	632	11	47.8	20	2	S29636	Jacalin beta-1 cha
560	11	47.8	19	2	I40063	shikimate 5-dehydr	633	11	47.8	20	2	S29635	Jacalin beta chain
561	11	47.8	19	2	A44854	L-2,4-diaminobuty	634	11	47.8	20	2	S03987	agglutinin beta-2
562	11	47.8	19	2	S29212	protein C - oat (f	635	11	47.8	20	2	S35460	alliin lyase (EC 4
563	11	47.8	19	2	S19532	globin - polychaet	636	11	47.8	20	2	PC2084	serine proteinase
564	11	47.8	19	2	S19613	globin - polychaet	637	11	47.8	20	2	S38763	S-adenosyl-L-methi
565	11	47.8	19	2	JX0124	tachyplesin I prec	638	11	47.8	20	2	A34817	collagenolytic pro
566	11	47.8	19	2	I52721	gene hMLH1 protein	639	11	47.8	20	2	A56899	serum heterodimer,
567	11	47.8	19	2	S12268	Qa-2 antigen - mou	640	11	47.8	20	2	A47105	dystroglycan - chi
568	11	47.8	19	2	A60505	hemoglobin Cl beta	641	11	47.8	20	2	A61506	alpha-1-antitrypsi
569	11	47.8	19	2	A58700	actagardine [valid	642	11	47.8	20	2	A56894	intracrystalline c
570	11	47.8	19	4	I54264	rhodopsin single b	643	11	47.8	20	2	B56894	intracrystalline c
571	11	47.8	20	2	A23739	cytochrome P450 MU	644	11	47.8	20	2	A85659	hypothetical prote
572	11	47.8	20	2	S21176	testosterone 6beta	645	11	47.8	20	2	AE0120	insertion element
573	11	47.8	20	2	A60728	cytochrome P450 3A	646	11	47.8	20	2	AC0269	probable trp opero
574	11	47.8	20	2	B61080	5-carboxymethyl-2-	647	11	47.8	20	2	B60505	hemoglobin A1-2 be
575	11	47.8	20	2	B37520	glutathione transf	648	11	47.8	20	2	S08605	hypothetical prote
576	11	47.8	20	2	S29099	glutathione transf	649	11	47.8	20	2	S27142	hypothetical prote
577	11	47.8	20	2	S29100	glutathione transf	650	11	47.8	20	2	DIRT	dental fluid tra
578	11	47.8	20	2	S71869	glutathione transf	651	8	34.8	15	2	A28856	fructose-bisphosph
579	11	47.8	20	2	S03381	glutathione transf	652	7	30.4	12	2	E41383	23K variable histo
580	11	47.8	20	2	PQ0751	self-incompatibili	653	7	30.4	20	2	I70108	microsomal triglyc
581	11	47.8	20	2	PH0111	style glycoprotein	654	6	26.1	3	3	S68328	blood cell protein
582	11	47.8	20	2	PH0110	base nonspecific a	655	6	26.1	4	1	ECXAA	antho-RFamide neur
583	11	47.8	20	2	PC2347	pancreatic elastas	656	6	26.1	4	2	D41654	hypothetical prote
584	11	47.8	20	2	S33787	chymotrypsin I (EC	657	6	26.1	4	2	S53508	starvation-induced
585	11	47.8	20	2	A56900	chymotrypsin I (EC	658	6	26.1	4	2	A25844	myosin-RF amide neu
586	11	47.8	20	2	B61333	chymotrypsin (EC 3	659	6	26.1	4	2	S39390	myosin-light-chain
587	11	47.8	20	2	I49423	cytotoxic T-lympho	660	6	26.1	4	2	JQ1273	neuropeptide Antho
588	11	47.8	20	2	S46205	comosain (EC 3.4.2	661	6	26.1	4	2	A35779	neuropeptide Antho
589	11	47.8	20	2	S46204	ananain (EC 3.4.22	662	6	26.1	4	2	A60418	FMRFamide - polych
590	11	47.8	20	2	C54052	phosphoribosyl-AMP	663	6	26.1	4	2	A32480	achatin-I - giant
591	11	47.8	20	2	A37111	ribulose-bisphosph	664	6	26.1	4	2	ECNK	cardioexcitatory n
592	11	47.8	20	2	C49164	chromogranin-B - r	665	6	26.1	5	2	A44955	alkanal monooxygen
593	11	47.8	20	2	PT0248	Ig heavy chain CDR	666	6	26.1	5	2	S70615	endo-1,4-beta-xyla
594	11	47.8	20	2	F49048	T-cell receptor be	667	6	26.1	5	2	PS0324	ribulose-bisphosph
595	11	47.8	20	2	A49048	T-cell receptor be	668	6	26.1	5	2	B45525	actin I - malaria
596	11	47.8	20	2	PL0192	Ig lambda 2 chain	669	6	26.1	5	2	B61445	Leu-enkephalin - b
597	11	47.8	20	2	S39049	cytotoxin-binding	670	6	26.1	5	2	A61445	Met-enkephalin - b
598	11	47.8	20	2	B33761	actin - Acanthamo	671	6	26.1	5	2	B61168	coconase (EC 3.4.
599	11	47.8	20	2	A05313	apolipoprotein A-I	672	6	26.1	5	2	PT0278	Ig heavy chain CRD
600	11	47.8	20	2	A36045	thrombospondin hom	673	6	26.1	5	2	A44692	fulicin - giant Af
601	11	47.8	20	2	S03335	photosystem II pho	674	6	26.1	5	2	JS0319	subesophageal gang
602	11	47.8	20	2	PW0003	chlorophyll a/b-bi	675	6	26.1	5	2	PT0644	T-cell receptor be
603	11	47.8	20	2	S04988	gag core shell pro	676	6	26.1	5	4	A58728	serrawettin W2 - S
604	11	47.8	20	2	A44773	pollen allergen I	677	6	26.1	6	2	A61049	halo-toxin - Pseud
605	11	47.8	20	2	A60372	pollen allergen Po	678	6	26.1	6	2	A60986	N-formyl oligopept
606	11	47.8	20	2	D37396	pollen allergen Fe	679	6	26.1	6	2	S11024	hydrogensulfite re
607	11	47.8	20	2	I64036	hypothetical prote	680	6	26.1	6	2	I51317	bHLH transcription
608	11	47.8	20	2	T46626	hypothetical prote	681	6	26.1	6	2	I37263	y protein - human
609	11	47.8	20	2	S16202	pyroline-5-carbox	682	6	26.1	6	2	I59142	platelet-derived g
610	11	47.8	20	2	D25507	proteinase inhibit	683	6	26.1	6	2	A41946	T-cell receptor ga
611	11	47.8	20	2	PC1152	equinotoxin 1D - s	684	6	26.1	6	2	A27696	contraction-inhibi
612	11	47.8	20	2	S10876	hypothetical prote	685	6	26.1	6	2	B27696	neuropeptide GNFR
613	11	47.8	20	2	S58382	hypothetical prote	686	6	26.1	6	2	A43129	

687	6	26.1	7	1	NYPG7	hypothalamic hepta	760	6	26.1	9	2	S36850	Ig heavy chain V r
688	6	26.1	7	1	A61324	dermorphin - Rohde	761	6	26.1	9	2	G41946	T-cell receptor ga
689	6	26.1	7	2	A60224	Met-enkephalin-Arg	762	6	26.1	9	2	A42266	peptidylglycine mo
690	6	26.1	7	2	S36662	dermorphin (Lys-7)	763	6	26.1	9	2	I52974	seminal vesicle pr
691	6	26.1	7	2	PH1408	Ig heavy chain V r	764	6	26.1	9	2	S39767	cardioactive pepti
692	6	26.1	7	2	B3127	phosphotransferase	765	6	26.1	9	2	S39040	lysine-conopressin
693	6	26.1	7	2	I40504	hypothetical prote	766	6	26.1	9	2	G58502	kidney and bladder
694	6	26.1	7	2	H33098	180K exoantigen -	767	6	26.1	9	2	S39523	orf AB protein - S
695	6	26.1	7	2	S68004	hucolin, 75K chain	768	6	26.1	9	2	A31576	xylose isomerase (
696	6	26.1	7	2	S39332	Ig mu chain D regl	769	6	26.1	9	2	S33333	alpha/beta-gliadin
697	6	26.1	7	2	PT0665	T-cell receptor be	770	6	26.1	9	2	PC2021	oxytocin-related p
698	6	26.1	7	2	A59489	protein kinase C i	771	6	26.1	9	2	A36363	cardioactive pepti
699	6	26.1	7	2	B35890	RNA-directed DNA p	772	6	26.1	9	2	A61620	locustamyotropin I
700	6	26.1	7	2	A25269	sex pheromone CAM3	773	6	26.1	9	2	S27233	cardioactive pepti
701	6	26.1	7	2	S39812	sex pheromone cCF1	774	6	26.1	9	2	A41978	calliFMRamide 1 -
702	6	26.1	7	2	S17976	glucose isomerase	775	6	26.1	9	2	A44787	calliFMRamide 10
703	6	26.1	7	2	PC2132	FMRamide-related	776	6	26.1	9	2	D44787	calliFMRamide 13
704	6	26.1	7	2	B44787	calliFMRamide 11	777	6	26.1	9	2	B41978	calliFMRamide 2 -
705	6	26.1	7	2	S08606	hypothetical prote	778	6	26.1	9	2	C41978	calliFMRamide 3 -
706	6	26.1	8	2	A35223	peptidyl-dipeptida	779	6	26.1	9	2	D41978	calliFMRamide 4 -
707	6	26.1	8	2	PH1407	Ig heavy chain V r	780	6	26.1	9	2	E41978	calliFMRamide 5 -
708	6	26.1	8	2	PL0184	capsid protein VP-	781	6	26.1	9	2	F41978	calliFMRamide 6 -
709	6	26.1	8	2	PA0032	protein QA300040 -	782	6	26.1	9	2	F41978	calliFMRamide 7 -
710	6	26.1	8	2	S13661	polygalacturonase	783	6	26.1	9	2	S10920	venom protein HR-3
711	6	26.1	8	2	B33099	158K exoantigen -	784	6	26.1	9	2	JN0027	[pre-6]-mosact - s
712	6	26.1	8	2	A38992	P element, P cytot	785	6	26.1	9	2	B20569	serum amyloid P-co
713	6	26.1	8	2	B45800	serum albumin - do	786	6	26.1	9	2	S77984	cytochrome-c oxida
714	6	26.1	8	2	A42057	fibroblast growth	787	6	26.1	9	2	PT0080	60K Ca binding pro
715	6	26.1	8	2	PH0803	T-cell receptor al	788	6	26.1	9	2	A61386	macrophage inhibit
716	6	26.1	8	2	PC4372	telomeric and tetr	789	6	26.1	9	2	B39504	octamer-binding pr
717	6	26.1	8	2	S66296	Na+-transporting A	790	6	26.1	9	2	S66635	alpha-2-macroglobu
718	6	26.1	8	2	S37141	tpsa protein - Erw	791	6	26.1	9	2	S10784	enamelin 1 - bovin
719	6	26.1	8	2	S21273	cellulase (EC 3.2.	792	6	26.1	9	2	A28924	fructose-bisphosph
720	6	26.1	8	2	A37521	R-phycoerythrin ga	793	6	26.1	9	2	PC7074	3-oxoacid CoA-tran
721	6	26.1	8	2	S11078	glucose-6-phosphat	794	6	26.1	9	2	A43065	translation elonga
722	6	26.1	8	2	PT0030	inulinase (EC 3.2.	795	6	26.1	9	2	P00027	hydroxyproline-3-b
723	6	26.1	8	2	A46306	spasmodic toxin.	796	6	26.1	9	2	P00027	pev-tachykinin - p
724	6	26.1	8	2	A23967	leucoperoxin - M	797	6	26.1	9	2	G85802	hypothetical prote
725	6	26.1	8	2	S66646	cardioacceleratory	798	6	26.1	9	2	S15850	vitamin D3 26-mono
726	6	26.1	8	2	B27867	homeotic protein U	799	6	26.1	9	2	A26744	bradykinin-like pe
727	6	26.1	8	2	H41978	calliFMRamide 8 -	800	6	26.1	9	2	A61057	Thr-6 bradykinin -
728	6	26.1	8	2	D47393	neuropeptide calla	801	6	26.1	9	2	A60579	bradykinin-like pe
729	6	26.1	8	2	E47393	neuropeptide calla	802	6	26.1	9	2	S19329	sperm-activating p
730	6	26.1	8	2	S71919	alcohol dehydrogen	803	6	26.1	9	2	B60246	ornitho-kinin - ch
731	6	26.1	8	2	A14683	aspartate transami	804	6	26.1	9	2	A61363	bradykinin - commo
732	6	26.1	8	2	A61328	trypsin (EC 3.4.21	805	6	26.1	9	2	A61358	bradykinin-like pe
733	6	26.1	8	2	A28719	thymic humoral fac	806	6	26.1	10	1	ECLQ1M	tachykinin I - mig
734	6	26.1	8	2	S65381	cytochrome-c oxida	807	6	26.1	10	1	ECLQ3M	tachykinin III - m
735	6	26.1	8	2	PC4373	telomeric and tetr	808	6	26.1	10	1	ECLQ4M	tachykinin IV - mi
736	6	26.1	8	2	A59028	MHC class I histoc	809	6	26.1	10	1	SPGNK	neuromedin K - pig
737	6	26.1	8	2	S20162	leghemoglobin III	810	6	26.1	10	1	GMROL2	leucosulfakinin-II
738	6	26.1	8	2	F60588	sperm-activating p	811	6	26.1	10	2	S28055	cytochrome b559 co
739	6	26.1	8	2	B24749	neuropeptide B - b	812	6	26.1	10	2	S15118	dihydrofolate redu
740	6	26.1	8	2	E60588	sperm-activating p	813	6	26.1	10	2	S39392	calpain (EC 3.4.22
741	6	26.1	8	2	G60588	sperm-activating p	814	6	26.1	10	2	A06624	angiotensin I - Ja
742	6	26.1	8	2	S43972	tumor-associated a	815	6	26.1	10	2	A60410	beta-neoendorphin
743	6	26.1	8	2	S43971	tumor-associated a	816	6	26.1	10	2	JN0024	neurokinin A - chi
744	6	26.1	9	2	A28495	conopressin G - co	817	6	26.1	10	2	S39374	mannose receptor -
745	6	26.1	9	2	A61230	calasequetrin, car	818	6	26.1	10	2	A61617	ecdysteroid UDPglu
746	6	26.1	9	2	D24180	fibrinogen beta ch	819	6	26.1	10	2	S66458	ferritin - Rhizo
747	6	26.1	9	2	D24180	fibrinogen beta ch	820	6	26.1	10	2	S70721	heat shock protein
748	6	26.1	9	2	E28854	fibrinopeptide B -	821	6	26.1	10	2	S48182	bacterioferritin -
749	6	26.1	9	2	F28854	fibrinopeptide B -	822	6	26.1	10	2	H28027	protein Pil - curl
750	6	26.1	9	2	D28854	fibrinopeptide B -	823	6	26.1	10	2	C61440	polygalacturonase
751	6	26.1	9	2	D58503	translation elonga	824	6	26.1	10	2	S85432	angiotensin I - ho
752	6	26.1	9	2	S66607	quinoline 2-oxidor	825	6	26.1	10	2	PT0230	Ig heavy chain CDR
753	6	26.1	9	2	S63491	disinfectant sulf	826	6	26.1	10	2	PT0251	Ig heavy chain CDR
754	6	26.1	9	2	S36898	ribosomal protein	827	6	26.1	10	2	PT0284	Ig heavy chain CDR
755	6	26.1	9	2	T31612	hypothetical prote	828	6	26.1	10	2	B45482	platelet activatin
756	6	26.1	9	2	S39766	cardioactive pepti	829	6	26.1	10	2	S23371	T-cell receptor al
757	6	26.1	9	2	S65433	bradykinin - horn	830	6	26.1	10	2	S66214	cartilage oligomer
758	6	26.1	9	2	PT0225	Ig heavy chain CDR	831	6	26.1	10	2	S71948	matrix metalloprot
759	6	26.1	9	2	PT0315	Ig heavy chain CDR	832	6	26.1	10	2	C39398	Fc mu (IgM) recept

833	10	2	A37268	Ig heavy chain C r	906	6	26.1	10	2	I60588	sperm-activating p
834	6	26.1	S36849	Ig heavy chain V r	907	6	26.1	10	2	B60589	sperm-activating p
835	6	26.1	PT0807	T-cell receptor al	908	6	26.1	10	2	G61033	ranatachykinin C -
836	6	26.1	PT0215	T-cell receptor be	909	6	26.1	10	2	B61033	ranatachykinin B -
837	6	26.1	S65385	cytochrome-c oxida	910	6	26.1	10	2	S27178	cardiolekinin A-relat
838	6	26.1	S68033	cytochrome P450 1A	911	6	26.1	10	2	A32543	cardioexcitatory n
839	6	26.1	D37397	hypothetical prote	912	6	26.1	10	4	S14943	UGA3 leader peptid
840	6	26.1	B46453	e antigen p20e pre	913	6	26.1	11	1	EC1Q2M	tachykinin II - mi
841	6	26.1	G58501	48K bile/gallblad	914	6	26.1	11	1	A60654	substance P - guin
842	6	26.1	I39702	nopaline synthase	915	6	26.1	11	1	EOOC	eledoisin - musky
843	6	26.1	S06964	hypothetical prote	916	6	26.1	11	1	EOOC	eledoisin - curled
844	6	26.1	S18396	probable glucose-6	917	6	26.1	11	1	SPHO	substance P - hors
845	6	26.1	S70251	nitrogenase (EC 1.	918	6	26.1	11	1	GMROL	leucosulfakinin -
846	6	26.1	I40032	trpE protein - Bac	919	6	26.1	11	2	G42762	proteasome endopep
847	6	26.1	A60476	S-layer protein -	920	6	26.1	11	2	A33917	dihydroorotase (EC
848	6	26.1	I44644	neurotoxin-associa	921	6	26.1	11	2	UN0023	substance P - chic
849	6	26.1	A39745	endo-glucosylceram	922	6	26.1	11	2	A38841	rhodopsin homolog
850	6	26.1	PC2044	beta-Kirilowin - M	923	6	26.1	11	2	D58502	27K bile and gallb
851	6	26.1	B59272	peptide-N4- (N-acet	924	6	26.1	11	2	A58502	38K kidney stone p
852	6	26.1	S38304	lectin GNL1 alpha	925	6	26.1	11	2	S33782	acetolactate synth
853	6	26.1	S38305	lectin GNL2 alpha	926	6	26.1	11	2	D60691	phycobillosome 8K 1
854	6	26.1	D28027	protein P7 - curle	927	6	26.1	11	2	D60691	phycobillosome 9K 1
855	6	26.1	B61440	polygalacturonase	928	6	26.1	11	2	PC2372	58K heat shock pro
856	6	26.1	D61440	polygalacturonase	929	6	26.1	11	2	B41835	translation elonga
857	6	26.1	FN0165	triose-phosphate i	930	6	26.1	11	2	S19301	endo-1,4-beta-xyla
858	6	26.1	A58365	neuropeptide FPRFa	931	6	26.1	11	2	PA0028	protein QA300042 -
859	6	26.1	B60566	leucosulfakinin II	932	6	26.1	11	2	T06383	hypothetical prote
860	6	26.1	A43977	FMRFamide-like pro	933	6	26.1	11	2	PU0029	33K protein 3218 -
861	6	26.1	C44787	callifMRPamide 12	934	6	26.1	11	2	S78026	ribosomal protein
862	6	26.1	A56633	neomysuppressin -	935	6	26.1	11	2	I33098	173K exoantigen -
863	6	26.1	D46285	formaldehyde dehyd	936	6	26.1	11	2	B60769	Ig H2 chain - Paci
864	6	26.1	A30823	bothropstoxin - ja	937	6	26.1	11	2	I52980	glucocerebrosidase
865	6	26.1	A90917	angiotensin precur	938	6	26.1	11	2	PT0250	Ig heavy chain CRD
866	6	26.1	A90345	angiotensin precur	939	6	26.1	11	2	PT0287	Ig heavy chain CRD
867	6	26.1	S65387	cytochrome-c oxida	940	6	26.1	11	2	S57575	T cell receptor V -
868	6	26.1	TL3838	cytochrome-c oxida	941	6	26.1	11	2	S23364	T-cell receptor al
869	6	26.1	A44871	monodehydroascorba	942	6	26.1	11	2	S23373	T-cell receptor al
870	6	26.1	S74147	glyceraldehyde-3-p	943	6	26.1	11	2	S51732	T-cell receptor al
871	6	26.1	B33710	ornithine decarbox	944	6	26.1	11	2	A54348	N-acetylglucosamin
872	6	26.1	A60527	sperm-activating p	945	6	26.1	11	2	PD0442	NIPSNAP2 protein -
873	6	26.1	B49581	sialokinin II - ye	946	6	26.1	11	2	PH1376	T antigen variant
874	6	26.1	A49581	sialokinin I - ye	947	6	26.1	11	2	PT0214	T-cell receptor be
875	6	26.1	H60787	sperm-activating p	948	6	26.1	11	2	I60434	68kDa neurofilamen
876	6	26.1	G60787	sperm-activating p	949	6	26.1	11	2	S53436	beta-D-galactosida
877	6	26.1	F60787	sperm-activating p	950	6	26.1	11	2	PH0906	T-cell receptor be
878	6	26.1	F60787	sperm-activating p	951	6	26.1	11	2	S58501	42K bile stone pro
879	6	26.1	C60787	sperm-activating p	952	6	26.1	11	2	S58244	pyrroloquinoline q
880	6	26.1	A60787	sperm-activating p	953	6	26.1	11	2	S35490	type II site-speci
881	6	26.1	D60787	sperm-activating p	954	6	26.1	11	2	B39853	LuxC protein - Pho
882	6	26.1	B60787	sperm-activating p	955	6	26.1	11	2	PC2330	cycloinulooligosac
883	6	26.1	D60588	sperm-activating p	956	6	26.1	11	2	A44755	20alpha-hydroxyste
884	6	26.1	B60588	sperm-activating p	957	6	26.1	11	2	A35594	buccalin - Califor
885	6	26.1	C60588	sperm-activating p	958	6	26.1	11	2	S69349	neuropeptide Ffami
886	6	26.1	I60527	sperm-activating p	959	6	26.1	11	2	A60656	perisulfakinin - A
887	6	26.1	A60588	sperm-activating p	960	6	26.1	11	2	I41978	califMRamide 9 -
888	6	26.1	A60788	sperm-activating p	961	6	26.1	11	2	S33300	probable substance
889	6	26.1	D60527	sperm-activating p	962	6	26.1	11	2	D42965	talin - chicken (f
890	6	26.1	C39572	sperm-activating p	963	6	26.1	11	2	E57789	gallbladder stone
891	6	26.1	F60527	sperm-activating p	964	6	26.1	11	2	S13279	ile-Ser-bradykinin
892	6	26.1	C60527	sperm-activating p	965	6	26.1	11	2	A32428	amine oxidase (cop
893	6	26.1	E60527	sperm-activating p	966	6	26.1	11	2	PN0042	statamin - mouse
894	6	26.1	G60527	sperm-activating p	967	6	26.1	11	2	A48973	glucosylase A1 (E
895	6	26.1	E39572	sperm-activating p	968	6	26.1	11	2	S09074	cytochrome P450-4b
896	6	26.1	D60788	sperm-activating p	969	6	26.1	11	2	A57458	gene Gax protein -
897	6	26.1	E60788	sperm-activating p	970	6	26.1	11	2	S07203	uperolein - frog
898	6	26.1	C60788	sperm-activating p	971	6	26.1	11	2	B26744	megascollakinin -
899	6	26.1	A24867	scyllorhinin I - s	972	6	26.1	11	2	C60409	kassinin-like pept
900	6	26.1	S23307	neurokinin A - rai	973	6	26.1	11	2	E60409	substance P-like p
901	6	26.1	S23186	neurokinin A - Atl	974	6	26.1	11	2	B60409	kassinin-like pept
902	6	26.1	S07202	phylomedulin - tw	975	6	26.1	11	2	F60409	substance P-like p
903	6	26.1	F60589	sperm-activating p	976	6	26.1	11	2	D60409	kassinin-like pept
904	6	26.1	C60589	sperm-activating p	977	6	26.1	11	2	YHBO	morphogenetic neur
905	6	26.1	D60589	sperm-activating p	978	6	26.1	11	2	YHBO	morphogenetic neur

979 morphogenetic neur 11 2 YHJPHY
 980 morphogenetic neur 11 2 YHXA
 981 substance P - rain 11 2 S23308
 982 substance P - Atia 11 2 S23306
 983 Crinia-angiotensin 11 2 S07207
 984 phylalaemin - frog 11 2 S07201
 985 phyllokinin - Rohd 11 2 A61365
 986 ranatachykinin A - 11 2 A61033
 987 ranatachykinin D - 11 2 D61033
 988 morphogenetic neur 11 2 YHRT
 989 morphogenetic neur 11 4 S41909
 990 aminotransferase c 11 4 PC2124
 991 hypothetical prote 11 4 S52252
 992 hypothetical prote 12 1 A43975
 993 locustamytotropin - 12 1 LFGCPE
 994 glutathione peptid 12 2 S17869
 995 1-aminocyclopropan 12 2 C6201
 996 glycoprotein hormo 12 2 A61309
 997 T-cell receptor be 12 2 S26552
 998 T-cell receptor be 12 2 S26549
 999 T-cell receptor be 12 2 S26544
 1000 Ig heavy chain - m 12 2 S25056

ALIGNMENTS

RESULT 1
 A4244
 adipokinetic hormone - bollworm
 N:Alternate names: Hex-AKH
 C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
 C>Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C:Accession: A24244
 R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
 Biochem. Biophys. Res. Commun. 135, 622-628, 1986
 A:Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helio
 A:Reference number: A24244; MUID:86186794; PMID:3964263
 A:Accession: A24244
 A:Molecule type: protein
 A:Residues: 1-9 <JAR>
 A:Cross-references: UNIPROT:P08901
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 73.9%; Score 17; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 DB 4 FTSSW 8

RESULT 2
 A28004
 adipokinetic hormone G - two-spotted cricket
 N:Alternate names: AKH-G
 C:Species: Gryllus bimaculatus (two-spotted cricket)
 C>Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
 C:Accession: A28004
 R:Gaede, G.; Rinehart, K.L.
 Biochem. Biophys. Res. Commun. 149, 908-914, 1987
 A:Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a pepti
 A:Reference number: A28004; MUID:88106553; PMID:3426616
 A:Accession: A28004
 A:Molecule type: protein
 A:Residues: 1-8 <GAE>
 A:Cross-references: UNIPROT:P14086
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 69.6%; Score 16; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 DB 4 FSTGW 8

RESULT 3
 A1571
 hypertrehalosemic/adipokinetic hormone - bollworm
 N:Alternate names: Hex-HrTH
 C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
 C>Date: 30-Jun-1989 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C:Accession: A1571
 R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.
 Biochem. Biophys. Res. Commun. 155, 344-350, 1988
 A:Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea wit
 A:Reference number: A31571; MUID:88326324; PMID:3415690
 A:Accession: A31571
 A:Molecule type: protein
 A:Residues: 1-10 <JAF>
 A:Cross-references: UNIPROT:P16353
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:10/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 69.6%; Score 16; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 6.3e+02;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 DB 4 FSSGW 8

RESULT 4
 S10596
 adipokinetic hormone - pond skimmer
 C:Species: Libellula auripennis
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S10596
 R:Gaede, G.
 Biol. Chem. Hoppe-Seyler 371, 475-483, 1990
 A:Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hor
 A:Reference number: S10596; MUID:90359055; PMID:2390213
 A:Accession: S10596
 A:Molecule type: protein
 A:Residues: 1-8 <BIO>
 A:Cross-references: UNIPROT:P25418
 C:Comment: This peptide has both adipokinetic and hypertrehalosemic activities.
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 65.2%; Score 15; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 DB 4 FTSPW 8

RESULT 5
 D57444

neuropeptide Grb-AST B4 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
C;Accession: D57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21109, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: D57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>
A;Cross-references: UNIPROT:Q7M3N6

Query Match 65.2%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.Be+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|
Db 5 FHGSW 9

RESULT 6
Tl17063
cytochrome-c oxidase (EC 1.9.3.1) chain I - Hoplocercus spinosus mitochondrion (fragment)
C;Species: mitochondrion Hoplocercus spinosus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: Tl17063
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gene
A;Reference number: Z18674; MUID:97315309; PMID:9169559
A;Accession: Tl17063
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: UNIPROT:Q79897; EMBL:U82683; NID:G3603127; PIDN:AAC622
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|
Db 2 FISRW 6

RESULT 7
Tl12325
cytochrome-c oxidase (EC 1.9.3.1) chain I - Leiocephalus carinatus mitochondrion (fragment)
C;Species: mitochondrion Leiocephalus carinatus
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: Tl12325
R;Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example used
A;Reference number: Z17488; MUID:99162288; PMID:100511389
A;Accession: Tl12325
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-10 <SCH>
A;Cross-references: UNIPROT:Q92YT2; EMBL:AF049864; NID:G4105754; PID:G4105757; PIDN:AAD0
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 65.2%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|
Db 2 FISRW 6

RESULT 8
S53789
neuropeptide Pec-HrTH - Platypleura capensis
C;Species: Platypleura capensis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S53789
R;Gaede, G.; Janssens, M.P.E.
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
A;Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehalose
A;Reference number: S53789; MUID:95225985; PMID:7710694
A;Accession: S53789
A;Molecule type: protein
A;Residues: 1-10 <GAE>
A;Cross-references: UNIPROT:Q7M465
C;Keywords: blocked amino end; blocked carboxyl end

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|
Db 4 FSPSW 8

RESULT 9
PH1613
IG H chain V-D-J region (clone B-less 17) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1613
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1613
A;Molecule type: DNA
A;Residues: 1-15 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 65.2%; Score 15; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|
Db 10 FTMLW 14

RESULT 10
A34704
protein-tyrosine kinase (EC 2.7.1.112) 1, neuron-specific - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34704
R;Pyper, J.M.; Bolen, J.B.
Mol. Cell. Biol. 10, 2035-2040, 1990
A;Title: Identification of a novel neuronal C-SRC exon expressed in human brain.
A;Reference number: A34704; MUID:90220588; PMID:1691439
A;Accession: A34704
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-17 <PYP>
A;Cross-references: UNIPROT:Q14925

C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 65.2%; Score 15; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 10 FTRW 14

RESULT 11

S77981

Cytochrome-c oxidase (EC 1.9.3.1) chain Va.1 - bigeye tuna (fragment)

C:Species: Thunnus obesus (bigeye tuna)
C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C:Accession: S77981

R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.

submitted to the Protein Sequence Database, June 1997

A:Reference number: S77980

A:Accession: S77981

A:Molecule type: protein

A:Residues: 1-20 <ARN>

A:Cross-references: UNIPROT:P80972

A:Experimental source: heart; liver

C:Genetics:

A:Genome: nuclear

C:Function:

A:Pathway: oxidative phosphorylation; respiratory chain

A:Superfamily: mammalian cytochrome-c oxidase chain Va

C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 65.2%; Score 15; DB 2; Length 20;

Best Local Similarity 40.0%; Pred. No. 1.9e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 11 FDRW 15

RESULT 12

PN0171

peptidylprolyl isomerase (EC 5.2.1.8) b, cytosolic - fungus (Fusarium sporotrichoides)

N:Contains: cyclophilin

C:Species: Fusarium sporotrichoides

C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 02-Sep-2000

C:Accession: PN0171

R:Fukaya, N.; Chow, L.P.; Sugitara, Y.; Taugita, A.; Ueno, Y.; Tabuchi, K.

submitted to JIPD, May 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich

A:Reference number: PN0160

A:Accession: PN0171

A:Molecule type: protein

A:Residues: 1-20 <PUK>

A:Experimental source: strain M-1-1

C:Superfamily: peptidylprolyl isomerase; cyclophilin homology

C:Keywords: cis-trans-isomerase; cyclosporin A binding; cytosol

Query Match 65.2%; Score 15; DB 2; Length 20;

Best Local Similarity 40.0%; Pred. No. 1.9e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 6 FDIW 10

RESULT 13

PH1380

alpha-amylose (EC 3.2.1.1) (Haim sensitive) - Bacillus sp. (fragment)

C:Species: Bacillus sp.

C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

C:Accession: PH1380
R:Kawaguchi, T.; Nagae, H.; Murao, S.; Arai, M.
Biosci. Biotechnol. Biochem. 56, 1792-1796, 1992
A:Title: Purification and some properties of a Haim-sensitive alpha-amylose from newly isolated *Bacillus* sp.
A:Reference number: PH1380; MUID:93113087; PMID:1369074
A:Accession: PH1380
A:Molecule type: protein
A:Residues: 1-20 <RAW>
A:Cross-references: UNIPROT:Q9R5E8
A:Experimental source: strain NO.195
C:Comment: This enzyme has an optimum pH of 7.0.

C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 65.2%; Score 15; DB 2; Length 20;

Best Local Similarity 40.0%; Pred. No. 1.9e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 13 FSWTW 17

RESULT 14

A33995

adipokinetic hormone - black horse fly

C:Species: Tabanus atratus (black horse fly)

C:Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-Jul-2004

C:Accession: A33995

R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Y.

Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989

A:Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehal

A:Reference number: A33995; MUID:90046758; PMID:2813385

A:Accession: A33995

A:Molecule type: protein

A:Residues: 1-8 <JAF>

A:Cross-references: UNIPROT:P14595

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F:8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 60.9%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 4 FTPGW 8

RESULT 15

A44960

neuropeptide Led-CC-I - Colorado potato beetle

C:Species: Leptinotarsa decemlineata (Colorado potato beetle)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: A44960

R:Gaede, G.; Kellner, R.

Peptides 10, 1287-1289, 1989

A:Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and t

A:Reference number: A44960; MUID:90160053; PMID:2576128

A:Accession: A44960

A:Molecule type: protein

A:Residues: 1-8 <GAE>

A:Cross-references: UNIPROT:P04548

C:Superfamily: adipokinetic hormone

C:Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0; Matches 2; Conservative 3;

QY 1 FXXW 5
|
Db 4 FSPW 8

RESULT 16

B44960
neuropeptide Led-CC-II - Colorado potato beetle
C:Species: Leptinotarsa decemlineata (Colorado potato beetle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: B44960
R:Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A:Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and
A:Reference number: A44960; MUID:90160053; PMID:2576128
A:Accession: B44960
A:Molecule type: protein
A:Residues: 1-8 <GAE>
A:Cross-references: UNIPROT:P04549
C:Superfamily: adipokinetic hormone
C:Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0; Matches 2; Conservative 3;

QY 1 FXXW 5
|
Db 4 FTPW 8

RESULT 17

A58620
adipokinetic hormone - damselfly (Ischnura senegalensis)
C:Species: Ischnura senegalensis
C:Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004
C:Accession: A58620
R:Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A:Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspic
A:Reference number: S55310; MUID:94379987; PMID:8093008
A:Accession: A58620
A:Molecule type: protein
A:Residues: 1-8 <JAN>
A:Cross-references: UNIPROT:Q7M4H6
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0; Matches 2; Conservative 3;

QY 1 FXXW 5
|
Db 4 FTPW 8

RESULT 18

S11545
adipokinetic hormone - nestling-sucking blowfly
C:Species: Protophormia terraenovae (nestling-sucking blowfly)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S11545
R:Gaede, G.; Wilps, H.; Kellner, R.
Biochem. J. 269, 309-313, 1990
A:Title: Isolation and structure of a novel charged member of the red-pigment-concentrat

erraenovae (Diptera).
A:Reference number: S11545; MUID:90351345; PMID:2386478
A:Accession: S11545
A:Molecule type: protein
A:Residues: 1-8 <GAE>
A:Cross-references: UNIPROT:P61856
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0; Matches 2; Conservative 3;

QY 1 FXXW 5
|
Db 4 FSPW 8

RESULT 19

S55310
adipokinetic hormone - damselfly (Pseudagrion inconspicuum)
N:Alternate names: Psi-AKH
C:Species: Pseudagrion inconspicuum
C:Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 09-Jul-2004
C:Accession: S55310
R:Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A:Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspic
A:Reference number: S55310; MUID:94379987; PMID:8093008
A:Accession: S55310
A:Molecule type: protein
A:Residues: 1-8 <JAN>
A:Cross-references: UNIPROT:Q7M4H7
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0; Matches 2; Conservative 3;

QY 1 FXXW 5
|
Db 4 FTPW 8

RESULT 20

A61348
red pigment-concentrating hormone - northern shrimp
N:Alternate names: blanching hormone
C:Species: Pandalus borealis (northern shrimp)
C:Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C:Accession: A61348; S07139
R:Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A:Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A:Reference number: A61348; MUID:72228738; PMID:5041363
A:Accession: A61348
A:Molecule type: protein
A:Residues: 1-8 <FER1>
A:Cross-references: UNIPROT:P08939
R:Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A:Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus bore

A:Reference number: S07139; MUID:75054965; PMID:4433569

A:Accession: S07139
A:Molecule type: protein
A:Residues: 'E', 2-8 <FER2>

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C:Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pi

zed pigment-containing cells.

C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

DB 4 FSPGW 8

RESULT 21

S08995 hyperrehalosemic hormone I - oriental cockroach

N:Alternate names: Pea-CAH-I

C:Species: Blatta orientalis (oriental cockroach)

C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004

C:Accession: S08995

R:Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hyperrehalosemic neuropeptides isolated from the corpora allata and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombardment mass spectrometry

A:Reference number: S08995; MUID:90253659; PMID:2340112

A:Accession: S08995

A:Molecule type: protein

A:Residues: 1-8 <GAE>

A:Cross-references: UNIPROT:P04548

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have assigned the sequence as shown

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

QY 1 FXXXW 5

DB 4 FSPNW 8

RESULT 22

S08996 hyperrehalosemic hormone II - oriental cockroach

N:Alternate names: Pea-CAH-II

C:Species: Blatta orientalis (oriental cockroach)

C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004

C:Accession: S08996

R:Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hyperrehalosemic neuropeptides isolated from the corpora allata and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombardment mass spectrometry

A:Reference number: S08996; MUID:90253659; PMID:2340112

A:Accession: S08996

A:Molecule type: protein

A:Residues: 1-8 <GAE>

A:Cross-references: UNIPROT:P04549

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have assigned the sequence as shown

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

QY 1 FXXXW 5

DB 4 FTPNW 8

RESULT 23

A49823

adipokinetic hormone I - American cockroach

N:Alternate names: periplanetin CC-1

C:Species: Periplaneta americana (American cockroach)

C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C:Accession: A49823

R:Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.F.

Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984

A:Title: Isolation and primary structure of two peptides with cardioacceleratory and hypotensive activities

A:Reference number: A49823; MUID:84298179; PMID:6591205

A:Accession: A49823

A:Molecule type: protein

A:Residues: 1-8 <SCA>

A:Cross-references: UNIPROT:P04548

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

DB 4 FSPNW 8

RESULT 24

B49823

adipokinetic hormone II - American cockroach

N:Alternate names: neuropeptide M-II; periplanetin CC-1

C:Species: Periplaneta americana (American cockroach)

C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C:Accession: B49823; A05170

R:Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.F.

Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984

A:Title: Isolation and primary structure of two peptides with cardioacceleratory and hypotensive activities

A:Reference number: A49823; MUID:84298179; PMID:6591205

A:Accession: B49823

A:Molecule type: protein

A:Residues: 1-8 <SCA>

A:Cross-references: UNIPROT:P04549

R:Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.

Biochem. Biophys. Res. Commun. 124, 350-358, 1984

A:Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry

A:Reference number: A90118; MUID:85046530; PMID:6548628

A:Accession: A05170

A:Molecule type: protein

A:Residues: 'E', 2-8 <WIT>

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

DB 4 FTPNW 8

RESULT 25

A43976

hyperrehalosemic hormone - yellow mealworm

C:Species: Tenebrio molitor (yellow mealworm)

C>Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C:Accession: A43976
R:Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A>Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle
A:Reference number: A43976; MUID:90341081; PMID:2381871
A:Accession: A43976
A:Molecule type: protein
A:Residues: 1-8 <GAE>
A:Cross-references: UNIPROT:P25419
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F;/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 4 FSPNW 8

RESULT 26
B43976
hypertrehalosemic hormone - beetle (Zophobas rugipes)
C:Species: Zophobas rugipes
C>Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C:Accession: B43976
R:Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A>Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle
A:Reference number: A43976; MUID:90341081; PMID:2381871
A:Accession: B43976
A:Molecule type: protein
A:Residues: 1-8 <GAE>
A:Cross-references: UNIPROT:P25419
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F;/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 4 FSPNW 8

RESULT 27
A05169
neuropeptide M-I - American cockroach
C:Species: Periplaneta americana (American cockroach)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C:Accession: A05169
R:Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.I.
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A>Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry
A:Reference number: A90118; MUID:85046530; PMID:6548628
A:Accession: A05169
A:Molecule type: protein
A:Residues: 1-8 <WIT>
A:Cross-references: UNIPROT:P04548
C:Keywords: neuropeptide

Query Match 60.9%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 4 FSPNW 8

Db 4 FSPNW 8

RESULT 28

B33995
hypertrehalosemic hormone - black horse fly
C:Species: Tabanus atratus (black horse fly)
C>Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-Jul-2004
C:Accession: B33995
R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Y.
Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A>Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activities
A:Reference number: A33995; MUID:90046758; PMID:2813385
A:Accession: B33995
A:Molecule type: protein
A:Residues: 1-10 <JAF>
A:Cross-references: UNIPROT:P14596
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F;/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match 60.9%; Score 14; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 2e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

Db 4 FPGW 8

RESULT 29

S08997
hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)
C:Species: Gromphadorina portentosa
C>Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C:Accession: S08997
R:Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A>Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora cardiaca and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bombardment mass spectrometry
A:Reference number: S08995; MUID:90253659; PMID:2340112
A:Accession: S08997
A:Molecule type: protein
A:Residues: 1-10 <GAE>
A:Cross-references: UNIPROT:P10939
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 2e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

Db 4 FSPGW 8

RESULT 30

A60421
hypertrehalosemic hormone - German cockroach
N:Alternate names: Bld-HrTH
C:Species: Blattella germanica (German cockroach)
C>Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C:Accession: A60421; S09137
R:Veenstra, J.A.; Camps, F.
Neuropeptides 15, 107-109, 1990
A>Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, *Blattella germanica*
A:Reference number: A60421; MUID:91179584; PMID:2080017
A:Accession: A60421

A:Molecule type: protein

A:Residues: 1-10 <VEE>

A:CROSS-references: UNIPROT:P10939

R:Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment

A:Reference number: S08995; PMID:90253659; PMID:2340112

A:Accession: S09137

A:Molecule type: protein

A:Residues: 1-10 <GAE>

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 2e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

DB 4 FSPGW 8

RESULT 31

S08998

Hypertrehalosaemic neuropeptide Bld-HrTH - Madeira cockroach

C:Species: Leucophaea maderae (Madeira cockroach)

C>Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004

A:Accession: S08998

R:Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment

A:Reference number: S08995; PMID:90253659; PMID:2340112

A:Accession: S08998

A:Molecule type: protein

A:Residues: 1-10 <GAE>

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 2e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

DB 4 FSPGW 8

RESULT 32

A26381

Hypertrehalosaemic hormone - gray cockroach

C:Species: Nauphoeta cinerea (gray cockroach)

C>Date: 31-Mar-1988 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004

A:Accession: A26381

R:Gaede, G.; Rinehart Jr., K.L.

Biochem. Biophys. Res. Commun. 141, 774-781, 1986

A:Title: Amino acid sequence of a hypertrehalosaemic neuropeptide from the corpora allata

A:Reference number: A26381; PMID:87100208; PMID:3801028

A:Accession: A26381

A:Molecule type: protein

A:Residues: 1-10 <GAU>

A:CROSS-references: UNIPROT:P10939

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 2e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

DB 4 FSPGW 8

RESULT 33

JC1416

Hypertrehalosaemic hormone I - stick insect (Carausius morosus)

N:Alternate names: neuropeptide Cam-HrTH-I

C:Contains: hypertrehalosaemic factor II

C:Species: Carausius morosus

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: JC1416; S07157

R:Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.

Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992

A:Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick insect

A:Reference number: JC1416; PMID:93129188; PMID:1482345

A:Accession: JC1416

A:Molecule type: protein

A:Residues: 1-10 <GAE1>

A:CROSS-references: UNIPROT:P11385

R:Gaede, G.; Rinehart Jr., K.L.

Biol. Chem. Hoppe-Seyler 368, 67-75, 1987

A:Title: Primary structure of the hypertrehalosaemic factor II from the corpus cardiacum

A:Reference number: S07157; PMID:87157103; PMID:3828078

A:Accession: S07157

A:Molecule type: protein

A:Residues: 1-10 <GAE2>

C:Comment: Hypertrehalosaemic factor II lacks the tryptophan modification.

C:Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplaneta

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Binding site: carbohydrate (Trp) (covalent) #status experimental

F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 2e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

DB 4 FFPNW 8

RESULT 34

S09138

Hypertrehalosaemic hormone II - stick insect (Extatosoma tiaratum)

N:Alternate names: Cam-HrTH-II

C:Species: Extatosoma tiaratum

C>Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004

C:Accession: S09138

R:Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A:Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment

A:Reference number: S08995; PMID:90253659; PMID:2340112

A:Accession: S09138

A:Molecule type: protein

A:Residues: 1-10 <GAE>

A:CROSS-references: UNIPROT:P11385

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 2e+03; Mismatches 0; Indels 3; Gaps 0;

QY 1 FXXW 5
DB 4 FPNW 8

RESULT 35

C39191

hypothetical protein 1 (Tex5' region) - Bacteroides fragilis

C;Species: Bacteroides fragilis

C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993

C;Accession: C39191

R;Speer, B.S.; Bedzyk, L.; Salvers, A.A.

J. Bacteriol. 173, 176-183, 1991

A;Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tra

A;Reference number: A39191; MUID:91100280; PMID:1846135

A;Accession: C39191

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-10 <SPE>

A;Cross-references: GB:M37699

Query Match 60.9%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 3 FSRPW 7

RESULT 36

PT0322

Ig heavy chain CDR3 region (clone J2-106A) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0322

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0322

A;Molecule type: DNA

A;Residues: 1-10 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 60.9%; Score 14; DB 2; Length 10;
Best Local Similarity 20.0%; Pred. No. 2e+03;
Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 3 YSSW 7

RESULT 37

T17066

cytochrome-c oxidase (EC 1.9.3.1) chain I - Oplurus cuvieri mitochondrion (fragment)

C;Species: Mitochondrion Oplurus cuvieri

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T17066

R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.

J. Mol. Evol. 44, 660-674, 1997

A;Title: Evolutionary shifts in three major structural features of the mitochondrial ge

A;Reference number: Z18674; MUID:97315309; PMID:9169559

A;Accession: T17066

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-10 <MAC>

A;Cross-references: UNIPROT:O79903; EMBL:U82685; NID:G3603136; PID:G3603139; PIDN:AAC622

C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 60.9%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 2 FINRW 6

RESULT 38

T17069

cytochrome-c oxidase (EC 1.9.3.1) chain I - Phrynosoma douglassii mitochondrion (fragment

C;Species: mitochondrion Phrynosoma douglassii

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T17069

R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.

J. Mol. Evol. 44, 660-674, 1997

A;Title: Evolutionary shifts in three major structural features of the mitochondrial gen

A;Reference number: Z18674; MUID:97315309; PMID:9169559

A;Accession: T17069

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-10 <MAC>

A;Cross-references: UNIPROT:O79906; EMBL:U82686; NID:G3603144; PID:G3603147; PIDN:AAC6229

C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match

60.9%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 2 FINRW 6

RESULT 39

T12329

cytochrome-c oxidase (EC 1.9.3.1) chain I - Stenocercus crassicaudatus mitochondrion (frag

C;Species: mitochondrion Stenocercus crassicaudatus

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004

C;Accession: T12329

R;Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 367-376, 1998

A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example usin

A;Reference number: Z17488; MUID:99162288; PMID:10051389

A;Accession: T12329

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-10 <SCH>

A;Cross-references: UNIPROT:Q9ZY56; EMBL:AF049866; NID:G4105762; PID:G4105765; PIDN:AADO

C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match

60.9%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 2 FINRW 6

RESULT 40

PT0274
Ig heavy chain CRD3 region (clone 3-109B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0274
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0274
A:Molecule type: DNA
A:Residues: 1-12 <VAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 60.9%; Score 14; DB 2; Length 12;
Best Local Similarity 20.0%; Pred. NO. 2.3e+03;
Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXW 5
Db 3 YSSW 7

Search completed: October 18, 2005, 15:59:21
Job time : 30.6471 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:32:19 ; Search time 104.471 Seconds
(without alignments)
39.213 Million cell updates/sec

Title: US-09-214-371-10

Perfect score: 23

Sequence: 1 FXXWXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 12050

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	73.9	9	1 AKH_HELZE	P67787 heliothis z
2	17	73.9	13	2 Q9XLI2	Q9XLI2 bemisia tab
3	16	69.6	8	1 AKHG_GRYBI	P67785 gryllus bim
4	16	69.6	8	1 AKH_ROMMI	P67786 romalea mic
5	16	69.6	10	1 HTF_HELZE	P16353 heliothis z
6	16	69.6	11	2 Q6E5N4	Q6E5N4 mantheyus p
7	16	69.6	11	2 Q9G649	Q9G649 otocryptis
8	16	69.6	17	2 O15276	O15276 homo sapien
9	16	69.6	17	2 Q7Y1X8	Q7Y1X8 lilium long
10	16	69.6	19	2 Q9L129	Q9L129 human immun
11	16	69.6	19	2 Q9WJB1	Q9WJB1 human immun
12	16	69.6	20	2 Q6LD18	Q6LD18 mus musculus
13	15	65.2	8	1 AKH_LIABU	P25418 libellula a
14	15	65.2	9	2 Q7M3N6	Q7M3N6 gryllus bim
15	15	65.2	9	2 Q8WGS6	Q8WGS6 procamburus
16	15	65.2	10	1 AKHX_LOCMI	P81626 locusta mig
17	15	65.2	10	2 Q7M465	Q7M465 platypleura
18	15	65.2	10	2 Q70F01	Q70F01 sus scrofa
19	15	65.2	10	2 Q79897	Q79897 hoplocercus
20	15	65.2	10	2 P92707	P92707 platysaurus
21	15	65.2	10	2 Q6UJL5	Q6UJL5 strophurus
22	15	65.2	10	2 Q6WB44	Q6WB44 sceloporos
23	15	65.2	10	2 Q6X0E7	Q6X0E7 anolis marc
24	15	65.2	10	2 Q71DW3	Q71DW3 polychrus m
25	15	65.2	10	2 Q71DW6	Q71DW6 polychrus a
26	15	65.2	10	2 Q71DW9	Q71DW9 anisolepis
27	15	65.2	10	2 Q71E17	Q71E17 morunasauru
28	15	65.2	10	2 Q71E20	Q71E20 enyalioides
29	15	65.2	10	2 Q9ZYF2	Q9ZYF2 leiocephalu
30	15	65.2	11	2 Q8WES0	Q8WES0 ceratophora
31	15	65.2	11	2 Q9G365	Q9G365 calotes emm

32	15	65.2	11	2 Q9G368	Q9G368 draco blanf
33	15	65.2	11	2 Q9G5Y9	Q9G5Y9 pseudocalot
34	15	65.2	11	2 Q9G5Z2	Q9G5Z2 pseudocalot
35	15	65.2	11	2 Q9G601	Q9G601 bronchocele
36	15	65.2	11	2 Q9G625	Q9G625 calotes ver
37	15	65.2	11	2 Q9G628	Q9G628 calotes mys
38	15	65.2	11	2 Q9G631	Q9G631 calotes nig
39	15	65.2	11	2 Q9G634	Q9G634 calotes lio
40	15	65.2	11	2 Q9G640	Q9G640 calotes cey
41	15	65.2	11	2 Q9G643	Q9G643 calotes cal
42	15	65.2	11	2 Q9G646	Q9G646 sitana pont
43	15	65.2	12	2 Q6WR31	Q6WR31 mycteria am
44	15	65.2	12	2 Q6WR52	Q6WR52 asio otus (
45	15	65.2	12	2 Q6WR67	Q6WR67 neomorphus
46	15	65.2	12	2 Q6WR73	Q6WR73 coccyzus er
47	15	65.2	12	2 Q6WR79	Q6WR79 cuculus can
48	15	65.2	14	2 Q71H30	Q71H30 andrena bra
49	15	65.2	16	2 Q76019	Q76019 aspergillus
50	15	65.2	19	2 Q7S645	Q7S645 neuospora
51	15	65.2	20	1 COXA_THUOB	P80972 thunnus obe
52	15	65.2	20	2 Q95MK5	Q95MK5 varecia var
53	15	65.2	20	2 Q673D5	Q673D5 dehalococco
54	15	65.2	20	2 Q9R5E8	Q9R5E8 bacillus sp
55	14	60.9	8	1 AKH_PROTE	P61856 protophormi
56	14	60.9	8	1 AKH_TABAT	P14595 tabanus atr
57	14	60.9	8	1 HTF1_PERAM	P04548 periplaneta
58	14	60.9	8	1 HTF2_PERAM	P04549 periplaneta
59	14	60.9	8	1 HTF_TENMO	P67789 tenebrio mo
60	14	60.9	8	1 HTF_ZOPRU	P67790 zophobas ru
61	14	60.9	8	1 RPH_PANBO	P08939 pandalus bo
62	14	60.9	8	2 Q7M4H6	Q7M4H6 ischnura se
63	14	60.9	8	2 Q7M4H7	Q7M4H7 pseudagrion
64	14	60.9	10	1 HTF1_ROMMI	P18110 romalea mic
65	14	60.9	10	1 HTF2_CARMO	P62542 carausius m
66	14	60.9	10	1 HTF2_EXITI	P62543 extatosoma
67	14	60.9	10	1 HTF_ELAGE	P84220 blattella g
68	14	60.9	10	1 HTF_GROPO	P84221 gromphadori
69	14	60.9	10	1 HTF_LEUMA	P84219 leucophaea
70	14	60.9	10	1 HTF_NAUCI	P84218 nauphoeta c
71	14	60.9	10	1 HTF_TABAT	P14596 tabanus atr
72	14	60.9	10	2 Q79885	Q79885 anolis pate
73	14	60.9	10	2 Q79903	Q79903 oplurus cuv
74	14	60.9	10	2 Q79906	Q79906 phrynosoma
75	14	60.9	10	2 Q8W7U4	Q8W7U4 anolis nite
76	14	60.9	10	2 Q8W8Q2	Q8W8Q2 anolis punc
77	14	60.9	10	2 Q8W8Q3	Q8W8Q3 anolis nite
78	14	60.9	10	2 Q8W8Q4	Q8W8Q4 anolis punc
79	14	60.9	10	2 Q8W969	Q8W969 anolis orto
80	14	60.9	10	2 Q8W970	Q8W970 anolis nite
81	14	60.9	10	2 Q8W971	Q8W971 anolis fusc
82	14	60.9	10	2 Q8WDG6	Q8WDG6 anolis trac
83	14	60.9	10	2 Q8WDH0	Q8WDH0 anolis limi
84	14	60.9	10	2 Q8WDH2	Q8WDH2 anolis temu
85	14	60.9	10	2 Q8WDH4	Q8WDH4 anolis carp
86	14	60.9	10	2 Q8WDH6	Q8WDH6 anolis west
87	14	60.9	10	2 Q8WDH8	Q8WDH8 anolis mood
88	14	60.9	10	2 Q8WDI8	Q8WDI8 anolis tran
89	14	60.9	10	2 Q6WB7	Q6WB7 sceloporos
90	14	60.9	10	2 Q6WER1	Q6WER1 sceloporos
91	14	60.9	10	2 Q6WB44	Q6WB44 sceloporos
92	14	60.9	10	2 Q6WB53	Q6WB53 sceloporos
93	14	60.9	10	2 Q6WB78	Q6WB78 sceloporos
94	14	60.9	10	2 Q6WB1	Q6WB1 sceloporos
95	14	60.9	10	2 Q6WB2	Q6WB2 phrynosoma
96	14	60.9	10	2 Q6WB5	Q6WB5 phrynosoma
97	14	60.9	10	2 Q6WB8	Q6WB8 phrynosoma
98	14	60.9	10	2 Q6WBX1	Q6WBX1 phrynosoma
99	14	60.9	10	2 Q6WBX4	Q6WBX4 phrynosoma
100	14	60.9	10	2 Q6WZ6	Q6WZ6 anolis cybo
101	14	60.9	10	2 Q6X061	Q6X061 anolis haet
102	14	60.9	10	2 Q6X071	Q6X071 anolis shre
103	14	60.9	10	2 Q6X0C3	Q6X0C3 anolis whit
104	14	60.9	10	2 Q6X0D2	Q6X0D2 anolis arm

105	14	60.9	10	2	Q6X0D8	Q6X0d8 anolis long	178	14	60.9	19	2	Q44506	Q44506 anabaena va
106	14	60.9	10	2	Q71DR5	Q71dr5 leiocephalu	179	14	60.9	19	2	Q6QLM2	Q6qlm2 influenza a
107	14	60.9	10	2	Q71DR8	Q71dr8 leiocephalu	180	14	60.9	20	1	CRBC_SPIOL	P30806 spinacia ol
108	14	60.9	10	2	Q71DS4	Q71ds4 tropidurus	181	14	60.9	20	1	GBB4_RAT	Q35353 rattus norv
109	14	60.9	10	2	Q71DS7	Q71ds7 tropidurus	182	14	60.9	20	2	Q95MJ7	Q95mj7 tarsius syr
110	14	60.9	10	2	Q71DT0	Q71dt0 uranoscodon	183	14	60.9	20	2	Q95MJ8	Q95mj8 galago moho
111	14	60.9	10	2	Q71DT3	Q71dt3 tropidurus	184	14	60.9	20	2	Q95MJ9	Q95mj9 pan troglod
112	14	60.9	10	2	Q71DT6	Q71dt6 uracentron	185	14	60.9	20	2	Q95MK0	Q95mk0 pongo pygma
113	14	60.9	10	2	Q71DT9	Q71dt9 stenocercus	186	14	60.9	20	2	Q95MK1	Q95mk1 colobus ang
114	14	60.9	10	2	Q71DU2	Q71du2 stenocercus	187	14	60.9	20	2	Q95MK2	Q95mk2 papio cynoc
115	14	60.9	10	2	Q71DU5	Q71du5 stenocercus	188	14	60.9	20	2	Q95MK3	Q95mk3 ateles belz
116	14	60.9	10	2	Q71DU8	Q71du8 sceloporos	189	14	60.9	20	2	Q95MK4	Q95mk4 cheirogaleu
117	14	60.9	10	2	Q71DM0	Q71dm0 phrynosoma	190	14	60.9	20	2	Q95MK6	Q95mk6 eulemur cor
118	14	60.9	10	2	Q71DX5	Q71dx5 urostephous	191	14	60.9	20	2	Q9TRA4	Q9tra4 sus scrofa
119	14	60.9	10	2	Q71DX8	Q71dx8 enyalisus le	192	14	60.9	20	2	Q66548	Q66548 human herpe
120	14	60.9	10	2	Q71DY1	Q71dy1 pristiadacty	193	13	56.5	6	1	EI01_LITRU	P82096 litoria rub
121	14	60.9	10	2	Q71DY4	Q71dy4 leiosaurus	194	13	56.5	9	2	Q28121	Q28121 bos taurus
122	14	60.9	10	2	Q71DY7	Q71dy7 leiosaurus	195	13	56.5	15	2	Q6JQC4	Q6jcq4 tetraeureod
123	14	60.9	10	2	Q71DZ0	Q71dz0 diplolaemus	196	13	56.5	15	2	Q6JCS2	Q6jcs2 aleuroplatu
124	14	60.9	10	2	Q71DZ3	Q71dz3 diplolaemus	197	13	56.5	16	2	Q697F2	Q697f2 bemiaia sp.
125	14	60.9	10	2	Q71E08	Q71e08 anolis cybo	198	13	56.5	16	2	Q9XNP6	Q9xnp6 boophilus m
126	14	60.9	10	2	Q71E11	Q71e11 chalarodon	199	13	56.5	18	2	Q7S173	Q7s173 neurospora
127	14	60.9	10	2	Q71E23	Q71e23 corytophane	200	13	56.5	18	2	Q8RU82	Q8ru82 zea mays (m
128	14	60.9	10	2	Q71E35	Q71e35 basiliscus	201	13	56.5	19	2	Q9TU41	Q9tu41 loxodonta a
129	14	60.9	10	2	Q71SD0	Q71sd0 liolaemus w	202	13	56.5	19	2	Q9TU42	Q9tu42 mammutus p
130	14	60.9	10	2	Q9T8U8	Q9t8u8 liolaemus p	203	13	56.5	19	2	Q99722	Q99722 lamprocorni
131	14	60.9	10	2	Q9T8X1	Q9t8x1 liolaemus a	204	13	56.5	20	2	Q90X92	Q90x92 gallus gall
132	14	60.9	10	2	Q9ZY56	Q9zy56 stenocercus	205	12	52.2	8	2	Q7GEM6	Q7gem6 branchiosto
133	14	60.9	12	2	Q6WR34	Q6wr34 phoenicopte	206	12	52.2	10	1	G0N1_PBTMA	P04378 petromyzon
134	14	60.9	12	2	Q6WR37	Q6wr37 buteo jamai	207	12	52.2	10	2	Q6UJL2	Q6ujl2 strophurus
135	14	60.9	12	2	Q6WR43	Q6wr43 scolopax ni	208	12	52.2	11	1	CA31_LITCI	P82089 litoria cit
136	14	60.9	12	2	Q6WR55	Q6wr55 crinifer pi	209	12	52.2	11	1	CA32_LITCI	P82090 litoria cit
137	14	60.9	12	2	Q6WR58	Q6wr58 musophaga v	210	12	52.2	11	1	CORZ_PERAM	P14496 periplaneta
138	14	60.9	12	2	Q6WR82	Q6wr82 urocolius m	211	12	52.2	11	2	Q6E5M8	Q6esm8 pyctolaemu
139	14	60.9	12	2	Q6WR88	Q6wr88 coracias sp	212	12	52.2	11	2	Q9G359	Q9g359 japalura fl
140	14	60.9	12	2	Q6WR91	Q6wr91 trogon curu	213	12	52.2	11	2	Q9G607	Q9g607 aphanotis
141	14	60.9	12	2	Q6WR94	Q6wr94 tockus eryt	214	12	52.2	12	2	Q92680	Q92680 trimersguru
142	14	60.9	12	2	Q6WR97	Q6wr97 anseranas s	215	12	52.2	16	2	Q9N237	Q9n237 pan troglod
143	14	60.9	12	2	Q6WRA0	Q6wra0 chauna torq	216	12	52.2	17	2	Q8MJ33	Q8mj33 sus scrofa
144	14	60.9	12	2	Q6WRA3	Q6wra3 megapodius	217	12	52.2	17	2	Q9TR22	Q9tr22 bos taurus
145	14	60.9	12	2	Q6WRA6	Q6wra6 alectura la	218	12	52.2	18	2	Q9QW51	Q9qw51 mus sp. . a
146	14	60.9	12	2	Q6WRA9	Q6wra9 crax rubra	219	12	52.2	19	2	Q7REEL	Q7reel plasmodium
147	14	60.9	12	2	Q8HN63	Q8hn63 sayornis ph	220	11	47.8	2	1	GWA_SEPOF	P83570 sepia offic
148	14	60.9	12	2	Q8HN66	Q8hn66 acryllium v	221	11	47.8	4	1	OCF3_OCTMI	P58649 octopus min
149	14	60.9	12	2	Q53579	Q53579 rhodobacter	222	11	47.8	5	1	BPP7_BOTIN	P30425 bothrops in
150	14	60.9	13	1	BML2_BOMVA	P84211 bomina var	223	11	47.8	5	1	UF01_MOUSE	P38639 mus musculu
151	14	60.9	13	1	YPNP_PHOLU	P41122 photorhabdu	224	11	47.8	6	1	LOK1_LOCM1	P41491 locusta mig
152	14	60.9	13	2	Q7M1F5	Q7m1f5 freesia ref	225	11	47.8	7	1	BRHP_CONIM	P58803 conus imper
153	14	60.9	13	2	Q6GNE7	Q6gne7 borrelia bu	226	11	47.8	7	1	TPPY_PACDA	P83455 pachymedusa
154	14	60.9	13	2	Q718T2	Q718t2 newcastle d	227	11	47.8	7	1	TV51_LITRU	P82065 litoria rub
155	14	60.9	15	2	Q6LCZ7	Q6lcz7 homo sapien	228	11	47.8	7	1	WWA1_ACHFU	P35919 achatina fu
156	14	60.9	15	2	Q9UC22	Q9uc22 homo sapien	229	11	47.8	7	1	WWA2_ACHFU	P35920 achatina fu
157	14	60.9	15	2	Q53580	Q53580 rhodobacter	230	11	47.8	7	1	WWA3_ACHFU	P35921 achatina fu
158	14	60.9	15	2	Q9R5D6	Q9r5d6 chromatium	231	11	47.8	7	2	Q9BRV4	Q9brv4 homo sapien
159	14	60.9	16	2	Q79B06	Q79b06 helicobacte	232	11	47.8	7	2	Q95945	Q95945 saccharomyc
160	14	60.9	16	2	Q9R4F2	Q9r4f2 streptomyce	233	11	47.8	7	2	Q49223	Q49223 glycine max
161	14	60.9	16	2	Q9QW76	Q9qw76 mus sp. hom	234	11	47.8	7	2	Q8KMS9	Q8kms9 enterobacte
162	14	60.9	16	2	Q8QGA1	Q8qga1 brachydanio	235	11	47.8	7	2	Q8GL00	Q8gl00 borrelia bu
163	14	60.9	17	2	Q8MIG9	Q8mig9 cynopterus	236	11	47.8	7	2	Q8GL04	Q8gl04 borrelia bu
164	14	60.9	17	2	Q9QUJ4	Q9quj4 mus sp. mep	237	11	47.8	7	2	Q8JE81	Q8je81 human immun
165	14	60.9	17	2	Q6QLL7	Q6ql17 influenza a	238	11	47.8	8	1	ACI_THUAL	P18691 thunnus alb
166	14	60.9	17	2	Q6QLL9	Q6ql19 influenza a	239	11	47.8	8	1	AKH_GEOST	P84241 geotrupes s
167	14	60.9	17	2	Q6QLM0	Q6qlm0 influenza a	240	11	47.8	8	1	AKH_MEML	P84240 meiolontha
168	14	60.9	17	2	Q6QLM1	Q6qlm1 influenza a	241	11	47.8	8	1	AKH_PACMA	P84242 pachnoda ma
169	14	60.9	18	2	Q8N0X8	Q8n0x8 homo sapien	242	11	47.8	8	1	C125_CYPDO	P83661 cyphononyx
170	14	60.9	18	2	Q71U72	Q71u72 homo sapien	243	11	47.8	8	1	CCKN_DASVI	P68125 dasyrus vi
171	14	60.9	18	2	Q9ZYW4	Q9zyw4 habrobracon	244	11	47.8	8	1	CCKN_NACEU	P81226 macropus eu
172	14	60.9	18	2	Q9ZYX7	Q9zyx7 perga conde	245	11	47.8	8	1	CONW_CONPU	P58785 conus purpu
173	14	60.9	19	2	P83003	P83003 entamoeba h	246	11	47.8	8	1	LCK1_LEUMA	P21140 leucophaea
174	14	60.9	19	2	Q9N1W2	Q9n1w2 equus cabal	247	11	47.8	8	1	LCK2_LEUMA	P21141 leucophaea
175	14	60.9	19	2	Q9T2V5	Q9t2v5 crithidia f	248	11	47.8	8	1	LCK3_LEUMA	P21142 leucophaea
176	14	60.9	19	2	Q9ZYW7	Q9zyw7 aphidius ro	249	11	47.8	8	1	LCK4_LEUMA	P21143 leucophaea
177	14	60.9	19	2	Q9ZYW8	Q9zyw8 ichneutes b	250	11	47.8	8	1	LCK5_LEUMA	P19987 leucophaea

251	11	47.8	8	1	LCK6_LEUMA	P19988 leucophaea	324	11	47.8	9	1	LITR_PHYRO	P08946 phyllomedus
252	11	47.8	8	1	LCK7_LEUMA	P19989 leucophaea	325	11	47.8	9	1	LMIP_LOCMI	P11799 locusta mig
253	11	47.8	8	1	LCK8_LEUMA	P19990 leucophaea	326	11	47.8	9	1	NEF_HV128	P12481 human immun
254	11	47.8	8	1	NGIF_RAT	P82598 rattus norv	327	11	47.8	9	1	PTSP_BOMMO	P82001 bombyx mori
255	11	47.8	8	1	PK1_PERAM	P82685 periplaneta	328	11	47.8	9	2	O95953	Q16386 homo sapien
256	11	47.8	8	1	PK2_PERAM	P82686 periplaneta	329	11	47.8	9	2	Q16386	Q16386 homo sapien
257	11	47.8	8	1	PK3_PERAM	P82687 periplaneta	330	11	47.8	9	2	O6LDB5	Q66f45 homo sapien
258	11	47.8	8	1	PK4_PERAM	P82688 periplaneta	331	11	47.8	9	2	O6QF45	Q66f45 homo sapien
259	11	47.8	8	1	PK5_PERAM	P82689 periplaneta	332	11	47.8	9	2	O71E39	Q71eb9 homo sapien
260	11	47.8	8	1	PLP_BRANA	P81707 brassica na	333	11	47.8	9	2	O7M4S2	Q7m4s2 homo sapien
261	11	47.8	8	1	RT31_BOVIN	P82929 bos taurus	334	11	47.8	9	2	O9H326	Q9h326 homo sapien
262	11	47.8	8	1	VAM6_MOUSE	P83853 mus musculu	335	11	47.8	9	2	O9H326	Q9h326 homo sapien
263	11	47.8	8	2	Q15888	Q15888 homo sapien	336	11	47.8	9	2	O9H3Y3	Q9h3y3 homo sapien
264	11	47.8	8	2	Q15890	Q15890 homo sapien	337	11	47.8	9	2	O9UC36	Q9uc36 homo sapien
265	11	47.8	8	2	Q81VK3	Q81vk3 homo sapien	338	11	47.8	9	2	O9UCQ9	Q9ucq9 homo sapien
266	11	47.8	8	2	O86SL0	Q86sl0 homo sapien	339	11	47.8	9	2	O9UK44	Q9uk44 homo sapien
267	11	47.8	8	2	O7M3S2	Q7m3s2 trypanosoma	340	11	47.8	9	2	O9UMAO	Q9uma0 homo sapien
268	11	47.8	8	2	O7M3S3	Q7m3s3 trypanosoma	341	11	47.8	9	2	O9UMF3	Q9umf3 homo sapien
269	11	47.8	8	2	O02B31	O02b31 oryctolagus	342	11	47.8	9	2	O9UQW0	Q9uqw0 homo sapien
270	11	47.8	8	2	O95M23	Q95m23 sus scrofa	343	11	47.8	9	2	O7M3N7	Q7m3n7 gryllus bim
271	11	47.8	8	2	O9TRY3	Q9try3 sus sp. ins	344	11	47.8	9	2	O7M3N8	Q7m3n8 gryllus bim
272	11	47.8	8	2	O8WBG2	Q8wbg2 diadema sav	345	11	47.8	9	2	O7M4D5	Q7m4d5 diadema set
273	11	47.8	8	2	O8WBG3	Q8wbg3 diadema pau	346	11	47.8	9	2	O9MW43	Q9mw43 homo sapien
274	11	47.8	8	2	O8WBG4	Q8wbg4 diadema mex	347	11	47.8	9	2	O8SHF0	Q8shf0 chamaeleo n
275	11	47.8	8	2	O8WBG5	Q8wbg5 diadema ant	348	11	47.8	9	2	O8W8W5	Q8w8w5 diadema set
276	11	47.8	8	2	O8WBG6	Q8wbg6 diadema mex	349	11	47.8	9	2	O8W8W6	Q8w8w6 diadema ant
277	11	47.8	8	2	O8WGD7	Q8wgd7 lomix hirta	350	11	47.8	9	2	O8W8X4	Q8w8x4 diadema mex
278	11	47.8	8	2	O94PX5	Q94px5 felis silve	351	11	47.8	9	2	O8WFS4	Q8wfs4 diadema mex
279	11	47.8	8	2	O94PX6	Q94px6 felis libyc	352	11	47.8	9	2	O94NA9	Q94na9 daubentonia
280	11	47.8	8	2	O94PX7	Q94px7 felis silve	353	11	47.8	9	2	O94NB0	Q94nb0 microcebus
281	11	47.8	8	2	O94V82	Q94v82 varanus yuw	354	11	47.8	9	2	O94NB1	Q94nb1 microcebus
282	11	47.8	8	2	O94V88	Q94v88 varanus tri	355	11	47.8	9	2	O94NB2	Q94nb2 microcebus
283	11	47.8	8	2	O94V91	Q94v91 varanus tim	356	11	47.8	9	2	O94VC6	Q94vc6 varanus pil
284	11	47.8	8	2	O94VA7	Q94va7 varanus sal	357	11	47.8	9	2	O94VD8	Q94vd8 varanus nil
285	11	47.8	8	2	O94VB2	Q94vb2 varanus sal	358	11	47.8	9	2	O94VE1	Q94ve1 varanus mer
286	11	47.8	8	2	O94VB5	Q94vb5 varanus sal	359	11	47.8	9	2	O94VG2	Q94vg2 varanus ind
287	11	47.8	8	2	O94VC1	Q94vc1 varanus rud	360	11	47.8	9	2	O94VH4	Q94vh4 varanus gla
288	11	47.8	8	2	O94VB4	Q94vb4 varanus mel	361	11	47.8	9	2	O94VI0	Q94vi0 varanus gig
289	11	47.8	8	2	O94VF6	Q94vf6 varanus job	362	11	47.8	9	2	O94VI8	Q94vi8 varanus ere
290	11	47.8	8	2	O94VF9	Q94vf9 varanus ind	363	11	47.8	9	2	O94VJ1	Q94vj1 varanus dor
291	11	47.8	8	2	O94VJ4	Q94vj4 varanus ben	364	11	47.8	9	2	O94XE6	Q94xe6 tectocoris
292	11	47.8	8	2	O70Y57	Q70y57 fueretia af	365	11	47.8	9	2	O69ID6	Q69id6 anolis sagr
293	11	47.8	8	2	O70Y84	Q70y84 plectranthu	366	11	47.8	9	2	O71DX2	Q71dx2 urostrophus
294	11	47.8	8	2	O71515	Q71515 varanus dum	367	11	47.8	9	2	O85DB0	Q85db0 lepitemur s
295	11	47.8	8	2	O9T4Y2	Q9t4y2 asterina pe	368	11	47.8	9	2	O85DB8	Q85db8 lepitemur e
296	11	47.8	8	2	O9TD02	Q9td02 terranatos	369	11	47.8	9	2	O9T688	Q9t688 gekko gekko
297	11	47.8	8	2	O6ZZ01	Q6zz01 silene con	370	11	47.8	9	2	O38366	Q38366 bacterioph
298	11	47.8	8	2	O6ZZ02	Q6zz02 lychnis cor	371	11	47.8	9	2	O6A1H7	Q6a1h7 hordeum vul
299	11	47.8	8	2	O85406	Q85406 coxiella bu	372	11	47.8	9	2	O6ZZ00	Q6zz00 silene rotu
300	11	47.8	8	2	O6LDP8	Q6ldp8 pseudomonas	373	11	47.8	9	2	O47410	Q47410 escherichia
301	11	47.8	8	2	O7M010	Q7m010 clostridium	374	11	47.8	9	2	O6VCK0	Q6vcx0 streptomyce
302	11	47.8	8	2	O7M124	Q7m124 kluuyvera ci	375	11	47.8	9	2	O8GL26	Q8gl26 borrelia bu
303	11	47.8	8	2	O8G940	Q8g940 borrelia bu	376	11	47.8	9	2	O8GLJ1	Q8glj1 borrelia bu
304	11	47.8	8	2	O8GLJ2	Q8glj2 borrelia bu	377	11	47.8	9	2	O9RSM1	Q9rsm1 staphylococ
305	11	47.8	8	2	O35835	Q35835 rattus sp.	378	11	47.8	9	2	O9R635	Q9rg635 chlamydia t
306	11	47.8	8	2	P70243	P70243 mus musculu	379	11	47.8	9	2	O9R9C4	Q9rg9c4 borrelia bu
307	11	47.8	8	2	O99MM0	Q99mm0 mus musculu	380	11	47.8	9	2	O6LQA1	Q6laq1 rattus norv
308	11	47.8	8	2	O62721	Q62721 rattus norv	381	11	47.8	9	2	O7M078	Q7m078 rattus norv
309	11	47.8	8	2	O9ET16	Q9et16 mesocricetu	382	11	47.8	9	2	O8OX07	Q8ox07 mus sp. thr
310	11	47.8	8	2	O9ET17	Q9et17 mus caroli	383	11	47.8	9	2	O90350	Q90350 gb virus c/
311	11	47.8	8	2	O9ET18	Q9et18 mus spretus	384	11	47.8	9	2	O65711	Q65711 berne virus
312	11	47.8	8	2	O64971	Q64971 alfalfa mos	385	11	47.8	9	2	O69100	Q69100 human herpe
313	11	47.8	8	2	P79940	P79940 xenopus lae	386	11	47.8	9	2	O89491	Q89491 murine minu
314	11	47.8	8	2	O98TU5	Q98tu5 xenopus lae	387	11	47.8	9	2	O673W5	Q673w5 tyrannus me
315	11	47.8	8	2	O68LF1	Q68lf1 myrmotherul	388	11	47.8	9	2	O673W6	Q673w6 terpsiphone
316	11	47.8	8	2	O68LGH	Q68lgh sakesphorus	389	11	47.8	9	2	O673W7	Q673w7 telophorus
317	11	47.8	8	2	O6R7U6	Q6r7u6 grypotoscin	390	11	47.8	9	2	O673W8	Q673w8 tchagra sen
318	11	47.8	8	2	O7LZ27	Q7lzz27 najia oxiana	391	11	47.8	9	2	O673W9	Q673w9 tchagra aus
319	11	47.8	9	1	CAER_PHYSA	Q71zc4 phyllomedus	392	11	47.8	9	2	O673X0	Q673x0 rhodophoneu
320	11	47.8	9	1	COW_CONVE	P83047 cow ventr	393	11	47.8	9	2	O673X1	Q673x1 rhididura a
321	11	47.8	9	1	D1_NEPNO	P24816 nephrops no	394	11	47.8	9	2	O673X2	Q673x2 pseudobias
322	11	47.8	9	1	DSIP_RABIT	P01158 oryctolagus	395	11	47.8	9	2	O673X3	Q673x3 prionops sc
323	11	47.8	9	1	LITO_LITAU	P08945 litoria aur	396	11	47.8	9	2	O673X4	Q673x4 prionops re

397	11	47.8	9	2	Q673X5	Q673x5 platysteira	470	11	47.8	10	2	Q9TR47	Q9tr47 bos taurus
398	11	47.8	9	2	Q673X6	Q673x6 oriolus xan	471	11	47.8	10	2	Q9TS43	Q9ts43 sus scrofa
399	11	47.8	9	2	Q673X7	Q673x7 nilaus afer	472	11	47.8	10	2	Q9TU33	Q9tu33 canis famil
400	11	47.8	9	2	Q673X8	Q673x8 bias flamm	473	11	47.8	10	2	Q9TU88	Q9tu88 basiliscus
401	11	47.8	9	2	Q673X9	Q673x9 malaconotus	474	11	47.8	10	2	Q79888	Q79889 crotaphytus
402	11	47.8	9	2	Q673Y0	Q673y0 lanius coll	475	11	47.8	10	2	Q79891	Q79891 gambelia wi
403	11	47.8	9	2	Q673Y1	Q673y1 lanioturdus	476	11	47.8	10	2	Q79894	Q79894 gambelia wi
404	11	47.8	9	2	Q673Y2	Q673y2 lanioturdus	477	11	47.8	10	2	Q79900	Q79900 liolaemus p
405	11	47.8	9	2	Q673Y3	Q673y3 laniarius l	478	11	47.8	10	2	Q79909	Q79909 saurumalus
406	11	47.8	9	2	Q673Y4	Q673y4 laniarius f	479	11	47.8	10	2	Q79912	Q79912 chamaeleo f
407	11	47.8	9	2	Q673Y5	Q673y5 laniarius a	480	11	47.8	10	2	Q79915	Q79915 leiolepis b
408	11	47.8	9	2	Q673Y6	Q673y6 platysteira	481	11	47.8	10	2	Q79924	Q79924 elgaria pan
409	11	47.8	9	2	Q673Y7	Q673y7 dryoscopus	482	11	47.8	10	2	P92616	P92616 aspidosceli
410	11	47.8	9	2	Q673Y8	Q673y8 dryoscopus	483	11	47.8	10	2	P92632	P92632 eremias gra
411	11	47.8	9	2	Q673Y9	Q673y9 dicrurus pa	484	11	47.8	10	2	P92648	P92648 lialis jica
412	11	47.8	9	2	Q673Z0	Q673z0 cyanolanius	485	11	47.8	10	2	P92733	P92733 euprepis au
413	11	47.8	9	2	Q673Z1	Q673z1 corvus coro	486	11	47.8	10	2	P92758	P92758 teratoscinc
414	11	47.8	9	2	Q673Z2	Q673z2 coracina me	487	11	47.8	10	2	P92762	P92762 uromastyx a
415	11	47.8	9	2	Q673Z3	Q673z3 telophorus	488	11	47.8	10	2	P92766	P92766 varanus gri
416	11	47.8	9	2	Q673Z4	Q673z4 telophorus	489	11	47.8	10	2	P92771	P92771 xenosauros
417	11	47.8	9	2	Q673Z5	Q673z5 telophorus	490	11	47.8	10	2	P92774	P92774 xantusia vi
418	11	47.8	9	2	Q673Z6	Q673z6 campephaga	491	11	47.8	10	2	Q8SH83	Q8sh83 brookesia t
419	11	47.8	9	2	Q673Z7	Q673z7 tchagra min	492	11	47.8	10	2	Q8SH85	Q8sh85 brookesia t
420	11	47.8	9	2	Q673Z8	Q673z8 bias musicu	493	11	47.8	10	2	Q8SH88	Q8sh88 brookesia t
421	11	47.8	9	2	Q673Z9	Q673z9 battis poens	494	11	47.8	10	2	Q8SH90	Q8sh90 brookesia s
422	11	47.8	9	2	Q78DU2	Q78du2 gallus gall	495	11	47.8	10	2	Q8SH93	Q8sh93 brookesia p
423	11	47.8	9	2	Q7LZ66	Q7lzx6 meleagris g	496	11	47.8	10	2	Q8SH96	Q8sh96 brookesia n
424	11	47.8	9	2	Q801K0	Q801k0 illicura mil	497	11	47.8	10	2	Q8SH99	Q8sh99 brookesia n
425	11	47.8	9	2	Q801K1	Q801k1 chirotophia	498	11	47.8	10	2	Q8SHA2	Q8sha2 brookesia b
426	11	47.8	9	2	Q801K2	Q801k2 antilophia	499	11	47.8	10	2	Q8SHA5	Q8sha5 brookesia a
427	11	47.8	9	2	Q9PRJ4	Q9prj4 lepisosteus	500	11	47.8	10	2	Q8SHA8	Q8sha8 rhampholeon
428	11	47.8	9	2	Q8S723	Q8s723 simian sarc	501	11	47.8	10	2	Q8SHB1	Q8shb1 rhampholeon
429	11	47.8	10	1	AEG_L_AGRAE	P83465 agroclype ae	502	11	47.8	10	2	Q8SHB4	Q8shb4 furcifer ve
430	11	47.8	10	1	APE_CARGI	P80474 capnocytoph	503	11	47.8	10	2	Q8SHB7	Q8shb7 furcifer ou
431	11	47.8	10	1	BPP2_BOTIN	P30422 bothrops in	504	11	47.8	10	2	Q8SHC0	Q8shc0 furcifer la
432	11	47.8	10	1	BPP2_BOTJA	P10122 bothrops ja	505	11	47.8	10	2	Q8SHC3	Q8shc3 furcifer la
433	11	47.8	10	1	BPP8_BOTIN	P30426 bothrops in	506	11	47.8	10	2	Q8SHC6	Q8shc6 furcifer ba
434	11	47.8	10	1	BPP_VIPAS	P31351 vipera aspi	507	11	47.8	10	2	Q8SHC9	Q8shc9 furcifer ba
435	11	47.8	10	1	BRK_ONCMY	Q9przi oncorhynch	508	11	47.8	10	2	Q8SHD2	Q8shd2 chamaeleo w
436	11	47.8	10	1	CA12_LITCI	P62540 litoria cit	509	11	47.8	10	2	Q8SHD5	Q8shd5 chamaeleo s
437	11	47.8	10	1	CA12_LITSP	P62541 litoria spl	510	11	47.8	10	2	Q8SHD8	Q8shd8 chamaeleo r
438	11	47.8	10	1	CABR_LITXA	P56264 litoria spl	511	11	47.8	10	2	Q8SHE1	Q8she1 chamaeleo q
439	11	47.8	10	1	GON1_ALLMI	P37041 alligator m	512	11	47.8	10	2	Q8SHE4	Q8she4 chamaeleo q
440	11	47.8	10	1	GON1_CHEPR	P80677 chelyosoma	513	11	47.8	10	2	Q8SHE7	Q8she7 chamaeleo p
441	11	47.8	10	1	GON1_CLUPA	P81749 clupea pall	514	11	47.8	10	2	Q8SHF3	Q8shf3 chamaeleo m
442	11	47.8	10	1	GON2_ALLMI	P68073 alligator m	515	11	47.8	10	2	Q8SHF6	Q8shf6 chamaeleo m
443	11	47.8	10	1	GON2_CHEPR	P80678 chelyosoma	516	11	47.8	10	2	Q8SHF9	Q8shf9 chamaeleo j
444	11	47.8	10	1	GON2_CHICK	P68072 gallus gall	517	11	47.8	10	2	Q8SHG2	Q8shg2 chamaeleo j
445	11	47.8	10	1	GON2_CLUPA	P68075 clupea pall	518	11	47.8	10	2	Q8SHG5	Q8shg5 chamaeleo h
446	11	47.8	10	1	GON2_HYDCO	P68076 hydrolegus	519	11	47.8	10	2	Q8SHG8	Q8shg8 chamaeleo g
447	11	47.8	10	1	GON2_SQUAC	P68074 squalus aca	520	11	47.8	10	2	Q8SHH1	Q8shh1 chamaeleo f
448	11	47.8	10	1	GON3_ONCKE	P20367 oncorhynch	521	11	47.8	10	2	Q8SHH4	Q8shh4 chamaeleo f
449	11	47.8	10	1	GON3_PETMA	P30948 petromyzon	522	11	47.8	10	2	Q8SHH7	Q8shh7 chamaeleo e
450	11	47.8	10	1	GONL_SQUAC	P27429 squalus aca	523	11	47.8	10	2	Q8SHI0	Q8shi0 chamaeleo d
451	11	47.8	10	1	GRP_RANRI	P23260 rana ridibu	524	11	47.8	10	2	Q8SHI3	Q8shi3 chamaeleo c
452	11	47.8	10	1	LABI_JATMU	P13270 jatropha mu	525	11	47.8	10	2	Q8SHI6	Q8shi6 chamaeleo c
453	11	47.8	10	1	MP2_MICOC	P81533 microplitis	526	11	47.8	10	2	Q8SHI9	Q8shi9 chamaeleo c
454	11	47.8	10	1	NO40_TOBAC	P55962 nicotiana t	527	11	47.8	10	2	Q8SHJ2	Q8shj2 chamaeleo a
455	11	47.8	10	1	PNAL_PRUDU	P81899 prunus dulc	528	11	47.8	10	2	Q8SHJ5	Q8shj5 calumma par
456	11	47.8	10	1	TPIS_NICPL	P19118 nicotiana p	529	11	47.8	10	2	Q8SHJ8	Q8shj8 calumma osh
457	11	47.8	10	2	Q7M530	Q7m530 pyrococcus	530	11	47.8	10	2	Q8SHK1	Q8shk1 calumma nas
458	11	47.8	10	2	Q7M4X1	Q7m4x1 basidiobolu	531	11	47.8	10	2	Q8SHK4	Q8shk4 calumma hil
459	11	47.8	10	2	Q7SA62	Q7sa62 neurospora	532	11	47.8	10	2	Q8SHK7	Q8shk7 calumma glo
460	11	47.8	10	2	Q15342	Q15342 homo sapien	533	11	47.8	10	2	Q8SHL0	Q8shl0 calumma gas
461	11	47.8	10	2	Q8WTT4	Q8wtt4 homo sapien	534	11	47.8	10	2	Q8SHL3	Q8shl3 calumma fur
462	11	47.8	10	2	Q96QA7	Q96qa7 homo sapien	535	11	47.8	10	2	Q8SHL6	Q8shl6 calumma cuc
463	11	47.8	10	2	Q6LA62	Q6la62 homo sapien	536	11	47.8	10	2	Q8SHL9	Q8shl9 calumma bre
464	11	47.8	10	2	Q25355	Q25355 locusta mig	537	11	47.8	10	2	Q8SHM2	Q8shm2 calumma boe
465	11	47.8	10	2	Q25356	Q25356 locusta mig	538	11	47.8	10	2	Q8SHM5	Q8shm5 bradypodion
466	11	47.8	10	2	Q7RRV6	Q7rrv6 plaemodium	539	11	47.8	10	2	Q8SHM8	Q8shm8 bradypodion
467	11	47.8	10	2	Q7M2Z8	Q7m2z8 bos taurus	540	11	47.8	10	2	Q8SHN1	Q8shn1 bradypodion
468	11	47.8	10	2	Q7M3E8	Q7m3e8 sus scrofa	541	11	47.8	10	2	Q8SHN4	Q8shn4 bradypodion
469	11	47.8	10	2	Q9N1X1	Q9n1x1 equus cabal	542	11	47.8	10	2	Q8SHN7	Q8shn7 bradypodion

543	11	47.8	10	2	Q8SHP0	Q8shp0 bradypodion	616	11	47.8	10	2	Q6WBL6	Q6wb16 sceloporos
544	11	47.8	10	2	Q8SIR8	Q8si18 xantusia ar	617	11	47.8	10	2	Q6WBL9	Q6wb19 sceloporos
545	11	47.8	10	2	Q8SIU1	Q8siu1 xantusia ar	618	11	47.8	10	2	Q6WBM2	Q6wbm2 sceloporos
546	11	47.8	10	2	Q8SIU4	Q8siu4 xantusia he	619	11	47.8	10	2	Q6WBM5	Q6wbm5 sceloporos
547	11	47.8	10	2	Q8W916	Q8w916 liolaemus m	620	11	47.8	10	2	Q6WBM8	Q6wbm8 sceloporos
548	11	47.8	10	2	Q8WDG8	Q8wdg8 anolis line	621	11	47.8	10	2	Q6WBN1	Q6wb11 sceloporos
549	11	47.8	10	2	Q8WDI0	Q8wdi0 anolis sagr	622	11	47.8	10	2	Q6WBN4	Q6wb14 sceloporos
550	11	47.8	10	2	Q8WFT5	Q8wft5 diadema ant	623	11	47.8	10	2	Q6WBP0	Q6wb10 sceloporos
551	11	47.8	10	2	Q8WFT6	Q8wft6 diadema ant	624	11	47.8	10	2	Q6WBP3	Q6wb13 sceloporos
552	11	47.8	10	2	Q94NH4	Q94nb4 rana muscos	625	11	47.8	10	2	Q6WBP6	Q6wb16 sceloporos
553	11	47.8	10	2	Q94PD8	Q94pd8 varanus sca	626	11	47.8	10	2	Q6WBP9	Q6wb19 sceloporos
554	11	47.8	10	2	Q94V85	Q94v85 varanus sca	627	11	47.8	10	2	Q6WBP2	Q6wb12 sceloporos
555	11	47.8	10	2	Q94V97	Q94v97 varanus spe	628	11	47.8	10	2	Q6WBQ5	Q6wb15 sceloporos
556	11	47.8	10	2	Q94VC9	Q94vc9 varanus pan	629	11	47.8	10	2	Q6WBQ8	Q6wb18 sceloporos
557	11	47.8	10	2	Q94VD2	Q94vd2 varanus pan	630	11	47.8	10	2	Q6WBQ7	Q6wb17 sceloporos
558	11	47.8	10	2	Q94VD5	Q94vd5 varanus oli	631	11	47.8	10	2	Q6WBS0	Q6wb10 sceloporos
559	11	47.8	10	2	Q94VF0	Q94vf0 varanus kin	632	11	47.8	10	2	Q6WBS6	Q6wb16 sceloporos
560	11	47.8	10	2	Q94VG5	Q94vg5 varanus gri	633	11	47.8	10	2	Q6WBS9	Q6wb19 sceloporos
561	11	47.8	10	2	Q94VH1	Q94vh1 varanus gle	634	11	47.8	10	2	Q6WBT2	Q6wb12 sceloporos
562	11	47.8	10	2	Q958J8	Q958j8 rana muscos	635	11	47.8	10	2	Q6WBT5	Q6wb15 sceloporos
563	11	47.8	10	2	Q958K0	Q958k0 rana cascad	636	11	47.8	10	2	Q6WBU7	Q6wb17 sceloporos
564	11	47.8	10	2	Q958K3	Q958k3 rana aurora	637	11	47.8	10	2	Q6WBV0	Q6wb10 sceloporos
565	11	47.8	10	2	Q958K6	Q958k6 rana pretio	638	11	47.8	10	2	Q6WBV3	Q6wb13 sceloporos
566	11	47.8	10	2	Q958K9	Q958k9 rana boylli	639	11	47.8	10	2	Q6WBV6	Q6wb16 sceloporos
567	11	47.8	10	2	Q958L2	Q958l2 rana tempor	640	11	47.8	10	2	Q6WBV9	Q6wb19 sceloporos
568	11	47.8	10	2	Q958L5	Q958l5 rana sylvat	641	11	47.8	10	2	Q6X0E4	Q6x0e4 anolis stra
569	11	47.8	10	2	Q958L8	Q958l8 rana catesb	642	11	47.8	10	2	Q71DS1	Q71ds1 microlophus
570	11	47.8	10	2	Q6UJG7	Q6ujg7 heteronotia	643	11	47.8	10	2	Q71DV1	Q71dv1 sceloporos
571	11	47.8	10	2	Q6UJH0	Q6ujh0 gehyra vari	644	11	47.8	10	2	Q71DV4	Q71dv4 sceloporos
572	11	47.8	10	2	Q6UJH3	Q6ujh3 liailis jica	645	11	47.8	10	2	Q71DV7	Q71dv7 sceloporos
573	11	47.8	10	2	Q6UJH6	Q6ujh6 pseudotheca	646	11	47.8	10	2	Q71E02	Q71e02 anolis dist
574	11	47.8	10	2	Q6UJH9	Q6ujh9 phyllurus c	647	11	47.8	10	2	Q71E05	Q71e05 anolis cris
575	11	47.8	10	2	Q6UJ12	Q6uj12 nephrurus m	648	11	47.8	10	2	Q71E14	Q71e14 brachylophu
576	11	47.8	10	2	Q6UJ15	Q6uj15 nephrurus w	649	11	47.8	10	2	Q71E26	Q71e26 corytophane
577	11	47.8	10	2	Q6UJ18	Q6uj18 nephrurus l	650	11	47.8	10	2	Q71E29	Q71e29 laemantus
578	11	47.8	10	2	Q6UJ11	Q6uj11 nephrurus v	651	11	47.8	10	2	Q71E32	Q71e32 basiliscus
579	11	47.8	10	2	Q6UJ34	Q6uj34 nephrurus l	652	11	47.8	10	2	Q71G22	Q71g22 andrena lim
580	11	47.8	10	2	Q6UJ37	Q6uj37 carphodactyl	653	11	47.8	10	2	Q71S88	Q71s88 liolaemus r
581	11	47.8	10	2	Q6UJK0	Q6ujk0 crenadactyl	654	11	47.8	10	2	Q71S81	Q71s81 liolaemus f
582	11	47.8	10	2	Q6UJK3	Q6ujk3 oedura marm	655	11	47.8	10	2	Q71S84	Q71s84 liolaemus a
583	11	47.8	10	2	Q6UJK6	Q6ujk6 rhynchoedur	656	11	47.8	10	2	Q71S87	Q71s87 liolaemus s
584	11	47.8	10	2	Q6UJK9	Q6ujk9 diploactyl	657	11	47.8	10	2	Q71S86	Q71s86 liolaemus a
585	11	47.8	10	2	Q6UJL8	Q6ujl8 strophurus	658	11	47.8	10	2	Q71S89	Q71s89 liolaemus a
586	11	47.8	10	2	Q6UJM1	Q6ujm1 strophurus	659	11	47.8	10	2	Q71S82	Q71s82 phymaturus
587	11	47.8	10	2	Q6UJM4	Q6ujm4 diploactyl	660	11	47.8	10	2	Q71S85	Q71s85 phymaturus
588	11	47.8	10	2	Q6UJM7	Q6ujm7 strophurus	661	11	47.8	10	2	Q71S88	Q71s88 ctenoblepha
589	11	47.8	10	2	Q6UJN0	Q6ujn0 diploactyl	662	11	47.8	10	2	Q76MK5	Q76mk5 eurypharynx
590	11	47.8	10	2	Q6UJN3	Q6ujn3 diploactyl	663	11	47.8	10	2	Q76ML6	Q76ml6 eurypharynx
591	11	47.8	10	2	Q6UJN6	Q6ujn6 diploactyl	664	11	47.8	10	2	Q76MM1	Q76mm1 eurypharynx
592	11	47.8	10	2	Q6UJN9	Q6ujn9 diploactyl	665	11	47.8	10	2	Q7J5U5	Q7j5u5 ovis aries
593	11	47.8	10	2	Q6UJP2	Q6ujp2 diploactyl	666	11	47.8	10	2	Q85J75	Q85j75 varanus bre
594	11	47.8	10	2	Q6UJP5	Q6ujp5 diploactyl	667	11	47.8	10	2	Q9B0Z6	Q9b0z6 salamandra
595	11	47.8	10	2	Q6UJP8	Q6ujp8 diploactyl	668	11	47.8	10	2	Q9B1W9	Q9b1w9 mertenstell
596	11	47.8	10	2	Q6UJQ1	Q6ujq1 diploactyl	669	11	47.8	10	2	Q9B1X0	Q9b1x0 mertenstell
597	11	47.8	10	2	Q6UJQ4	Q6ujq4 strophurus	670	11	47.8	10	2	Q9B4S0	Q9b4s0 mertenstell
598	11	47.8	10	2	Q6UJQ7	Q6ujq7 strophurus	671	11	47.8	10	2	Q9B4S5	Q9b4s5 mertenstell
599	11	47.8	10	2	Q6UJQ0	Q6ujq0 strophurus	672	11	47.8	10	2	Q9B4S8	Q9b4s8 mertenstell
600	11	47.8	10	2	Q6WBQ8	Q6wbq8 liolaemus c	673	11	47.8	10	2	Q9B4T1	Q9b4t1 mertenstell
601	11	47.8	10	2	Q6WBH1	Q6wbh1 liolaemus x	674	11	47.8	10	2	Q9B4U2	Q9b4u2 mertenstell
602	11	47.8	10	2	Q6WBH4	Q6wbh4 liolaemus r	675	11	47.8	10	2	Q9B4U5	Q9b4u5 mertenstell
603	11	47.8	10	2	Q6WBH7	Q6wbh7 liolaemus h	676	11	47.8	10	2	Q9B4U8	Q9b4u8 salamandra
604	11	47.8	10	2	Q6WB10	Q6wb10 liolaemus s	677	11	47.8	10	2	Q9B4V5	Q9b4v5 mertenstell
605	11	47.8	10	2	Q6WB13	Q6wb13 liolaemus p	678	11	47.8	10	2	Q9B4V8	Q9b4v8 chioglossa
606	11	47.8	10	2	Q6WB16	Q6wb16 liolaemus k	679	11	47.8	10	2	Q9B4W1	Q9b4w1 triturus vu
607	11	47.8	10	2	Q6WB19	Q6wb19 liolaemus h	680	11	47.8	10	2	Q9B4W4	Q9b4w4 pachytriton
608	11	47.8	10	2	Q6WB22	Q6wb22 liolaemus p	681	11	47.8	10	2	Q9B4W7	Q9b4w7 tylocotrito
609	11	47.8	10	2	Q6WB25	Q6wb25 liolaemus g	682	11	47.8	10	2	Q9B4X0	Q9b4x0 notophthalm
610	11	47.8	10	2	Q6WB28	Q6wb28 liolaemus n	683	11	47.8	10	2	Q9G362	Q9g362 acanthosaur
611	11	47.8	10	2	Q6WBK1	Q6wbk1 sceloporos	684	11	47.8	10	2	Q9G694	Q9g694 leirolepis g
612	11	47.8	10	2	Q6WBK4	Q6wbk4 sceloporos	685	11	47.8	10	2	Q9G697	Q9g697 chamaeleo d
613	11	47.8	10	2	Q6WBK7	Q6wbk7 sceloporos	686	11	47.8	10	2	Q9MQ05	Q9mq05 podospora c
614	11	47.8	10	2	Q6WB10	Q6wb10 sceloporos	687	11	47.8	10	2	Q9T4P9	Q9t4p9 liolaemus d
615	11	47.8	10	2	Q6WB13	Q6wb13 sceloporos	688	11	47.8	10	2	Q9T8F5	Q9t8f5 liolaemus b

689	11	47.8	10	2	Q9T8G0	Q9T8G0 liolaemus 1	762	11	47.8	10	2	Q9TG74	Q9Tg74 wetmorena h
690	11	47.8	10	2	Q9T8G5	Q9T8G5 liolaemus o	763	11	47.8	10	2	Q9TG77	Q9Tg77 sauresia ag
691	11	47.8	10	2	Q9T8G8	Q9T8G8 liolaemus c	764	11	47.8	10	2	Q9TG80	Q9Tg80 ophiodes st
692	11	47.8	10	2	Q9T8H1	Q9T8H1 liolaemus u	765	11	47.8	10	2	Q9TG83	Q9Tg83 diploglossu
693	11	47.8	10	2	Q9T8H4	Q9T8H4 liolaemus i	766	11	47.8	10	2	Q9TG86	Q9Tg86 diploglossu
694	11	47.8	10	2	Q9T8H7	Q9T8H7 liolaemus a	767	11	47.8	10	2	Q9TG89	Q9Tg89 celestus en
695	11	47.8	10	2	Q9T8I0	Q9T8I0 liolaemus o	768	11	47.8	10	2	Q9TG92	Q9Tg92 anniella pu
696	11	47.8	10	2	Q9T8I3	Q9T8I3 liolaemus q	769	11	47.8	10	2	Q9TG95	Q9Tg95 anniella ge
697	11	47.8	10	2	Q9T8I6	Q9T8I6 liolaemus k	770	11	47.8	10	2	Q9TG98	Q9Tg98 shinisaurus
698	11	47.8	10	2	Q9T8I9	Q9T8I9 liolaemus a	771	11	47.8	10	2	Q9TGA1	Q9Tga1 heloderma s
699	11	47.8	10	2	Q9T8J2	Q9T8J2 liolaemus r	772	11	47.8	10	2	Q9XMB4	Q9xmb4 aegilops ta
700	11	47.8	10	2	Q9T8J5	Q9T8J5 liolaemus m	773	11	47.8	10	2	Q9ZY59	Q9zy59 phymaturus
701	11	47.8	10	2	Q9T8J8	Q9T8J8 liolaemus w	774	11	47.8	10	2	Q9ZYT5	Q9zyt5 uta stansbu
702	11	47.8	10	2	Q9T8K1	Q9T8K1 liolaemus s	775	11	47.8	10	2	Q9ZYT8	Q9zyt8 urosaurus g
703	11	47.8	10	2	Q9T8K4	Q9T8K4 liolaemus s	776	11	47.8	10	2	Q9ZYU1	Q9zyul uma scopari
704	11	47.8	10	2	Q9T8K7	Q9T8K7 liolaemus m	777	11	47.8	10	2	Q9ZI04	Q9zyu4 sceloporue
705	11	47.8	10	2	Q9T8L0	Q9T8L0 liolaemus o	778	11	47.8	10	2	Q9ZY07	Q9zyu7 sator angus
706	11	47.8	10	2	Q9T8L3	Q9T8L3 liolaemus l	779	11	47.8	10	2	Q9ZYV0	Q9zyv0 petrosaurus
707	11	47.8	10	2	Q9T8L6	Q9T8L6 liolaemus p	780	11	47.8	10	2	Q9ZYV3	Q9zyv3 dipsoosaurus
708	11	47.8	10	2	Q9T8L9	Q9T8L9 liolaemus f	781	11	47.8	10	2	P82443	P82443 nicotiana t
709	11	47.8	10	2	Q9T8M2	Q9T8M2 liolaemus c	782	11	47.8	10	2	Q9Z213	Q9z213 aegilops ta
710	11	47.8	10	2	Q9T8M5	Q9T8M5 liolaemus a	783	11	47.8	10	2	Q9TS30	Q6t630 lycopersico
711	11	47.8	10	2	Q9T8M8	Q9T8M8 liolaemus m	784	11	47.8	10	2	Q8GZC8	Q8gzc8 hordeum vul
712	11	47.8	10	2	Q9T8N1	Q9T8N1 liolaemus p	785	11	47.8	10	2	Q8KH9	Q8kh9 clostridium
713	11	47.8	10	2	Q9T8N4	Q9T8N4 liolaemus d	786	11	47.8	10	2	Q93LX4	Q93lx4 vibrio chol
714	11	47.8	10	2	Q9T8N7	Q9T8N7 liolaemus o	787	11	47.8	10	2	Q93T35	Q93t35 acinetobact
715	11	47.8	10	2	Q9T8P0	Q9T8P0 liolaemus f	788	11	47.8	10	2	Q47561	Q47561 escherichia
716	11	47.8	10	2	Q9T8P3	Q9T8P3 liolaemus a	789	11	47.8	10	2	Q60L97	Q6l97 neisseria g
717	11	47.8	10	2	Q9T8P6	Q9T8P6 liolaemus r	790	11	47.8	10	2	Q6R101	Q6r101 clostridium
718	11	47.8	10	2	Q9T8P9	Q9T8P9 liolaemus m	791	11	47.8	10	2	Q79AV7	Q79av7 klebsiella
719	11	47.8	10	2	Q9T8Q2	Q9T8Q2 liolaemus s	792	11	47.8	10	2	Q8G8W5	Q8g8w5 borrelia bu
720	11	47.8	10	2	Q9T8Q5	Q9T8Q5 liolaemus l	793	11	47.8	10	2	Q9F9H5	Q9f9h5 helicobacte
721	11	47.8	10	2	Q9T8Q8	Q9T8Q8 liolaemus e	794	11	47.8	10	2	Q9R5N2	Q9r5n2 clostridium
722	11	47.8	10	2	Q9T8R1	Q9T8R1 liolaemus a	795	11	47.8	10	2	Q70580	Q76lbt3 mus musculu
723	11	47.8	10	2	Q9T8R4	Q9T8R4 liolaemus p	796	11	47.8	10	2	Q6LBT3	Q6lbt3 mus musculu
724	11	47.8	10	2	Q9T8R7	Q9T8R7 liolaemus c	797	11	47.8	10	2	Q8CJE0	Q8cje0 rattus norv
725	11	47.8	10	2	Q9T8R9	Q9T8R9 liolaemus b	798	11	47.8	10	2	Q9ESU5	Q9eesu5 mus musculu
726	11	47.8	10	2	Q9T8S1	Q9T8S1 liolaemus l	799	11	47.8	10	2	O42355	O42355 brachydanio
727	11	47.8	10	2	Q9T8S4	Q9T8S4 liolaemus n	800	11	47.8	10	2	Q8JFE7	Q8jfe7 ficedula al
728	11	47.8	10	2	Q9T8S7	Q9T8S7 liolaemus c	801	11	47.8	10	2	Q8UJ33	Q8uj33 ficedula hy
729	11	47.8	10	2	Q9T8T0	Q9T8T0 liolaemus f	802	11	47.8	10	2	Q7LZC5	Q7lzc5 kassina mac
730	11	47.8	10	2	Q9T8T3	Q9T8T3 liolaemus n	803	11	47.8	10	2	Q9PRU9	Q9pru9 sparus aua
731	11	47.8	10	2	Q9T8T6	Q9T8T6 liolaemus m	804	11	47.8	10	2	Q8UT83	Q8ut83 human immun
732	11	47.8	10	2	Q9T8T9	Q9T8T9 liolaemus l	805	11	47.8	11	1	CEP1_ACHFU	P22790 achatina fu
733	11	47.8	10	2	Q9T8U2	Q9T8U2 liolaemus t	806	11	47.8	11	1	CX5A_CONAL	P58848 conus aulic
734	11	47.8	10	2	Q9T8U5	Q9T8U5 liolaemus z	807	11	47.8	11	1	CX5B_CONAL	P58849 conus aulic
735	11	47.8	10	2	Q9T8V0	Q9T8V0 liolaemus c	808	11	47.8	11	1	LPW_THETH	P05624 thermus the
736	11	47.8	10	2	Q9T8V3	Q9T8V3 liolaemus b	809	11	47.8	11	1	MLG_THETS	P41989 theromyzon
737	11	47.8	10	2	Q9T8V6	Q9T8V6 liolaemus b	810	11	47.8	11	1	OAIF_SARBU	P83518 sarcophaga
738	11	47.8	10	2	Q9T8V9	Q9T8V9 liolaemus g	811	11	47.8	11	1	RANC_RANPI	P08951 rana pipien
739	11	47.8	10	2	Q9T8W2	Q9T8W2 liolaemus b	812	11	47.8	11	2	R82_CONAM	P42341 conopholis
740	11	47.8	10	2	Q9T8W5	Q9T8W5 liolaemus r	813	11	47.8	11	2	Q9CIR7	Q9c1r7 saccharomyc
741	11	47.8	10	2	Q9T8W8	Q9T8W8 liolaemus b	814	11	47.8	11	2	Q8TDA8	Q8tda8 homo sapien
742	11	47.8	10	2	Q9T8X4	Q9T8X4 liolaemus c	815	11	47.8	11	2	Q9UCR1	Q9ucr1 homo sapien
743	11	47.8	10	2	Q9T8X7	Q9T8X7 phymaturus	816	11	47.8	11	2	Q9UE69	Q9ue69 homo sapien
744	11	47.8	10	2	Q9T8U6	Q9T8U6 teratoscinc	817	11	47.8	11	2	Q9UEL0	Q9uel0 homo sapien
745	11	47.8	10	2	Q9T8U9	Q9T8U9 teratoscinc	818	11	47.8	11	2	Q6UZ55	Q6uz55 littorina s
746	11	47.8	10	2	Q9T8V2	Q9T8V2 teratoscinc	819	11	47.8	11	2	Q7RH63	Q7rh63 plaemodium
747	11	47.8	10	2	Q9T8V5	Q9T8V5 eublepharus	820	11	47.8	11	2	Q6DW13	Q6dw13 bos taurus
748	11	47.8	10	2	Q9TG32	Q9TG32 ophisaurus	821	11	47.8	11	2	Q9GL48	Q9gl48 sus scrofa
749	11	47.8	10	2	Q9TG35	Q9TG35 ophisaurus	822	11	47.8	11	2	Q77884	Q77884 oreochromis
750	11	47.8	10	2	Q9TG38	Q9TG38 ophisaurus	823	11	47.8	11	2	Q77885	Q77885 oreochromis
751	11	47.8	10	2	Q9TG41	Q9TG41 ophisaurus	824	11	47.8	11	2	Q77892	Q77892 oreochromis
752	11	47.8	10	2	Q9TG44	Q9TG44 anguis frag	825	11	47.8	11	2	Q77893	Q77893 oreochromis
753	11	47.8	10	2	Q9TG47	Q9TG47 ophisaurus	826	11	47.8	11	2	Q77894	Q77894 oreochromis
754	11	47.8	10	2	Q9TG50	Q9TG50 elgaria mul	827	11	47.8	11	2	Q77895	Q77895 oreochromis
755	11	47.8	10	2	Q9TG53	Q9TG53 elgaria pau	828	11	47.8	11	2	Q77896	Q77896 oreochromis
756	11	47.8	10	2	Q9TG56	Q9TG56 elgaria kin	829	11	47.8	11	2	Q77898	Q77898 oreochromis
757	11	47.8	10	2	Q9TG59	Q9TG59 elgaria coe	830	11	47.8	11	2	Q77906	Q77906 oreochromis
758	11	47.8	10	2	Q9TG62	Q9TG62 mesaepia mo	831	11	47.8	11	2	Q77908	Q77908 oreochromis
759	11	47.8	10	2	Q9TG65	Q9TG65 abronia oax	832	11	47.8	11	2	Q77913	Q77913 oreochromis
760	11	47.8	10	2	Q9TG68	Q9TG68 gerthnotus	833	11	47.8	11	2	Q77914	Q77914 oreochromis
761	11	47.8	10	2	Q9TG71	Q9TG71 barisia imb	834	11	47.8	11	2	Q77918	Q77918 pseudotroph

835	11	47.8	11	2	078118	078118 oreochromis	908	11	47.8	11	2	07Y9G4	07Y9G4 hypsilurus
836	11	47.8	11	2	078120	078120 oreochromis	909	11	47.8	11	2	07Y9G7	07Y9G7 hypsilurus
837	11	47.8	11	2	09UEX7	09UEX7 homo sapien	910	11	47.8	11	2	07Y9H0	07Y9H0 hypsilurus
838	11	47.8	11	2	079636	079636 laudakia hi	911	11	47.8	11	2	07Y9H3	07Y9H3 hypsilurus
839	11	47.8	11	2	079639	079639 laudakia le	912	11	47.8	11	2	07Y9H6	07Y9H6 hypsilurus
840	11	47.8	11	2	079642	079642 laudakia mi	913	11	47.8	11	2	07Y9H9	07Y9H9 diporiphora
841	11	47.8	11	2	079644	079644 laudakia mi	914	11	47.8	11	2	07Y9I2	07Y9I2 diporiphora
842	11	47.8	11	2	079921	079921 phrynoceph	915	11	47.8	11	2	07Y9I5	07Y9I5 diporiphora
843	11	47.8	11	2	079985	079985 laudakia ca	916	11	47.8	11	2	07Y9I8	07Y9I8 diporiphora
844	11	47.8	11	2	079986	079986 laudakia er	917	11	47.8	11	2	07Y9J1	07Y9J1 diporiphora
845	11	47.8	11	2	08MAZ1	08MAZ1 maripa pani	918	11	47.8	11	2	07Y9J4	07Y9J4 diporiphora
846	11	47.8	11	2	08MAZ3	08MAZ3 maripa repe	919	11	47.8	11	2	07Y9J7	07Y9J7 diporiphora
847	11	47.8	11	2	08MB39	08MB39 wilsonia hu	920	11	47.8	11	2	07Y9K0	07Y9K0 diporiphora
848	11	47.8	11	2	08MB58	08MB58 seddera hir	921	11	47.8	11	2	07Y9K3	07Y9K3 diporiphora
849	11	47.8	11	2	08MB77	08MB77 odonellia h	922	11	47.8	11	2	07Y9K6	07Y9K6 diporiphora
850	11	47.8	11	2	08MB79	08MB79 aniseia arg	923	11	47.8	11	2	07Y9K9	07Y9K9 amphiboluru
851	11	47.8	11	2	08MB97	08MB97 merremia pe	924	11	47.8	11	2	07Y9L3	07Y9L3 amphiboluru
852	11	47.8	11	2	08MBE1	08MBE1 ipomoea alb	925	11	47.8	11	2	07Y9L5	07Y9L5 amphiboluru
853	11	47.8	11	2	08SKN0	08SKN0 ctenophorus	926	11	47.8	11	2	09G2N4	09G2N4 chlamydosau
854	11	47.8	11	2	08SKN3	08SKN3 ctenophorus	927	11	47.8	11	2	09G3S0	09G3S0 laudakia sa
855	11	47.8	11	2	08SKN6	08SKN6 ctenophorus	928	11	47.8	11	2	09G3S3	09G3S3 trapelus sa
856	11	47.8	11	2	08SKN9	08SKN9 ctenophorus	929	11	47.8	11	2	09G3S6	09G3S6 agama atra
857	11	47.8	11	2	08SKP2	08SKP2 ctenophorus	930	11	47.8	11	2	09G371	09G371 pogona barb
858	11	47.8	11	2	08SKP5	08SKP5 ctenophorus	931	11	47.8	11	2	09G374	09G374 moloch horr
859	11	47.8	11	2	08SKP8	08SKP8 ctenophorus	932	11	47.8	11	2	09G3V0	09G3V0 laudakia st
860	11	47.8	11	2	08SKQ1	08SKQ1 ctenophorus	933	11	47.8	11	2	09G5V3	09G5V3 phrynoceph
861	11	47.8	11	2	08SKQ4	08SKQ4 ctenophorus	934	11	47.8	11	2	09G5V6	09G5V6 phrynoceph
862	11	47.8	11	2	08SKQ7	08SKQ7 ctenophorus	935	11	47.8	11	2	09G5V9	09G5V9 laudakia st
863	11	47.8	11	2	08SKR0	08SKR0 rankinia di	936	11	47.8	11	2	09G5W2	09G5W2 laudakia tu
864	11	47.8	11	2	08WC29	08WC29 ctenophorus	937	11	47.8	11	2	09G5W5	09G5W5 laudakia nu
865	11	47.8	11	2	08WD02	08WD02 ctenophorus	938	11	47.8	11	2	09G5W8	09G5W8 trapelus sa
866	11	47.8	11	2	08WD05	08WD05 ctenophorus	939	11	47.8	11	2	09G5X1	09G5X1 trapelus pe
867	11	47.8	11	2	08WD08	08WD08 ctenophorus	940	11	47.8	11	2	09G5X4	09G5X4 trapelus ag
868	11	47.8	11	2	08WD11	08WD11 ctenophorus	941	11	47.8	11	2	09G5X7	09G5X7 trapelus ru
869	11	47.8	11	2	08WD14	08WD14 ctenophorus	942	11	47.8	11	2	09G5Y0	09G5Y0 pseudotrapi
870	11	47.8	11	2	08WD17	08WD17 ctenophorus	943	11	47.8	11	2	09G5Y3	09G5Y3 agama impal
871	11	47.8	11	2	08WD20	08WD20 ctenophorus	944	11	47.8	11	2	09G5Y6	09G5Y6 agama agama
872	11	47.8	11	2	08WD23	08WD23 ctenophorus	945	11	47.8	11	2	09G5Z5	09G5Z5 japalura sp
873	11	47.8	11	2	08WD26	08WD26 ctenophorus	946	11	47.8	11	2	09G5Z8	09G5Z8 acanthosaur
874	11	47.8	11	2	08WD29	08WD29 ctenophorus	947	11	47.8	11	2	09G604	09G604 gonoccephal
875	11	47.8	11	2	08WD50	08WD50 ceratophora	948	11	47.8	11	2	09G610	09G610 lyriocephal
876	11	47.8	11	2	08WER4	08WER4 ceratophora	949	11	47.8	11	2	09G613	09G613 cophotis ce
877	11	47.8	11	2	08WER7	08WER7 ceratophora	950	11	47.8	11	2	09G616	09G616 ceratophora
878	11	47.8	11	2	094V74	094V74 lantthanotus	951	11	47.8	11	2	09G619	09G619 ceratophora
879	11	47.8	11	2	094V77	094V77 heloderma s	952	11	47.8	11	2	09G622	09G622 salea horsf
880	11	47.8	11	2	094V94	094V94 varanus sto	953	11	47.8	11	2	09G637	09G637 calotes lio
881	11	47.8	11	2	094VB8	094VB8 varanus sal	954	11	47.8	11	2	09G652	09G652 japalura va
882	11	47.8	11	2	094VE7	094VE7 varanus kom	955	11	47.8	11	2	09G655	09G655 japalura tr
883	11	47.8	11	2	094VG8	094VG8 varanus gou	956	11	47.8	11	2	09G658	09G658 hydrosaurus
884	11	47.8	11	2	094VH7	094VH7 varanus gil	957	11	47.8	11	2	09G661	09G661 tympanocryp
885	11	47.8	11	2	094VT5	094VT5 varanus exa	958	11	47.8	11	2	09G664	09G664 diporiphora
886	11	47.8	11	2	094VK1	094VK1 varanus aca	959	11	47.8	11	2	09G667	09G667 caimanops a
887	11	47.8	11	2	06ESN1	06ESN1 ptyctolaemu	960	11	47.8	11	2	09G670	09G670 rankinia ad
888	11	47.8	11	2	06WR61	06WR61 nandayus ne	961	11	47.8	11	2	09G673	09G673 ctenophorus
889	11	47.8	11	2	06WR64	06WR64 neophema el	962	11	47.8	11	2	09G676	09G676 amphiboluru
890	11	47.8	11	2	07M2E6	07M2E6 solanum tub	963	11	47.8	11	2	09G679	09G679 hypsilurus
891	11	47.8	11	2	07M2F2	07M2F2 lycopersico	964	11	47.8	11	2	09G682	09G682 chelosania
892	11	47.8	11	2	07Y9B6	07Y9B6 amphiboluru	965	11	47.8	11	2	09G685	09G685 arua modest
893	11	47.8	11	2	07Y9B9	07Y9B9 tympanocryp	966	11	47.8	11	2	09G688	09G688 physignathu
894	11	47.8	11	2	07Y9C2	07Y9C2 tympanocryp	967	11	47.8	11	2	09G691	09G691 lophognathu
895	11	47.8	11	2	07Y9C5	07Y9C5 tympanocryp	968	11	47.8	11	2	09G691	09G691 lophognathu
896	11	47.8	11	2	07Y9C8	07Y9C8 tympanocryp	969	11	47.8	11	2	09G698	09G698 elaeis guin
897	11	47.8	11	2	07Y9D1	07Y9D1 tympanocryp	970	11	47.8	11	2	094IR5	094IR5 pinus radia
898	11	47.8	11	2	07Y9D4	07Y9D4 tympanocryp	971	11	47.8	11	2	06T302	06T302 chlamydomon
899	11	47.8	11	2	07Y9D7	07Y9D7 pogona vitt	972	11	47.8	11	2	07MLU2	07MLU2 oryza sativ
900	11	47.8	11	2	07Y9E0	07Y9E0 pogona null	973	11	47.8	11	2	07MLW2	07MLW2 canavalie e
901	11	47.8	11	2	07Y9E3	07Y9E3 pogona mitc	974	11	47.8	11	2	047602	047602 escherichia
902	11	47.8	11	2	07Y9E6	07Y9E6 pogona mino	975	11	47.8	11	2	056413	056413 escherichia
903	11	47.8	11	2	07Y9E9	07Y9E9 pogona mini	976	11	47.8	11	2	0700S6	0700S6 mycoplasma
904	11	47.8	11	2	07Y9F2	07Y9F2 pogona henr	977	11	47.8	11	2	0798K4	0798K4 bacillus su
905	11	47.8	11	2	07Y9F5	07Y9F5 pogona brev	978	11	47.8	11	2	08GL19	08GL19 borrelia bu
906	11	47.8	11	2	07Y9F8	07Y9F8 lophognathu	979	11	47.8	11	2	08GL24	08GL24 borrelia bu
907	11	47.8	11	2	07Y9G1	07Y9G1 hypsilurus	980	11	47.8	11	2	08K432	08K432 spalax juda
												08K433	08K433 spalax galli

981 11 47.8 11 2 Q99JC3
 982 11 47.8 11 2 Q6LD68
 983 11 47.8 11 2 Q80W11
 984 11 47.8 11 2 Q8CQW6
 985 11 47.8 11 2 Q9QVH3
 986 11 47.8 11 2 Q80GP0
 987 11 47.8 11 2 Q65CG7
 988 11 47.8 11 2 Q90735
 989 11 47.8 11 2 Q7LZ10
 990 11 47.8 11 2 Q83410
 991 11 47.8 11 2 Q8ADI8
 992 11 47.8 11 2 Q9DZ32
 993 11 47.8 12 1 LICA_BACSU
 994 11 47.8 12 1 NO40_LOTJA
 995 11 47.8 12 1 NO40_SSSRO
 996 11 47.8 12 1 NO40_SOYBN
 997 11 47.8 12 1 RFL_CONSP
 998 11 47.8 12 1 UP01_CAEEL
 999 11 47.8 12 1 UR2A_CATCO
 1000 11 47.8 12 2 Q90XU4

ALIGNMENTS

RESULT 1
 AKH_HELZE STANDARD; PRT; 9 AA.
 AC P67787; P08901;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Adipokinetic hormone (Hez-AKH).
 OS Heliothis zea (Corn earworm) (Bollworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
 OC Noctuidae; Heliothinae; Helicoverpa.
 OX NCBI_TaxID=7113;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86196794; PubMed=3964263;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Holman G.M.,
 RA Wagner R.M., Ridgway R.L., Hayes D.K.;
 RT "Isolation and primary structure of a peptide from the corpora
 RT cardiaca of *Heliothis zea* with adipokinetic activity."
 RL Biochem. Biophys. Res. Commun. 135:622-628(1986).
 CC -!- FUNCTION: This hormone, released from cells in the corpora
 CC cardiaca after the beginning of flight, causes release of
 CC diglycerides from the fat body and then stimulates the flight
 CC muscles to use these diglycerides as an energy source.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; A24244; A24244.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Amidation; Direct protein sequencing; Flight; Neuropeptide;
 KW Pyrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrolidone carboxylic acid.
 FT MOD_RES 9 9 Glycine amide.
 SQ SEQUENCE 9 AA; 1026 MW; 403665A5A1A9D1A7 CRC64;

Query Match 73.9%; Score 17; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 |
 Db 4 FTSSW 8

RESULT 2
 Q9XLI2 PRELIMINARY; PRT; 13 AA.
 ID Q9XLI2

AC Q9XLI2;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Cytochrome oxidase I (Fragment).
 OS Bemisia tabaci (Sweetpotato whitefly).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleyrodiformes;
 OC Aleyrodioidea; Aleyrodidae; Aleyrodinae; Bemisia.
 OX NCBI_TaxID=7038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=10583831;
 RA Brown J.K.;
 RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,
 RT "A phylogeographical analysis of the Bemisia tabaci species complex
 RT based on mitochondrial DNA markers.";
 RL Mol. Ecol. 8:1683-1691(1999).
 DR EMBL; AF110703; RAD28415.1;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 13;
 Best Local Similarity 40.0%; Pred. No. 2.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 |
 Db 3 FTSSW 7

RESULT 3
 AKHG_GRYBI STANDARD; PRT; 8 AA.
 AC P67785; P14086;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Adipokinetic hormone G (AKH-G).
 OS Gryllus bimaculatus (Two-spotted cricket).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
 OC Gryllus.
 OX NCBI_TaxID=6999;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RC MEDLINE=88106553; PubMed=3426616;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary sequence analysis by fast atom bombardment mass spectrometry
 RT of a peptide with adipokinetic activity from the corpora cardiaca of
 RT the cricket *Gryllus bimaculatus*."
 RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
 CC -!- FUNCTION: This hormone, released from cells in the corpora
 CC cardiaca after the beginning of flight, causes release of
 CC diglycerides from the fat body and then stimulates the flight
 CC muscles to use these diglycerides as an energy source.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; A28004; A28004.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Amidation; Direct protein sequencing; Flight; Neuropeptide;
 KW Pyrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrolidone carboxylic acid.
 FT MOD_RES 8 8 Typtophan amide.
 SQ SEQUENCE 8 AA; 938 MW; 86786185B9C452D6 CRC64;

Query Match 69.6%; Score 16; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
Db 4 FSTGW 8

RESULT 4

AKH_ROMMI
ID AKH_ROMMI STANDARD; PRT; 8 AA.
AC P67786; P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adipokinetic hormone (AKH) (RO II).
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
OX NCBI_TaxID=7007;
RN [1]
RP SEQUENCE.

RC TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3225948; DOI=10.1016/0196-9781(88)90107-6;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RL Peptides 9:681-688(1988)."

CC -!- FUNCTION: This hormone, released from cells in the corpora
cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.

DR InterPro: IPR002047; AKH.

DR PROSITE: PS00256; AKH; 1.

KW Amidation; Direct protein sequencing; Flight; Neuropeptide;

KW Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 Pyrrolidone carboxylic acid.

FT MOD_RES 8 8 Tryptophan amide.

FT SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 69.6%; Score 16; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
Db 4 FSTGW 8

RESULT 5

HTF_HELZE
ID HTF_HELZE STANDARD; PRT; 10 AA.
AC P16353;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypertrehalosaemic hormone (HeZ-HRTH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=7113;
RN [1]
RP SEQUENCE.

RC TISSUE=Corpora cardiaca;
RX MEDLINE=88326324; PubMed=3415690;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G., Tseng C.M.,
RA Zhang Y.S., Hayes D.K.;
RT "Isolation and primary structure of a neuropeptide hormone from
RT Heliothis zea with hypertrehalosaemic and adipokinetic activities.";
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).

CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph of insects).
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.

DR PIR; A31571; A31571.

DR InterPro; IPR002047; AKH.

DR PROSITE; PS00256; AKH; 1.

KW Amidation; Direct protein sequencing; Neuropeptide;

KW Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 Pyrrolidone carboxylic acid.

FT MOD_RES 10 10 Asparagine amide.

FT SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

Query Match 69.6%; Score 16; DB 1; Length 10;

Best Local Similarity 40.0%; Pred. No. 3.8e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

|

Db 4 FSSGW 8

RESULT 6

Q6ESN4 PRELIMINARY; PRT; 11 AA.

ID Q6ESN4

AC Q6ESN4

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Cytochrome c oxidase subunit I (fragment).

GN Names=COI;

OS Mantheyus phuwanensis.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidodonta; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;

OC Mantheyus.

OX NCBI_TaxID=282162;

RN [1]

RP SEQUENCE FROM N.A.

RA Schulte J.A. II, Vindum J.V., Win H., Thin T., Lwin K.S., Shein A.K.,
Tun H.;

RT "Phylogenetic relationships of the genus Ptycolaelmus (Squamata:
RT Agamidae), with a description of a new species from the Chin Hills of
RT Western Myanmar.";

RL Proceedings Calif. Acad. Sci. 55:222-247(2004).

DR EMBL; AY555836; AAT74867.1;--

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON_TER 11

FT SEQUENCE 11 AA; 1343 MW; 932D371E336411B1 CRC64;

Query Match 69.6%; Score 16; DB 2; Length 11;

Best Local Similarity 40.0%; Pred. No. 4.1e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

|

Db 3 FTTRW 7

RESULT 7

Q9G649 PRELIMINARY; PRT; 11 AA.

ID Q9G649

AC Q9G649

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Cytochrome c oxidase subunit I (fragment).

GN Names=COI;

OS Oocryptis wiegmanni.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Ootocryptis
 OX NCBI_TaxID=118220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and phylogenetic information content of mitochondrial
 genomic structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating trans-tethys migration: an example using acrodont lizard
 phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128480; AA00677.1; -;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1347 MW; 9323710D3640DC1 CRC64;
 Query Match 69.6%; Score 16; DB 2; Length 11;
 Best Local Similarity 40.0%; Pred. No. 4.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 Db 3 FTARW 7
 RESULT 8
 O15276 PRELIMINARY; PRT; 17 AA.
 AC O15276;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mitochondrial translation elongation factor EF-Tu (Fragment).
 GN Names:TFPM;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jacobs H.T., Smurthwaite L., Koshiy R.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y11797; CAA72493.1; -;
 DR GO; GO:0003746; F:translation elongation factor activity; IEA.
 KW Elongation factor.
 FT NON_TER 1
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 2019 MW; BF737D12D2AB0A7E CRC64;
 Query Match 69.6%; Score 16; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 5.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 Db 1 FSLTW 5
 RESULT 9
 Q7Y1X8 PRELIMINARY; PRT; 17 AA.
 ID Q7Y1X8
 AC Q7Y1X8;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Male gametic cell-specific (Fragment).
 GN Name=LGCl;
 OS Lilium longiflorum (Trumpet lily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
 OX NCBI_TaxID=4690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22815576; PubMed=12729896; DOI=10.1016/S0014-5793(03)00335-1;
 RA Singh M., Bhalla P.L., Xu H., Singh M.B.;
 RT "Isolation and characterization of a flowering plant male gametic
 cell-specific promoter(1).";
 RL FEBS Lett. 542:47-52(2003).
 DR EMBL; AY207012; AAP37155.1; -;
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1880 MW; 661B6348496979F CRC64;
 Query Match 69.6%; Score 16; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 5.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 Db 11 FSSVW 15
 RESULT 10
 O91329 PRELIMINARY; PRT; 19 AA.
 ID O91329
 AC O91329;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98285741; PubMed=9621043;
 RA Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,
 RA Safar M., Barre-Sinoussi F., Kazatchkine M.D.;
 RT "Genetically related human immunodeficiency virus type 1 in three
 adults of a family with no identified risk factor for intrafamilial
 transmission.";
 RL J. Virol. 72:5831-5839(1998).
 DR EMBL; U87220; AAC32980.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF0516; GP120; 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 19 AA; 2324 MW; 379CB14A9E073911 CRC64;
 Query Match 69.6%; Score 16; DB 2; Length 19;
 Best Local Similarity 40.0%; Pred. No. 6.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 Db 10 FNSTW 14
 RESULT 11
 Q9WJB1 PRELIMINARY; PRT; 19 AA.
 ID Q9WJB1
 AC Q9WJB1;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)


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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285741; PubMed=9621043;
RA Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,
SAfar M., Barre-Sinoussi F., Kazatchkine M.D.;
RT "Genetically related human immunodeficiency virus type 1 in three
RT adults of a family with no identified risk factor for intrafamilial
RT transmission.";
RL J. Virol. 72:5831-5839(1998).
DR EMBL; U87216; AAC32976.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2294 MW; 3781714A9E073911 CRC64;

Query Match 69.6%; Score 16; DB 2; Length 19;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 10 FNSTW 14

RESULT 12
Q6LD18
ID Q6LD18 PRELIMINARY; PRT; 20 AA.
AC Q6LD18;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interferon alpha/beta receptor (Fragment).
GN Name=IFNAR;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95047447; PubMed=7958966; DOI=10.1016/0378-1119(94)90710-2;
RA Lutfalla G., Uze G.;
RT "Structure of the murine interferon alpha/beta receptor-encoding gene:
RT high-frequency rearrangements in the interferon-resistant L1210 cell
RT line.";
RL Gene 148:343-346(1994).
DR EMBL; U06242; AAA65007.1; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
KW Receptor.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2204 MW; 9B9C1DF0C12EBC43 CRC64;

Query Match 69.6%; Score 16; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 2 FSTIW 6

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RESULT 13
AKH_LIBAU
ID AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -1- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; S10596; S10596.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Flight; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 8 8 Tryptophan amide.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 65.2%; Score 15; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 4 FTFSW 8

RESULT 14
Q7M3N6
ID Q7M3N6 PRELIMINARY; PRT; 9 AA.
AC Q7M3N6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Neuropeptide Grb-AST B4.
OS Gryllus bimaculatus (Two-spotted cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthoptera; Orthopteroidea; Ensifera; Gryllidae; Gryllinae;
OX Gryllus.
OX NCBI_TaxID=6999;
RN [1]
RP SEQUENCE.
RX MEDLINE=95403341; PubMed=7673141; DOI=10.1074/jbc.270.36.21103;
RA Lorenz M.W., Kellner R., Hoffmann K.H.;
RT "A family of neuropeptides that inhibit juvenile hormone biosynthesis
RT in the cricket, Gryllus bimaculatus.";
RL J. Biol. Chem. 270:21103-21108(1995).
DR PIR; D57444; D57444.
SQ SEQUENCE 9 AA; 1175 MW; 3860B871E9D40B03 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5

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Db 5 FHGSW 9 | | | | |

Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 15
Q8WGSE6 PRELIMINARY; PRT; 9 AA.

ID Q8WGSE6 AC Q8WGSE6
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 1 (Fragment).
OS Procamburus clarkii (Red swamp crayfish).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacodea; Cambaridae; Procambarus.
OX NCBI_TaxID=6728;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21884466; PubMed=11886621; DOI=10.1098/rspb.2001.1886;
RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
Cunningham C.W.;
RT "Mitochondrial gene rearrangements confirm the parallel evolution of
the crab-like form.";
RL EMBL; R. Soc. Lond., B, Biol. Sci. 269:345-350(2002).
RL EMBL; AF436024; AAL31599.1;
DR GO; GO:0005739; C:mitchondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1185 MW; 936BB9C733640321 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5 | | | | |
DB 1 FTXRW 5

RESULT 16
AKHX LOCFMI ID AKHX LOCFMI STANDARD; PRT; 10 AA.

ID P816726 AC P816726
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peptide hormone.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE
RC TISSUE=Corpora cardiaca;
RA Siegart K.J.;
RA Submitted (DEC-1998) to Swiss-Prote.
CC -|- FUNCTION: Probably involved in the regulation of locust
intermediary metabolism, behavior and/or development.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR InterPro; IPR02047; ANK.
DR PROSITE; PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Neuropeptide;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 10 10 Proline amide.
SQ SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match 65.2%; Score 15; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EXXXW 5 | | | | |
DB 4 FSRDW 8

RESULT 17
Q7M465 PRELIMINARY; PRT; 10 AA.

ID Q7M465 AC Q7M465
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Neuropeptide Pec-HrTH.
OS Platypleura capensis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Cicadoidea; Cicadidae;
OC Cicadinae; Platypleurini; Platypleura.
OX NCBI_TaxID=70904;
RN [1]
RP SEQUENCE.
RA Gaede C.G., Janssens M.P.E.;
RT "Cicadas contain novel members of the AKH/RPCH family peptides with
hypertrehalosaemic activity.";
RL Biol. Chem. Hoppe-Seyler 375:803-809(1994).
DR PIR; S53789; S53789.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
SQ SEQUENCE 10 AA; 1135 MW; 10823665A775B9C4 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EXXXW 5 | | | | |
DB 4 FSPSW 8

RESULT 18
Q70F01 PRELIMINARY; PRT; 10 AA.

ID Q70F01 AC Q70F01
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Calpastatin type 2 (Fragment).
GN Names-CAST;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21531263; PubMed=11673859; DOI=10.1006/abbi.2001.2546;
RA Parr T., Sensky P.L., Bardaley R.G., Buttery P.J.;
RT "Calpastatin expression in porcine cardiac and skeletal muscle and
partial gene structure.";
RL Arch. Biochem. Biophys. 395:1-13(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Parr T.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ583410; CAE47431.1; --
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1291 MW; CFF912436365BDD9 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
Db 3 FASW 7

RESULT 19

O79897 PRELIMINARY; PRT; 10 AA.
AC O79897
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Hoplocercus spinosus (Club-tail iguana).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hoplocercinae;
OC Hoplocercus.
OX NCBI_TaxID=52193;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97315309; PubMed=9169559;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Evolutionary shifts in three major structural features of the
RT Mitochondrial genome among iguanian lizards.";
RL J. Mol. Evol. 44:660-674(1997).
DR ENBL; U82683; AAC62284.1; -.
DR PIR; T17063; T17063.
DR GO; GO:0005739; C:mitochondrion; IEA.
FT NON TER 10
KW Mitochondrion.
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
Db 2 FISRW 6

RESULT 20

P92707 PRELIMINARY; PRT; 10 AA.
AC P92707
DT 01-MAY-1997 (T-EMBLrel. 03, Created)
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Platysaurus capensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Scincophora; Scincoidea;
OC Cardylidae; Platysaurus.
OX NCBI_TaxID=521175;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153826; PubMed=9000757;
RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
RT "Two novel gene orders and the role of light-strand replication in
RT rearrangement of the vertebrate mitochondrial genome.";
RL Mol. Biol. Evol. 14:91-104(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
RT structures of mitochondrial transfer RNAs.";

RL Mol. Biol. Evol. 14:30-39(1997).
DR ENBL; U71329; AAB48286.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1322 MW; 0A3480C9D36415B0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
Db 2 FISRW 6

RESULT 21

Q6UJL5 PRELIMINARY; PRT; 10 AA.
AC Q6UJL5
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Strophurus pulcher.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Strophurus.
OX NCBI_TaxID=255186;
RN [1]
RP SEQUENCE FROM N.A.
RA Melville J., Schulte J.A. II, Larson A.;
RT "A Molecular Study of Phylogenetic Relationships and Evolution of
RT Antipredator Strategies in Australian Diploctylus Geckos, Subgenus
RT Strophurus.";
RL Biol. J. Linn. Soc. Lond. 82:123-138(2004).
DR ENBL; AY369011; AAR18865.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
Db 2 FISRW 6

RESULT 22

Q6WBU4 PRELIMINARY; PRT; 10 AA.
AC Q6WBU4
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Sceloporus siniferus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Sceloporus.
OX NCBI_TaxID=59719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";
RL Science 301:961-964(2003).

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DR EMBL; AV297494; AAP84453.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1303 MW; 933480C733640451 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 2 FTNRW 6

RESULT 23
Q6X0E7 PRELIMINARY; PRT; 10 AA.
AC Q6X0E7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Anolis marcanoi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=75264;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990428; PubMed=14628926;
RA Glor R.E., Kolbe J.J., Powell R., Larson A., Losos J.B.;
RT "Phylogenetic analysis of ecological and morphological diversification
in Hispaniolan trunk-ground anoles (Anolis cybotes group).";
RL Evolution 57:2383-2397(2003).
DR EMBL; AV263006; AAP94301.1; -.
DR EMBL; AV263005; AAP94298.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1370 MW; C93480C9D36411A9 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 2 FTNRW 6

RESULT 24
Q71DW3 PRELIMINARY; PRT; 10 AA.
AC Q71DW3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Polychrus marmoratus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Polychrus.
OX NCBI_TaxID=38934;
RN [1]
RP SEQUENCE FROM N.A.
RX Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
and morphological data and a phylogenetic taxonomy of iguanian
lizards.";
RL Herpetologica 59:399-419(2003).
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RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528738; AAQ09176.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 2 FITRW 6

RESULT 25
Q71DW6 PRELIMINARY; PRT; 10 AA.
AC Q71DW6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Polychrus acutirostris (Iguanid lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Polychrus.
OX NCBI_TaxID=161137;
RN [1]
RP SEQUENCE FROM N.A.
RX Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
and morphological data and a phylogenetic taxonomy of iguanian
lizards.";
RL Herpetologica 59:399-419(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528737; AAQ09173.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 2 FITRW 6

RESULT 26
Q71DW9 PRELIMINARY; PRT; 10 AA.
AC Q71DW9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Anisolepis longicauda.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anisolepis.
OX NCBI_TaxID=161142;
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RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
RT and morphological data and a phylogenetic taxonomy of Iguanian
RT lizards.";
RL Herpetologica 59:399-419 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528736; AA009170.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 2 FISRW 6

RESULT 27
Q71E17 PRELIMINARY; PRT; 10 AA.
AC Q71E17;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Morunasaurus annularis;
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hoplacercinae;
OC Morunasaurus;
OX NCBI_TaxID=211988;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
RT and morphological data and a phylogenetic taxonomy of Iguanian
RT lizards.";
RL Herpetologica 59:399-419 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528720; AA009122.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 2 FISRW 6

RESULT 28
Q71E20 PRELIMINARY; PRT; 10 AA.
AC Q71E20;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Emyalioides laticeps (Amazon wood lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hoplacercinae;
OC Emyalioides;
OX NCBI_TaxID=51206;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
RT and morphological data and a phylogenetic taxonomy of Iguanian
RT lizards.";
RL Herpetologica 59:399-419 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528719; AA009119.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 2 FISRW 6

RESULT 29
Q9ZYT2 PRELIMINARY; PRT; 10 AA.
AC Q9ZYT2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Leiocephalus carinatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae;
OC Leiocephalus;
OX NCBI_TaxID=81825;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99162288; PubMed=10051389; DOI=10.1006/mpev.1998.0541;
RA Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT "Molecular tests of phylogenetic taxonomies: a general procedure and
RT example using four subfamilies of the lizard family Iguanidae.";
RL Mol. Phylogenet. Evol. 10:367-376(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Macey J.R., Larson A., Papenfuss T.J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF049864; AA002535.1; -.
DR PIR; T12325; T12325.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

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Db      2 FITRW 6
RESULT 30
Q8WESO
ID Q8WESO PRELIMINARY; PRT; 11 AA.
AC Q8WESO;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Ceratophora karu.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Ceratophora.
OX NCBI_TaxID=118086;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2165505; PubMed=11796034; DOI=10.1006/mpev.2001.1041;
RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;
RT "Rostral horn evolution among agamid lizards of the genus Ceratophora
RT endemic to Sri Lanka.";
RL Mol. Phylogenet. Evol. 22:111-117(2002).
DR EMBL; AF128520; AAL67604.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 3 FLTRW 7

RESULT 31
Q9G365
ID Q9G365 PRELIMINARY; PRT; 11 AA.
AC Q9G365;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Calotes emma.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=52214;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
RT structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128477; AAG00668.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1341 MW; 4B2D371E336415B7 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128487; AAG00698.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 3 FLTRW 7

RESULT 32
Q9G368
ID Q9G368 PRELIMINARY; PRT; 11 AA.
AC Q9G368;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Draco blanfordii.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Draco.
OX NCBI_TaxID=89021;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
RT structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128477; AAG00668.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1341 MW; 4B2D371E336415B7 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 FXXW 5
Db 3 FLGRW 7

RESULT 33
Q9G5Y9
ID Q9G5Y9 PRELIMINARY; PRT; 11 AA.
AC Q9G5Y9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Pseudocalotes flavigula.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Pseudocalotes.
OX NCBI_TaxID=118227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AFI28503; AAG00746.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 3 FLTRW 7

RESULT 34
Q9G5Z2
ID Q9G5Z2 PRELIMINARY; PRT; 11 AA.
AC Q9G5Z2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Pseudocalotes brevipes;
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Pseudocalotes.
OX NCBI_TaxID=118226;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).

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[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AFI28502; AAG00743.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1389 MW; C92D371E336411A9 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 3 FLTRW 7

RESULT 35
Q9G601
ID Q9G601 PRELIMINARY; PRT; 11 AA.
AC Q9G601;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Bronchocele cristatella (Green crested lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Bronchocele.
OX NCBI_TaxID=118090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AFI28497; AAG00728.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 3 FLTRW 7

RESULT 36
Q9G625
ID Q9G625 PRELIMINARY; PRT; 11 AA.
AC Q9G625;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)

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DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Names=COI;
OS Calotes versicolor.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=48253;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128489; AAG00704.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03; 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 1 FXXXW 5
DB 3 FLTRW 7

RESULT 37
Q9G628 PRELIMINARY; PRT; 11 AA.
ID Q9G628
AC Q9G628
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Names=COI;
OS Calotes mystaceus.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=118097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128488; AAG00701.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.

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FT NON_TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03; 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 1 FXXXW 5
DB 3 FLTRW 7

RESULT 38
Q9G631 PRELIMINARY; PRT; 11 AA.
ID Q9G631
AC Q9G631
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Names=COI;
OS Calotes nigrilabris.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=118098;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128486; AAG00695.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03; 3; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 1 FXXXW 5
DB 3 FLTRW 7

RESULT 39
Q9G634 PRELIMINARY; PRT; 11 AA.
ID Q9G634
AC Q9G634
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Calotes liolepis.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=118096;
RN [1]

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Job time : 118.471 secs

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RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pathiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128485; AAC00692.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 3 FLTRW 7

RESULT 40
Q9G640
ID Q9G640 PRELIMINARY; PRT; 11 AA.
AC Q9G640;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (fragment).
GN Name=COI;
OS Calotes ceylonensis.
OC Mitochondrion.
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=118094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pathiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128483; AAC00686.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;
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Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 3 FLTRW 7

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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:58:45 ; Search time 102.588 Seconds
(without alignments)
32.505 Million cell updates/sec

Title: US-09-214-371-10

Perfect score: 23

Sequence: 1 FXXWXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1860064 seqs, 416830855 residues

Total number of hits satisfying chosen parameters: 377382

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 1000 summaries

Database : Published Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	17	73.9	9	14	US-10-072-419-8
7	17	73.9	9	16	US-10-869-768-3
8	17	73.9	9	16	US-10-869-768-8
9	17	73.9	9	18	US-10-818-036-14
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11	17	73.9	9	18	US-10-818-036-23
12	17	73.9	8	18	US-10-818-036-24
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131	16	69.6	13	9	US-09-785-215-19	Sequence 19, Appl	204	15	65.2	6	9	US-09-732-384-5	Sequence 34, Appl
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237	15	65.2	8	9	US-09-214-371-49	Sequence 49, Appl	310	15	65.2	8	18	US-10-946-647-346	Sequence 346, Appl
238	15	65.2	8	9	US-09-214-371-52	Sequence 52, Appl	311	15	65.2	8	18	US-10-946-647-621	Sequence 621, Appl
239	15	65.2	8	9	US-09-214-371-52	Sequence 52, Appl	312	15	65.2	8	18	US-10-946-647-621	Sequence 621, Appl
240	15	65.2	8	10	US-09-783-931-83	Sequence 83, Appl	313	15	65.2	8	18	US-10-776-521B-338	Sequence 338, Appl
241	15	65.2	8	14	US-10-209-372-31	Sequence 31, Appl	314	15	65.2	8	20	US-10-820-067A-848	Sequence 848, Appl
242	15	65.2	8	14	US-10-190-082-265	Sequence 265, Appl	315	15	65.2	8	20	US-11-051-411-203	Sequence 203, Appl
243	15	65.2	8	14	US-10-072-419-16	Sequence 16, Appl	316	15	65.2	8	20	US-11-051-411-345	Sequence 345, Appl
244	15	65.2	8	14	US-10-072-419-17	Sequence 17, Appl	317	15	65.2	8	20	US-11-051-411-475	Sequence 475, Appl
245	15	65.2	8	15	US-10-325-810-154	Sequence 154, Appl	318	15	65.2	8	20	US-11-051-411-690	Sequence 690, Appl
246	15	65.2	8	15	US-10-387-957-36	Sequence 36, Appl	319	15	65.2	8	20	US-11-051-411-902	Sequence 902, Appl
247	15	65.2	8	15	US-10-387-957-37	Sequence 37, Appl	320	15	65.2	8	20	US-11-051-411-1052	Sequence 1052, Appl
248	15	65.2	8	15	US-10-387-957-38	Sequence 38, Appl	321	15	65.2	8	20	US-11-013-537-39	Sequence 39, Appl
249	15	65.2	8	15	US-10-387-957-39	Sequence 39, Appl	322	15	65.2	9	8	US-08-821-739A-49	Sequence 49, Appl
250	15	65.2	8	15	US-10-387-934-36	Sequence 36, Appl	323	15	65.2	9	8	US-08-821-739A-53	Sequence 53, Appl
251	15	65.2	8	15	US-10-387-934-37	Sequence 37, Appl	324	15	65.2	9	9	US-09-214-371-37	Sequence 37, Appl
252	15	65.2	8	15	US-10-387-934-38	Sequence 38, Appl	325	15	65.2	9	9	US-09-214-371-38	Sequence 38, Appl
253	15	65.2	8	15	US-10-387-934-39	Sequence 39, Appl	326	15	65.2	9	9	US-09-764-304-12	Sequence 12, Appl
254	15	65.2	8	16	US-10-340-179-2	Sequence 2, Appl	327	15	65.2	9	9	US-09-862-260A-13	Sequence 13, Appl
255	15	65.2	8	16	US-10-340-179-3	Sequence 3, Appl	328	15	65.2	9	9	US-09-780-053-130	Sequence 130, Appl
256	15	65.2	8	16	US-10-387-955-36	Sequence 36, Appl	329	15	65.2	9	10	US-09-884-456-5	Sequence 5, Appl
257	15	65.2	8	16	US-10-387-955-37	Sequence 37, Appl	330	15	65.2	9	10	US-09-884-456-8	Sequence 8, Appl
258	15	65.2	8	16	US-10-387-955-38	Sequence 38, Appl	331	15	65.2	9	10	US-09-884-456-11	Sequence 11, Appl
259	15	65.2	8	16	US-10-387-955-39	Sequence 39, Appl	332	15	65.2	9	10	US-09-884-456-14	Sequence 14, Appl
260	15	65.2	8	16	US-10-869-768-16	Sequence 16, Appl	333	15	65.2	9	10	US-09-809-638-117	Sequence 117, Appl
261	15	65.2	8	16	US-10-869-768-17	Sequence 17, Appl	334	15	65.2	9	10	US-09-809-638-255	Sequence 255, Appl
262	15	65.2	8	16	US-10-877-124-154	Sequence 154, Appl	335	15	65.2	9	10	US-09-809-638-347	Sequence 347, Appl
263	15	65.2	8	16	US-10-877-022-154	Sequence 154, Appl	336	15	65.2	9	10	US-09-884-455-5	Sequence 5, Appl
264	15	65.2	8	16	US-10-488-219-36	Sequence 36, Appl	337	15	65.2	9	10	US-09-884-455-8	Sequence 8, Appl
265	15	65.2	8	16	US-10-488-219-37	Sequence 37, Appl	338	15	65.2	9	10	US-09-884-455-11	Sequence 11, Appl
266	15	65.2	8	16	US-10-488-219-38	Sequence 38, Appl	339	15	65.2	9	10	US-09-884-455-14	Sequence 14, Appl
267	15	65.2	8	16	US-10-488-219-39	Sequence 39, Appl	340	15	65.2	9	10	US-09-865-548A-186	Sequence 186, Appl
268	15	65.2	8	17	US-10-877-146-154	Sequence 154, Appl	341	15	65.2	9	11	US-09-920-480B-3	Sequence 3, Appl
269	15	65.2	8	17	US-10-480-954-49	Sequence 49, Appl	342	15	65.2	9	12	US-09-957-806A-62	Sequence 62, Appl
270	15	65.2	8	17	US-10-480-954-84	Sequence 84, Appl	343	15	65.2	9	13	US-09-957-806A-69	Sequence 69, Appl
271	15	65.2	8	17	US-10-480-954-86	Sequence 86, Appl	344	15	65.2	9	13	US-10-047-539-13	Sequence 13, Appl
272	15	65.2	8	17	US-10-480-954-88	Sequence 88, Appl	345	15	65.2	9	14	US-10-265-713-12	Sequence 12, Appl
273	15	65.2	8	17	US-10-480-954-90	Sequence 90, Appl	346	15	65.2	9	14	US-10-190-082-169	Sequence 169, Appl
274	15	65.2	8	17	US-10-480-954-92	Sequence 92, Appl	347	15	65.2	9	14	US-10-190-082-180	Sequence 180, Appl
275	15	65.2	8	17	US-10-480-954-94	Sequence 94, Appl	348	15	65.2	9	14	US-10-190-082-212	Sequence 212, Appl
276	15	65.2	8	17	US-10-480-954-96	Sequence 96, Appl	349	15	65.2	9	14	US-10-166-626-12	Sequence 12, Appl
277	15	65.2	8	17	US-10-480-954-98	Sequence 98, Appl	350	15	65.2	9	15	US-10-245-871-297	Sequence 297, Appl
278	15	65.2	8	17	US-10-480-954-113	Sequence 113, Appl	351	15	65.2	9	15	US-10-363-204-198	Sequence 198, Appl
279	15	65.2	8	17	US-10-480-954-115	Sequence 115, Appl	352	15	65.2	9	16	US-10-363-204-198	Sequence 198, Appl
280	15	65.2	8	17	US-10-480-954-117	Sequence 117, Appl	353	15	65.2	9	16	US-10-793-943-7	Sequence 7, Appl
281	15	65.2	8	17	US-10-480-954-119	Sequence 119, Appl	354	15	65.2	9	17	US-10-705-459-186	Sequence 186, Appl
282	15	65.2	8	17	US-10-480-954-121	Sequence 121, Appl	355	15	65.2	9	17	US-10-654-601-2374	Sequence 2374, Appl
283	15	65.2	8	17	US-10-480-954-123	Sequence 123, Appl	356	15	65.2	9	18	US-10-927-262A-37	Sequence 37, Appl
284	15	65.2	8	17	US-10-480-954-125	Sequence 125, Appl	357	15	65.2	9	18	US-10-927-262A-38	Sequence 38, Appl
285	15	65.2	8	17	US-10-480-954-143	Sequence 143, Appl	358	15	65.2	9	18	US-10-149-137A-540	Sequence 540, Appl
286	15	65.2	8	17	US-10-480-954-145	Sequence 145, Appl	359	15	65.2	9	18	US-10-953-901-690	Sequence 690, Appl
287	15	65.2	8	17	US-10-480-954-147	Sequence 147, Appl	360	15	65.2	9	18	US-10-953-901-690	Sequence 690, Appl
288	15	65.2	8	17	US-10-480-954-149	Sequence 149, Appl	361	15	65.2	9	18	US-10-510-523-33	Sequence 33, Appl
289	15	65.2	8	17	US-10-480-954-151	Sequence 151, Appl	362	15	65.2	9	18	US-10-510-523-34	Sequence 34, Appl
290	15	65.2	8	17	US-10-480-954-153	Sequence 153, Appl	363	15	65.2	9	20	US-11-051-411-73	Sequence 73, Appl
291	15	65.2	8	17	US-10-480-954-155	Sequence 155, Appl	364	15	65.2	9	20	US-11-051-411-281	Sequence 281, Appl
292	15	65.2	8	17	US-10-480-954-157	Sequence 157, Appl	365	15	65.2	9	20	US-11-051-411-346	Sequence 346, Appl
293	15	65.2	8	17	US-10-480-954-166	Sequence 166, Appl	366	15	65.2	9	20	US-11-051-411-473	Sequence 473, Appl
294	15	65.2	8	17	US-10-480-954-168	Sequence 168, Appl	367	15	65.2	9	20	US-11-051-411-607	Sequence 607, Appl
295	15	65.2	8	17	US-10-480-954-170	Sequence 170, Appl	368	15	65.2	9	20	US-11-051-411-1053	Sequence 1053, Appl
296	15	65.2	8	17	US-10-480-954-172	Sequence 172, Appl	369	15	65.2	9	20	US-09-214-371-35	Sequence 35, Appl
297	15	65.2	8	17	US-10-480-954-174	Sequence 174, Appl	370	15	65.2	10	9	US-09-214-371-36	Sequence 36, Appl
298	15	65.2	8	17	US-10-480-954-176	Sequence 176, Appl	371	15	65.2	10	9	US-09-767-460-53	Sequence 53, Appl
299	15	65.2	8	17	US-10-480-954-178	Sequence 178, Appl	372	15	65.2	10	9	US-09-767-460-53	Sequence 53, Appl
300	15	65.2	8	17	US-10-480-954-180	Sequence 180, Appl	373	15	65.2	10	9	US-09-767-460-53	Sequence 53, Appl
301	15	65.2	8	18	US-10-927-262A-12	Sequence 12, Appl	374	15	65.2	10	9	US-09-767-460-53	Sequence 53, Appl
302	15	65.2	8	18	US-10-927-262A-13	Sequence 13, Appl	375	15	65.2	10	9	US-09-767-460-53	Sequence 53, Appl
303	15	65.2	8	18	US-10-927-262A-21	Sequence 21, Appl	376	15	65.2	10	9	US-09-767-460-53	Sequence 53, Appl

377	15	65.2	10	9	US-09-780-053-175	Sequence 175, App	450	15	65.2	10	18	US-10-818-036-20	Sequence 20, Appl
378	15	65.2	10	9	US-09-826-290-390	Sequence 390, App	451	15	65.2	10	20	US-11-003-951-93	Sequence 93, Appl
379	15	65.2	10	10	US-09-809-638-187	Sequence 187, App	452	15	65.2	10	20	US-11-009-443-85	Sequence 85, Appl
380	15	65.2	10	10	US-09-809-638-273	Sequence 273, App	453	15	65.2	10	20	US-11-051-411-15	Sequence 15, Appl
381	15	65.2	10	10	US-09-995-529-26	Sequence 26, Appl	454	15	65.2	10	20	US-11-051-411-74	Sequence 74, Appl
382	15	65.2	10	10	US-09-995-529-43	Sequence 43, Appl	455	15	65.2	10	20	US-11-051-411-282	Sequence 282, App
383	15	65.2	10	10	US-09-995-529-44	Sequence 44, Appl	456	15	65.2	10	20	US-11-051-411-474	Sequence 474, App
384	15	65.2	10	10	US-09-995-529-45	Sequence 45, Appl	457	15	65.2	10	20	US-11-051-411-502	Sequence 502, App
385	15	65.2	10	10	US-09-995-529-46	Sequence 46, Appl	458	15	65.2	11	10	US-09-840-085-31	Sequence 31, Appl
386	15	65.2	10	10	US-09-995-529-47	Sequence 47, Appl	459	15	65.2	11	14	US-10-014-340-216	Sequence 216, App
387	15	65.2	10	10	US-09-995-798-10	Sequence 10, Appl	460	15	65.2	11	15	US-10-398-104-162	Sequence 162, App
388	15	65.2	10	11	US-09-995-529-26	Sequence 26, Appl	461	15	65.2	11	16	US-10-793-943-5	Sequence 5, Appli
389	15	65.2	10	11	US-09-995-529-43	Sequence 43, Appl	462	15	65.2	11	17	US-10-659-207-444	Sequence 444, App
390	15	65.2	10	11	US-09-995-529-44	Sequence 44, Appl	463	15	65.2	11	17	US-10-656-250-46	Sequence 46, Appl
391	15	65.2	10	11	US-09-995-529-45	Sequence 45, Appl	464	15	65.2	11	17	US-10-656-250-171	Sequence 171, App
392	15	65.2	10	11	US-09-995-529-46	Sequence 46, Appl	465	15	65.2	11	20	US-11-051-411-21	Sequence 21, Appl
393	15	65.2	10	11	US-09-995-529-47	Sequence 47, Appl	466	15	65.2	11	20	US-11-051-411-162	Sequence 162, App
394	15	65.2	10	14	US-10-094-401-172	Sequence 172, App	467	15	65.2	11	20	US-11-051-411-222	Sequence 222, App
395	15	65.2	10	14	US-10-190-082-167	Sequence 167, App	468	15	65.2	11	20	US-11-051-411-325	Sequence 325, App
396	15	65.2	10	14	US-10-190-082-170	Sequence 170, App	469	15	65.2	11	20	US-11-051-411-584	Sequence 584, App
397	15	65.2	10	14	US-10-190-082-171	Sequence 171, App	470	15	65.2	11	20	US-11-051-411-744	Sequence 744, App
398	15	65.2	10	14	US-10-190-082-178	Sequence 178, App	471	15	65.2	11	20	US-11-051-411-949	Sequence 949, App
399	15	65.2	10	14	US-10-190-082-276	Sequence 276, App	472	15	65.2	12	9	US-09-214-371-7	Sequence 7, Appli
400	15	65.2	10	14	US-10-190-082-230	Sequence 290, App	473	15	65.2	12	9	US-09-214-371-17	Sequence 17, Appl
401	15	65.2	10	14	US-10-160-506-29	Sequence 29, Appl	474	15	65.2	12	9	US-09-214-371-18	Sequence 18, Appl
402	15	65.2	10	14	US-10-072-419-32	Sequence 32, Appl	475	15	65.2	12	9	US-09-214-371-20	Sequence 20, Appl
403	15	65.2	10	14	US-10-031-874A-16	Sequence 16, Appl	476	15	65.2	12	9	US-09-214-371-24	Sequence 24, Appl
404	15	65.2	10	15	US-10-463-262-140	Sequence 140, App	477	15	65.2	12	9	US-09-214-371-25	Sequence 25, Appl
405	15	65.2	10	15	US-10-264-309-407	Sequence 407, App	478	15	65.2	12	9	US-09-214-371-26	Sequence 26, Appl
406	15	65.2	10	16	US-10-449-379-29	Sequence 29, Appl	479	15	65.2	12	9	US-09-214-371-31	Sequence 31, Appl
407	15	65.2	10	16	US-10-338-552-35	Sequence 35, Appl	480	15	65.2	12	9	US-09-214-371-64	Sequence 64, Appl
408	15	65.2	10	16	US-10-338-552-37	Sequence 37, Appl	481	15	65.2	12	10	US-09-820-053A-98	Sequence 98, Appl
409	15	65.2	10	16	US-10-338-552-39	Sequence 39, Appl	482	15	65.2	12	14	US-10-032-818-31	Sequence 31, Appl
410	15	65.2	10	16	US-10-338-552-41	Sequence 41, Appl	483	15	65.2	12	14	US-10-109-171-98	Sequence 98, Appl
411	15	65.2	10	16	US-10-338-627-35	Sequence 35, Appl	484	15	65.2	12	14	US-10-190-082-252	Sequence 252, App
412	15	65.2	10	16	US-10-338-627-37	Sequence 37, Appl	485	15	65.2	12	15	US-10-180-648-18	Sequence 18, Appl
413	15	65.2	10	16	US-10-338-627-39	Sequence 39, Appl	486	15	65.2	12	15	US-10-609-217-131	Sequence 131, App
414	15	65.2	10	16	US-10-338-627-41	Sequence 41, Appl	487	15	65.2	12	15	US-10-609-217-132	Sequence 132, App
415	15	65.2	10	16	US-10-688-015-29	Sequence 29, App	488	15	65.2	12	15	US-10-609-217-133	Sequence 133, App
416	15	65.2	10	16	US-10-450-036A-16	Sequence 16, Appl	489	15	65.2	12	15	US-10-609-217-134	Sequence 134, App
417	15	65.2	10	16	US-10-361-275-42	Sequence 42, App	490	15	65.2	12	15	US-10-609-217-137	Sequence 137, App
418	15	65.2	10	16	US-10-327-598-450	Sequence 450, App	491	15	65.2	12	15	US-10-609-217-143	Sequence 143, App
419	15	65.2	10	16	US-10-327-598-457	Sequence 457, App	492	15	65.2	12	15	US-10-609-217-144	Sequence 144, App
420	15	65.2	10	16	US-10-327-598-458	Sequence 458, App	493	15	65.2	12	15	US-10-609-217-145	Sequence 145, App
421	15	65.2	10	16	US-10-160-505-29	Sequence 29, Appl	494	15	65.2	12	15	US-10-609-217-146	Sequence 146, App
422	15	65.2	10	16	US-10-869-768-32	Sequence 32, Appl	495	15	65.2	12	15	US-10-632-388-131	Sequence 131, App
423	15	65.2	10	16	US-10-451-315A-8	Sequence 8, Appli	496	15	65.2	12	15	US-10-632-388-132	Sequence 132, App
424	15	65.2	10	17	US-10-823-253-1	Sequence 1, Appli	497	15	65.2	12	15	US-10-632-388-133	Sequence 133, App
425	15	65.2	10	17	US-10-823-253-11	Sequence 11, Appl	498	15	65.2	12	15	US-10-632-388-134	Sequence 134, App
426	15	65.2	10	17	US-10-823-253-19	Sequence 19, Appl	499	15	65.2	12	15	US-10-632-388-137	Sequence 137, App
427	15	65.2	10	17	US-10-823-253-26	Sequence 26, Appl	500	15	65.2	12	15	US-10-632-388-143	Sequence 143, App
428	15	65.2	10	17	US-10-769-308-29	Sequence 29, Appl	501	15	65.2	12	15	US-10-632-388-144	Sequence 144, App
429	15	65.2	10	17	US-10-725-962-61	Sequence 61, Appl	502	15	65.2	12	15	US-10-632-388-145	Sequence 145, App
430	15	65.2	10	17	US-10-777-829-53	Sequence 53, App	503	15	65.2	12	15	US-10-632-388-146	Sequence 146, App
431	15	65.2	10	17	US-10-777-829-72	Sequence 72, Appl	504	15	65.2	12	15	US-10-651-723-131	Sequence 131, App
432	15	65.2	10	17	US-10-879-994-67	Sequence 67, Appl	505	15	65.2	12	15	US-10-651-723-132	Sequence 132, App
433	15	65.2	10	17	US-10-726-332-128	Sequence 128, App	506	15	65.2	12	15	US-10-651-723-133	Sequence 133, App
434	15	65.2	10	17	US-10-769-074-29	Sequence 29, App	507	15	65.2	12	15	US-10-651-723-137	Sequence 137, App
435	15	65.2	10	17	US-10-818-067-53	Sequence 53, Appl	508	15	65.2	12	15	US-10-651-723-143	Sequence 143, App
436	15	65.2	10	17	US-10-818-067-72	Sequence 72, Appl	509	15	65.2	12	15	US-10-651-723-144	Sequence 144, App
437	15	65.2	10	18	US-10-996-316-138	Sequence 138, App	510	15	65.2	12	15	US-10-651-723-145	Sequence 145, App
438	15	65.2	10	18	US-10-996-316-147	Sequence 147, App	511	15	65.2	12	15	US-10-651-723-146	Sequence 146, App
439	15	65.2	10	18	US-10-996-316-148	Sequence 148, App	512	15	65.2	12	15	US-10-645-761-131	Sequence 131, App
440	15	65.2	10	18	US-10-927-262A-35	Sequence 35, Appl	513	15	65.2	12	15	US-10-645-761-132	Sequence 132, App
441	15	65.2	10	18	US-10-927-262A-36	Sequence 36, Appl	514	15	65.2	12	15	US-10-645-761-133	Sequence 133, App
442	15	65.2	10	18	US-10-823-810-1	Sequence 1, Appli	515	15	65.2	12	15	US-10-645-761-134	Sequence 134, App
443	15	65.2	10	18	US-10-823-810-11	Sequence 11, Appl	516	15	65.2	12	15	US-10-645-761-137	Sequence 137, App
444	15	65.2	10	18	US-10-823-810-19	Sequence 19, Appl	517	15	65.2	12	15	US-10-645-761-143	Sequence 143, App
445	15	65.2	10	18	US-10-823-810-26	Sequence 26, Appl	518	15	65.2	12	15	US-10-645-761-144	Sequence 144, App
446	15	65.2	10	18	US-10-727-737-19	Sequence 19, Appl	519	15	65.2	12	15	US-10-645-761-145	Sequence 145, App
447	15	65.2	10	18	US-10-727-737-21	Sequence 21, Appl	520	15	65.2	12	15	US-10-645-761-146	Sequence 146, App
448	15	65.2	10	18	US-10-727-737-22	Sequence 22, Appl	521	15	65.2	12	15	US-10-666-696-131	Sequence 131, App
449	15	65.2	10	18	US-10-264-309-407	Sequence 407, App	522	15	65.2	12	15		

523	15	65.2	12	15	US-10-666-696-132	Sequence 132, App	596	15	65.2	14	15	US-10-632-388-68	Sequence 68, Appl
524	15	65.2	12	15	US-10-666-696-133	Sequence 133, App	597	15	65.2	14	15	US-10-651-723-68	Sequence 68, Appl
525	15	65.2	12	15	US-10-666-696-134	Sequence 134, App	598	15	65.2	14	15	US-10-645-761-68	Sequence 68, Appl
526	15	65.2	12	15	US-10-666-696-137	Sequence 137, App	599	15	65.2	14	15	US-10-275-427A-13	Sequence 13, Appl
527	15	65.2	12	15	US-10-666-696-143	Sequence 143, App	600	15	65.2	14	15	US-10-666-696-68	Sequence 68, Appl
528	15	65.2	12	15	US-10-666-696-144	Sequence 144, App	601	15	65.2	14	15	US-10-653-048-68	Sequence 68, Appl
529	15	65.2	12	15	US-10-666-696-145	Sequence 145, App	602	15	65.2	14	15	US-10-387-955-61	Sequence 61, Appl
530	15	65.2	12	15	US-10-666-696-146	Sequence 146, App	603	15	65.2	14	16	US-10-712-447-158	Sequence 158, App
531	15	65.2	12	15	US-10-653-048-131	Sequence 131, App	604	15	65.2	14	16	US-10-712-447-159	Sequence 159, App
532	15	65.2	12	15	US-10-653-048-132	Sequence 132, App	605	15	65.2	14	16	US-10-712-447-160	Sequence 160, App
533	15	65.2	12	15	US-10-653-048-133	Sequence 133, App	606	15	65.2	14	16	US-10-712-447-194	Sequence 194, App
534	15	65.2	12	15	US-10-653-048-134	Sequence 134, App	607	15	65.2	14	16	US-10-712-447-195	Sequence 195, App
535	15	65.2	12	15	US-10-653-048-137	Sequence 137, App	608	15	65.2	14	16	US-10-712-447-196	Sequence 196, App
536	15	65.2	12	15	US-10-653-048-143	Sequence 143, App	609	15	65.2	14	16	US-10-712-447-204	Sequence 204, App
537	15	65.2	12	15	US-10-653-048-144	Sequence 144, App	610	15	65.2	14	16	US-10-865-478-854	Sequence 854, App
538	15	65.2	12	15	US-10-653-048-145	Sequence 145, App	611	15	65.2	14	17	US-10-808-187-1052	Sequence 1052, App
539	15	65.2	12	15	US-10-653-048-146	Sequence 146, App	612	15	65.2	14	18	US-10-645-784-68	Sequence 68, Appl
540	15	65.2	12	16	US-10-467-758-27	Sequence 27, App	613	15	65.2	14	18	US-10-853-973A-80	Sequence 80, Appl
541	15	65.2	12	16	US-10-467-758-31	Sequence 31, App	614	15	65.2	14	18	US-10-927-262A-33	Sequence 33, Appl
542	15	65.2	12	16	US-10-467-758-33	Sequence 33, App	615	15	65.2	14	18	US-10-927-262A-34	Sequence 34, Appl
543	15	65.2	12	16	US-10-467-758-36	Sequence 36, App	616	15	65.2	14	18	US-10-807-807-1052	Sequence 1052, App
544	15	65.2	12	16	US-10-363-204-228	Sequence 228, App	617	15	65.2	14	20	US-11-093-103-45	Sequence 45, Appl
545	15	65.2	12	16	US-10-649-873-61	Sequence 61, App	618	15	65.2	15	9	US-09-214-371-8	Sequence 8, Appl
546	15	65.2	12	16	US-10-839-525-98	Sequence 98, App	619	15	65.2	15	9	US-09-214-371-29	Sequence 29, Appl
547	15	65.2	12	17	US-10-873-848B-1	Sequence 1, Appl	620	15	65.2	15	9	US-09-214-371-30	Sequence 30, Appl
548	15	65.2	12	18	US-10-645-784-131	Sequence 131, App	621	15	65.2	15	9	US-09-214-371-66	Sequence 66, Appl
549	15	65.2	12	18	US-10-645-784-132	Sequence 132, App	622	15	65.2	15	9	US-09-829-549A-23	Sequence 23, Appl
550	15	65.2	12	18	US-10-645-784-133	Sequence 133, App	623	15	65.2	15	9	US-09-258-981-3	Sequence 3, Appl
551	15	65.2	12	18	US-10-645-784-134	Sequence 134, App	624	15	65.2	15	9	US-09-950-692-6	Sequence 6, Appl
552	15	65.2	12	18	US-10-645-784-137	Sequence 137, App	625	15	65.2	15	9	US-09-953-510-51	Sequence 51, Appl
553	15	65.2	12	18	US-10-645-784-143	Sequence 143, App	626	15	65.2	15	9	US-09-953-510-52	Sequence 52, Appl
554	15	65.2	12	18	US-10-645-784-144	Sequence 144, App	627	15	65.2	15	9	US-09-732-384-6	Sequence 6, Appl
555	15	65.2	12	18	US-10-645-784-145	Sequence 145, App	628	15	65.2	15	10	US-09-894-594-31	Sequence 31, Appl
556	15	65.2	12	18	US-10-645-784-146	Sequence 146, App	629	15	65.2	15	10	US-09-894-594-43	Sequence 43, Appl
557	15	65.2	12	18	US-10-927-262A-7	Sequence 7, Appl	630	15	65.2	15	10	US-09-952-680A-55	Sequence 55, Appl
558	15	65.2	12	18	US-10-927-262A-17	Sequence 17, App	631	15	65.2	15	10	US-09-840-085-33	Sequence 33, Appl
559	15	65.2	12	18	US-10-927-262A-18	Sequence 18, App	632	15	65.2	15	10	US-09-840-085-37	Sequence 37, Appl
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561	15	65.2	12	18	US-10-927-262A-24	Sequence 24, App	634	15	65.2	15	11	US-09-953-413-52	Sequence 52, Appl
562	15	65.2	12	18	US-10-927-262A-25	Sequence 25, App	635	15	65.2	15	14	US-10-067-649-90	Sequence 90, Appl
563	15	65.2	12	18	US-10-927-262A-26	Sequence 26, App	636	15	65.2	15	14	US-10-186-867-28	Sequence 28, Appl
564	15	65.2	12	18	US-10-927-262A-31	Sequence 31, App	637	15	65.2	15	14	US-10-186-867-29	Sequence 29, Appl
565	15	65.2	12	18	US-10-927-262A-64	Sequence 64, App	638	15	65.2	15	14	US-10-211-088-141	Sequence 141, App
566	15	65.2	12	18	US-10-312-637-1	Sequence 1, App	639	15	65.2	15	14	US-10-147-255-51	Sequence 51, Appl
567	15	65.2	12	20	US-11-136-186-98	Sequence 98, App	640	15	65.2	15	14	US-10-147-255-52	Sequence 52, Appl
568	15	65.2	13	14	US-10-058-053A-275	Sequence 275, App	641	15	65.2	15	14	US-10-239-313A-667	Sequence 667, App
569	15	65.2	13	14	US-10-300-694A-18	Sequence 18, App	642	15	65.2	15	14	US-10-080-608A-165	Sequence 165, App
570	15	65.2	13	14	US-10-113-512-1	Sequence 1, Appl	643	15	65.2	15	14	US-10-293-693-90	Sequence 90, Appl
571	15	65.2	13	16	US-10-838-226-275	Sequence 275, App	644	15	65.2	15	15	US-10-370-685-74	Sequence 74, Appl
572	15	65.2	13	16	US-10-468-496-692	Sequence 692, App	645	15	65.2	15	15	US-10-375-157-64	Sequence 64, Appl
573	15	65.2	13	16	US-10-468-496-693	Sequence 693, App	646	15	65.2	15	15	US-10-609-217-139	Sequence 139, App
574	15	65.2	13	16	US-10-468-496-694	Sequence 694, App	647	15	65.2	15	15	US-10-609-217-140	Sequence 140, App
575	15	65.2	13	16	US-10-468-496-695	Sequence 695, App	648	15	65.2	15	15	US-10-609-217-141	Sequence 141, App
576	15	65.2	13	16	US-10-468-496-1718	Sequence 1718, App	649	15	65.2	15	15	US-10-425-970-4	Sequence 4, Appl
577	15	65.2	13	16	US-10-468-496-1719	Sequence 1719, App	650	15	65.2	15	15	US-10-632-388-139	Sequence 139, App
578	15	65.2	13	16	US-10-468-496-1720	Sequence 1720, App	651	15	65.2	15	15	US-10-632-388-140	Sequence 140, App
579	15	65.2	13	16	US-10-468-496-1721	Sequence 1721, App	652	15	65.2	15	15	US-10-632-388-141	Sequence 141, App
580	15	65.2	13	16	US-10-495-146-185	Sequence 185, App	653	15	65.2	15	15	US-10-651-723-139	Sequence 139, App
581	15	65.2	13	16	US-10-495-146-186	Sequence 186, App	654	15	65.2	15	15	US-10-651-723-140	Sequence 140, App
582	15	65.2	13	16	US-10-495-146-187	Sequence 187, App	655	15	65.2	15	15	US-10-651-723-141	Sequence 141, App
583	15	65.2	13	16	US-10-495-146-188	Sequence 188, App	656	15	65.2	15	15	US-10-645-761-139	Sequence 139, App
584	15	65.2	13	16	US-10-793-943-4	Sequence 4, Appl	657	15	65.2	15	15	US-10-645-761-140	Sequence 140, App
585	15	65.2	13	18	US-10-948-707-1379	Sequence 1379, App	658	15	65.2	15	15	US-10-645-761-141	Sequence 141, App
586	15	65.2	13	20	US-11-093-103-7	Sequence 7, Appl	659	15	65.2	15	15	US-10-666-696-139	Sequence 139, App
587	15	65.2	14	9	US-09-214-371-33	Sequence 33, App	660	15	65.2	15	15	US-10-666-696-140	Sequence 140, App
588	15	65.2	14	9	US-09-214-371-34	Sequence 34, App	661	15	65.2	15	15	US-10-666-696-141	Sequence 141, App
589	15	65.2	14	14	US-10-186-867-7	Sequence 7, Appl	662	15	65.2	15	15	US-10-653-048-139	Sequence 139, App
590	15	65.2	14	14	US-10-083-768-33	Sequence 33, App	663	15	65.2	15	15	US-10-653-048-140	Sequence 140, App
591	15	65.2	14	14	US-10-083-768-213	Sequence 213, App	664	15	65.2	15	16	US-10-653-048-141	Sequence 141, App
592	15	65.2	14	15	US-10-435-766-80	Sequence 80, App	665	15	65.2	15	16	US-10-775-965-74	Sequence 74, Appl
593	15	65.2	14	15	US-10-436-715-430	Sequence 430, App	666	15	65.2	15	16	US-10-213-982-55	Sequence 55, Appl
594	15	65.2	14	15	US-10-436-715-442	Sequence 442, App	667	15	65.2	15	16	US-10-695-155-51	Sequence 51, Appl
595	15	65.2	14	15	US-10-609-217-68	Sequence 68, App	668	15	65.2	15	16	US-10-695-155-52	Sequence 52, Appl

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670	15	65.2	15	16	US-10-695-155-111	Sequence 111, App	743	15	18	20	US-11-093-103-48	Sequence 48, Appl	
671	15	65.2	15	16	US-10-495-146-23	Sequence 23, Appl	744	15	19	9	US-09-214-371-1	Sequence 1, Appl	
672	15	65.2	15	16	US-10-495-146-24	Sequence 24, App	745	15	65.2	19	9	US-09-732-357A-9	Sequence 9, Appl
673	15	65.2	15	16	US-10-495-146-25	Sequence 25, Appl	746	15	65.2	19	9	US-09-732-384-7	Sequence 7, Appl
674	15	65.2	15	16	US-10-495-146-26	Sequence 26, App	747	15	65.2	19	10	US-09-774-639-342	Sequence 342, App
675	15	65.2	15	16	US-10-793-943-3	Sequence 3, Appl	748	15	65.2	19	10	US-09-229-173-45	Sequence 45, Appl
676	15	65.2	15	17	US-10-182-613A-6	Sequence 6, Appl	749	15	65.2	19	10	US-09-977-797A-116	Sequence 116, App
677	15	65.2	15	17	US-10-182-613A-7	Sequence 7, Appl	750	15	65.2	19	10	US-09-969-730-289	Sequence 289, App
678	15	65.2	15	18	US-10-645-784-139	Sequence 139, App	751	15	65.2	19	13	US-10-155-059-13	Sequence 13, Appl
679	15	65.2	15	18	US-10-645-784-140	Sequence 140, App	752	15	65.2	19	14	US-10-144-929-231	Sequence 231, App
680	15	65.2	15	18	US-10-645-784-141	Sequence 141, App	753	15	65.2	19	14	US-10-225-567A-1318	Sequence 1318, Ap
681	15	65.2	15	18	US-10-927-262A-8	Sequence 8, Appl	754	15	65.2	19	14	US-10-300-694A-42	Sequence 42, Appl
682	15	65.2	15	18	US-10-927-262A-29	Sequence 29, Appl	755	15	65.2	19	14	US-10-029-386-28258	Sequence 28258, A
683	15	65.2	15	18	US-10-927-262A-30	Sequence 30, Appl	756	15	65.2	19	14	US-10-029-386-33510	Sequence 33510, A
684	15	65.2	15	18	US-10-927-262A-66	Sequence 66, Appl	757	15	65.2	19	15	US-10-120-885A-45	Sequence 45, Appl
685	15	65.2	15	18	US-10-862-195-2239	Sequence 2239, Ap	758	15	65.2	19	15	US-10-144-929-231	Sequence 231, App
686	15	65.2	15	18	US-10-754-473-30	Sequence 30, Appl	759	15	65.2	19	15	US-10-621-363-289	Sequence 289, App
687	15	65.2	15	20	US-11-051-411-1069	Sequence 1069, Ap	760	15	65.2	19	15	US-10-616-279-9	Sequence 9, Appl
688	15	65.2	15	20	US-11-051-411-1109	Sequence 1109, Ap	761	15	65.2	19	15	US-10-257-864A-100	Sequence 100, App
689	15	65.2	15	20	US-11-051-411-11469	Sequence 11469, Ap	762	15	65.2	19	15	US-10-328-953-14	Sequence 14, Appl
690	15	65.2	16	9	US-09-214-371-39	Sequence 39, Appl	763	15	65.2	19	15	US-10-399-518-129	Sequence 129, App
691	15	65.2	16	9	US-09-214-371-40	Sequence 40, Appl	764	15	65.2	19	16	US-10-624-884-9	Sequence 9, Appl
692	15	65.2	16	9	US-09-214-371-41	Sequence 41, Appl	765	15	65.2	19	16	US-10-754-457-9	Sequence 9, Appl
693	15	65.2	16	9	US-09-019-679-3	Sequence 3, Appl	766	15	65.2	19	16	US-10-399-585-128	Sequence 128, App
694	15	65.2	16	9	US-09-962-805-13	Sequence 13, Appl	767	15	65.2	19	16	US-10-645-085A-100	Sequence 100, App
695	15	65.2	16	9	US-09-813-333-20	Sequence 20, Appl	768	15	65.2	19	17	US-10-895-183-9	Sequence 9, Appl
696	15	65.2	16	10	US-09-825-517A-56	Sequence 56, Appl	769	15	65.2	19	17	US-10-637-317-58	Sequence 58, Appl
697	15	65.2	16	10	US-09-825-517A-105	Sequence 105, App	770	15	65.2	19	17	US-10-866-831-231	Sequence 231, App
698	15	65.2	16	10	US-09-825-517A-130	Sequence 130, App	771	15	65.2	19	17	US-10-947-352-37	Sequence 37, Appl
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700	15	65.2	16	13	US-10-044-703-20	Sequence 20, Appl	773	15	65.2	20	9	US-09-735-705-234	Sequence 234, App
701	15	65.2	16	14	US-10-223-047-19	Sequence 19, App	774	15	65.2	20	9	US-09-735-705-381	Sequence 381, App
702	15	65.2	16	14	US-10-094-401-220	Sequence 220, App	775	15	65.2	20	9	US-09-850-716A-381	Sequence 234, App
703	15	65.2	16	15	US-10-462-262-188	Sequence 188, App	776	15	65.2	20	9	US-09-850-716A-381	Sequence 381, App
704	15	65.2	16	15	US-10-239-103-20	Sequence 20, Appl	777	15	65.2	20	9	US-09-897-778-234	Sequence 234, App
705	15	65.2	16	16	US-10-467-758-14	Sequence 14, Appl	778	15	65.2	20	9	US-09-897-778-381	Sequence 381, App
706	15	65.2	16	18	US-10-927-262A-39	Sequence 39, Appl	779	15	65.2	20	10	US-09-764-891-4348	Sequence 4348, Ap
707	15	65.2	16	18	US-10-927-262A-40	Sequence 40, Appl	780	15	65.2	20	13	US-10-155-059-8	Sequence 8, Appl
708	15	65.2	16	18	US-10-927-262A-41	Sequence 41, Appl	781	15	65.2	20	13	US-10-155-059-10	Sequence 10, Appl
709	15	65.2	16	20	US-11-045-477-56	Sequence 56, Appl	782	15	65.2	20	13	US-10-155-059-11	Sequence 11, Appl
710	15	65.2	16	20	US-11-045-477-105	Sequence 105, App	783	15	65.2	20	13	US-10-155-059-14	Sequence 14, Appl
711	15	65.2	16	20	US-11-045-477-130	Sequence 130, App	784	15	65.2	20	13	US-10-155-059-15	Sequence 15, Appl
712	15	65.2	16	20	US-11-045-477-137	Sequence 137, App	785	15	65.2	20	13	US-10-155-059-16	Sequence 16, Appl
713	15	65.2	17	14	US-10-280-066-83	Sequence 83, Appl	786	15	65.2	20	13	US-10-155-059-19	Sequence 19, Appl
714	15	65.2	17	14	US-10-029-386-27504	Sequence 27504, A	787	15	65.2	20	13	US-10-155-059-20	Sequence 20, Appl
715	15	65.2	17	14	US-10-029-386-28133	Sequence 28133, A	788	15	65.2	20	14	US-10-007-700-234	Sequence 234, App
716	15	65.2	17	16	US-10-120-885A-44	Sequence 44, Appl	789	15	65.2	20	14	US-10-007-700-381	Sequence 381, App
717	15	65.2	17	16	US-10-258-144-248	Sequence 248, App	790	15	65.2	20	14	US-10-205-428-377	Sequence 377, App
718	15	65.2	17	16	US-10-258-144-258	Sequence 258, App	791	15	65.2	20	14	US-10-162-538-11	Sequence 11, Appl
719	15	65.2	17	16	US-10-258-144-442	Sequence 442, App	792	15	65.2	20	14	US-10-117-982-234	Sequence 234, App
720	15	65.2	17	16	US-10-695-155-155	Sequence 155, App	793	15	65.2	20	14	US-10-117-982-381	Sequence 381, App
721	15	65.2	17	17	US-10-661-156-93	Sequence 93, Appl	794	15	65.2	20	14	US-10-280-066-286	Sequence 286, App
722	15	65.2	17	18	US-10-946-647-66	Sequence 66, Appl	795	15	65.2	20	14	US-10-280-066-316	Sequence 316, App
723	15	65.2	18	9	US-09-214-371-74	Sequence 74, Appl	796	15	65.2	20	14	US-10-280-066-343	Sequence 343, App
724	15	65.2	18	10	US-09-896-841A-48	Sequence 48, Appl	797	15	65.2	20	14	US-10-029-386-33058	Sequence 33058, A
725	15	65.2	18	10	US-09-896-841A-49	Sequence 49, Appl	798	15	65.2	20	15	US-10-329-087-26	Sequence 26, Appl
726	15	65.2	18	14	US-10-225-567A-2147	Sequence 2147, Ap	799	15	65.2	20	15	US-10-329-087-31	Sequence 31, Appl
727	15	65.2	18	14	US-10-187-215-48	Sequence 48, Appl	800	15	65.2	20	15	US-10-313-986-234	Sequence 234, App
728	15	65.2	18	14	US-10-187-215-49	Sequence 49, Appl	801	15	65.2	20	15	US-10-313-986-381	Sequence 381, App
729	15	65.2	18	15	US-10-273-386-48	Sequence 48, Appl	802	15	65.2	20	15	US-10-644-703-14	Sequence 14, Appl
730	15	65.2	18	15	US-10-273-386-49	Sequence 49, Appl	803	15	65.2	20	16	US-10-666-480-5	Sequence 5, Appl
731	15	65.2	18	16	US-10-258-144-268	Sequence 268, App	804	15	65.2	20	16	US-10-467-758-8	Sequence 8, Appl
732	15	65.2	18	16	US-10-258-144-358	Sequence 358, App	805	15	65.2	20	16	US-10-467-758-9	Sequence 9, Appl
733	15	65.2	18	16	US-10-742-379-68	Sequence 68, App	806	15	65.2	20	16	US-10-775-972-234	Sequence 234, App
734	15	65.2	18	16	US-10-468-655-28	Sequence 28, Appl	807	15	65.2	20	16	US-10-775-972-381	Sequence 381, App
735	15	65.2	18	16	US-10-649-378A-51	Sequence 51, Appl	808	15	65.2	20	16	US-10-660-370-154	Sequence 154, App
736	15	65.2	18	16	US-10-649-378A-52	Sequence 52, Appl	809	15	65.2	20	17	US-10-660-370-154	Sequence 154, App
737	15	65.2	18	16	US-10-423-830-48	Sequence 48, Appl	810	15	65.2	20	17	US-10-661-156-181	Sequence 181, App
738	15	65.2	18	17	US-10-423-830-49	Sequence 49, Appl	811	15	65.2	20	17	US-10-661-156-181	Sequence 181, App
739	15	65.2	18	17	US-10-913-937-8	Sequence 8, Appl	812	15	65.2	20	17	US-10-926-683-1481	Sequence 1481, Ap
740	15	65.2	18	17	US-10-661-156-107	Sequence 107, App	813	15	65.2	20	17	US-10-690-276-394	Sequence 394, App
741	15	65.2	18	18	US-10-927-262A-74	Sequence 74, Appl	814	15	65.2	20	17	US-10-690-276-443	Sequence 443, App

815	15	65.2	20	18	US-10-922-124-234	Sequence 234, App	888	14	60.9	8	15	US-10-260-937-89	Sequence 89, Appl
816	15	65.2	20	18	US-10-922-124-381	Sequence 381, App	889	14	60.9	8	15	US-10-367-580-156	Sequence 156, App
817	15	65.2	20	18	US-10-792-582-456	Sequence 456, App	890	14	60.9	8	15	US-10-367-580-211	Sequence 211, App
818	15	65.2	20	18	US-10-518-358-1	Sequence 1, Appli	891	14	60.9	8	15	US-10-367-593-156	Sequence 156, App
819	15	65.2	20	18	US-10-518-358-2	Sequence 2, Appli	892	14	60.9	8	15	US-10-367-593-211	Sequence 211, App
820	15	65.2	20	18	US-10-518-358-3	Sequence 3, Appli	893	14	60.9	8	15	US-10-367-594-156	Sequence 156, App
821	15	65.2	20	20	US-11-066-697-1366	Sequence 1366, Ap	894	14	60.9	8	15	US-10-367-594-211	Sequence 211, App
822	15	65.2	20	20	US-11-065-970-27	Sequence 27, Appl	895	14	60.9	8	15	US-10-367-654-156	Sequence 156, App
823	15	65.2	20	20	US-11-075-234-257	Sequence 257, App	896	14	60.9	8	15	US-10-367-654-211	Sequence 211, App
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826	14	60.9	5	9	US-09-281-717-3	Sequence 3, Appli	899	14	60.9	8	15	US-10-367-668-156	Sequence 156, App
827	14	60.9	5	12	US-09-957-806A-226	Sequence 226, App	900	14	60.9	8	15	US-10-367-668-211	Sequence 211, App
828	14	60.9	5	15	US-10-436-549-16	Sequence 16, App	901	14	60.9	8	16	US-10-440-390-52	Sequence 52, Appl
829	14	60.9	5	15	US-10-126-962-3	Sequence 3, Appli	902	14	60.9	8	16	US-10-440-390-89	Sequence 89, Appl
830	14	60.9	5	16	US-10-777-053-801	Sequence 801, App	903	14	60.9	8	16	US-10-367-674-156	Sequence 156, App
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833	14	60.9	5	16	US-10-712-425-16	Sequence 16, Appl	906	14	60.9	8	16	US-10-869-768-5	Sequence 6, Appli
834	14	60.9	5	16	US-10-837-217-801	Sequence 801, App	907	14	60.9	8	16	US-10-869-768-6	Sequence 7, Appli
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854	14	60.9	7	10	US-09-750-754-70	Sequence 70, Appl	927	14	60.9	8	17	US-10-480-954-23	Sequence 23, Appl
855	14	60.9	7	10	US-09-750-754-79	Sequence 79, Appl	928	14	60.9	8	17	US-10-480-954-25	Sequence 25, Appl
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858	14	60.9	7	15	US-10-126-962-7	Sequence 7, Appli	931	14	60.9	8	17	US-10-480-954-31	Sequence 31, Appl
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862	14	60.9	7	18	US-10-989-462-182	Sequence 182, App	935	14	60.9	8	17	US-10-480-954-64	Sequence 64, Appl
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996 14 60.9 9 14 US-10-197-954-148 Sequence 148, App
997 14 60.9 9 14 US-10-190-082-613 Sequence 613, App
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ALIGNMENTS

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RESULT 1
US-10-818-036-24
; Sequence 24, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: AMIDATION
US-10-818-036-28
Query Match 73.9%; Score 17; DB 18; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db | 4 FTASW 8

RESULT 2
US-10-818-036-28
; Sequence 28, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: AMIDATION
US-10-818-036-28
Query Match 73.9%; Score 17; DB 18; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db | 4 FTASW 8

RESULT 3
US-10-818-036-28
; Sequence 28, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: AMIDATION
US-10-818-036-28
Query Match 73.9%; Score 17; DB 18; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db | 4 FTASW 8

RESULT 4
US-10-818-036-30
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; Sequence 30, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-818-036-30

Query Match      73.9%; Score 17; DB 18; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
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Db      4 FTASW 8

RESULT 5
US-10-072-419-3
; Sequence 3, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Apis mellifera
US-10-072-419-3

Query Match      73.9%; Score 17; DB 14; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
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Db      4 FTSSW 8

RESULT 6
US-10-072-419-8
; Sequence 8, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-072-419-8

Query Match      73.9%; Score 17; DB 16; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
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Db      4 FTSSW 8
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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-072-419-8

Query Match      73.9%; Score 17; DB 14; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
      | | |
Db      4 FTSSW 8

RESULT 7
US-10-869-768-3
; Sequence 3, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Apis mellifera
US-10-869-768-3

Query Match      73.9%; Score 17; DB 16; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
      | | |
Db      4 FTSSW 8

RESULT 8
US-10-869-768-8
; Sequence 8, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-869-768-8

Query Match      73.9%; Score 17; DB 16; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
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Db      4 FTSSW 8
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RESULT 9
US-10-818-036-14
; Sequence 14, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-818-036-14

Query Match      73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
Db      4 FTASW 8

RESULT 10
US-10-818-036-15
; Sequence 15, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-818-036-15

Query Match      73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
Db      4 FTASW 8

RESULT 11
US-10-818-036-23
; Sequence 23, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; NAME/KEY: MOD RES
; LOCATION: (9)-(9)
; OTHER INFORMATION: AMIDATION
US-10-818-036-23

Query Match      73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
Db      4 FTASW 8

RESULT 12
US-10-818-036-25
; Sequence 25, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-818-036-25

Query Match      73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
Db      4 FTASW 8

RESULT 13
US-10-818-036-26
; Sequence 26, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)-(9)
; OTHER INFORMATION: AMIDATION
; US-10-818-036-26

Query Match 73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 4 FTASW 8

RESULT 14

US-10-818-036-29
; Sequence 29, Application US/10818036
; Publication No. US2005022040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)-(9)
; OTHER INFORMATION: AMIDATION
; US-10-818-036-29

Query Match 73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 4 FTASW 8

RESULT 15

US-09-842-776A-28
; Sequence 28, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR1) of an
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease
; OTHER INFORMATION: epitope (alternative sequence)
; US-09-842-776A-28

Query Match 73.9%; Score 17; DB 11; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 4 FSTSW 8

RESULT 16

US-10-996-316-139
; Sequence 139, Application US/10996316
; Publication No. US20050129690A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: McWhirter, John
; APPLICANT: Kretz-Rommel, Anke
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC
; TITLE OF INVENTION: LEUKEMIA CELLS AND USES THEREOF
; FILE REFERENCE: 60 CIP IV (1087-43 CIP IV)
; CURRENT APPLICATION NUMBER: US/10/996,316
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/894,672
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/736,188
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/379,151
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 10
; TYPE: PRT
; ORGANISM: murine
; US-10-996-316-139

Query Match 73.9%; Score 17; DB 18; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 4 FSAW 8

RESULT 17

US-10-072-419-37
; Sequence 37, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanessa cardui

US-10-072-419-37

Query Match 73.9%; Score 17; DB 14; Length 11;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 4 FTSSW 8

RESULT 18

US-10-869-768-37

; Sequence 37, Application US/10869768

; Publication No. US20040224898A1

; GENERAL INFORMATION:

; APPLICANT: Schacter, Bernie

; APPLICANT: Schacter, Lee

; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human

; FILE REFERENCE: 10739-1

; CURRENT APPLICATION NUMBER: US/10/869,768

; CURRENT FILING DATE: 2004-06-16

; PRIOR APPLICATION NUMBER: US 10/072,419

; PRIOR FILING DATE: 2002-02-07

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 37

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Vanessa cardui

US-10-869-768-37

Query Match

73.9%; Score 17; DB 16; Length 11;

Best Local Similarity 40.0%; Pred. No. 6.6e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 4 FTSSW 8

RESULT 19

US-10-354-240-87

; Sequence 87, Application US/10354240

; Publication No. US20030185847A1

; GENERAL INFORMATION:

; APPLICANT: Sone, Toshio

; APPLICANT: Kume, Akinori

; APPLICANT: Dairiki, Kazuo

; APPLICANT: Iwama, Akiko

; APPLICANT: Kino, Kohsuke

; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease

; FILE REFERENCE: SPO-103D1

; CURRENT APPLICATION NUMBER: US/10/354,240

; CURRENT FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: PCT/JP97/00740

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: US 09/142,524

; PRIOR FILING DATE: 1998-09-09

; NUMBER OF SEQ ID NOS: 174

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 87

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Cryptomeria japonica

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)-(15)

; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4

US-10-354-240-87

Query Match

73.9%; Score 17; DB 14; Length 15;

Best Local Similarity 40.0%; Pred. No. 8e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 9 FSTAW 13

RESULT 20

US-10-354-240-88

; Sequence 88, Application US/10354240

; Publication No. US20030185847A1

; GENERAL INFORMATION:

; APPLICANT: Sone, Toshio

; APPLICANT: Kume, Akinori

; APPLICANT: Dairiki, Kazuo

; APPLICANT: Iwama, Akiko

; APPLICANT: Kino, Kohsuke

; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease

; FILE REFERENCE: SPO-103D1

; CURRENT APPLICATION NUMBER: US/10/354,240

; CURRENT FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: PCT/JP97/00740

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: US 09/142,524

; PRIOR FILING DATE: 1998-09-09

; NUMBER OF SEQ ID NOS: 174

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 88

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Cryptomeria japonica

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)-(15)

; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5

US-10-354-240-88

Query Match

73.9%; Score 17; DB 14; Length 15;

Best Local Similarity 40.0%; Pred. No. 8e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 4 FSTAW 8

RESULT 21

US-09-963-339-10

; Sequence 10, Application US/09963339

; Publication No. US20030049700A1

; GENERAL INFORMATION:

; APPLICANT: Bandaru, Rajasekhar

; TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN

; TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF

; FILE REFERENCE: 10448-090001

; CURRENT APPLICATION NUMBER: US/09/963,339

; CURRENT FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: 60/235,049

; PRIOR FILING DATE: 2000-09-25

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-963-339-10

Query Match

73.9%; Score 17; DB 10; Length 19;

Best Local Similarity 40.0%; Pred. No. 9.3e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 4 FSTAW 8

Db 4 FSATW 8

RESULT 22

US-10-145-586-59

Sequence 59, Application US/10145586

Publication No. US20030138890A1

GENERAL INFORMATION:

APPLICANT: Alexandra Glucksmann, Maria

APPLICANT: Silos-Santiago, Inmaculada

APPLICANT: M. Galvin, Katherine

APPLICANT: Weich, Nadine

APPLICANT: Curtis, Rory A.J.

APPLICANT: Bandaru, Rajasekhar

APPLICANT: Kapeller-Liebermann, Rosana

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS.

TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH

TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER

FILE REFERENCE: 10448-188001

CURRENT APPLICATION NUMBER: US/10/145,586

Prior Filing Date: 2002-05-14

NUMBER OF SEQ ID NOS: 95

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 59

LENGTH: 19

TYPE: PRT

ORGANISM: Homo sapiens

US-10-145-586-59

Query Match 73.9%; Score 17; DB 14; Length 19;

Best Local Similarity 40.0%; Pred. No. 9.3e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5

Db 4 FSATW 8

RESULT 23

US-10-931-260-265

Sequence 265, Application US/10931260

Publication No. US20050152927A1

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;

Pollock, Joanne;

Bond, Julian F.;

Garman, Richard D.;

Kuo, Mei-Chang;

Powers, Stephen P.;

Exley, Mark A.;

Chen, Xian;

Shaked, Ze'ev

TITLE OF INVENTION: Allergenic Proteins And Peptides From Japanese Cedar Pollen

NUMBER OF SEQUENCES: 283

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lahive & Cockfield, LLP

STREET: 28 State St

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/931,260

FILING DATE: 30-Aug-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/240,203

FILING DATE: 29-Jan-1999

APPLICATION NUMBER: 08/467,023

FILING DATE: 1995-JUN-06

APPLICATION NUMBER: 08/350,225

FILING DATE: 1994-DEC-06

APPLICATION NUMBER: 08/226,248

FILING DATE: 1994-APR-08

APPLICATION NUMBER: PCT/US93/00139

FILING DATE: 1993-JAN-15

APPLICATION NUMBER: 07/938,990

FILING DATE: 1992-SEP-01

APPLICATION NUMBER: 07/730,452

FILING DATE: 1991-JUL-15

APPLICATION NUMBER: 07/729,134

FILING DATE: 1991-JUL-12

APPLICATION NUMBER: 07/975,179

FILING DATE: 1992-NOV-12

APPLICATION NUMBER: PCT/US92/05661

FILING DATE: 1992-JUL-10

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras, Esq.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-10-931-260-265

Query Match 73.9%; Score 17; DB 18; Length 20;

Best Local Similarity 40.0%; Pred. No. 9.6e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5

Db 12 FSTAW 16

RESULT 24

US-10-190-082-36

Sequence 36, Application US/10190082

Publication No. US20030148264A1

GENERAL INFORMATION:

APPLICANT: Lasky, Lawrence A.

APPLICANT: Sidhu, Sachdev S.

APPLICANT: Heid, Heike A.

TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS

FILE REFERENCE: P1905R1

CURRENT APPLICATION NUMBER: US/10/190,082

CURRENT FILING DATE: 2002-07-03

PRIOR APPLICATION NUMBER: US 60/303,634

PRIOR FILING DATE: 2001-07-06

NUMBER OF SEQ ID NOS: 683

SEQ ID NO 36

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-190-082-36

Query Match 69.6%; Score 16; DB 14; Length 6;

Best Local Similarity 40.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 1 FSDTW 5

RESULT 25

US-09-774-639-284
; Sequence 284, Application US/09774639
; Publication No. US20030003555A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; CURRENT APPLICATION NUMBER: US/09/774,639
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/056,365
; PRIOR FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-284

Query Match 69.6%; Score 16; DB 10; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 2 FGTSW 6

RESULT 26

US-09-969-730-267
; Sequence 267, Application US/09969730
; Publication No. US2003005443A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2
; CURRENT APPLICATION NUMBER: US/09/969,730
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US99/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,367
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,365
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,731
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,557
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,563
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/055,970

; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,986
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,311
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,808
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,803
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,809
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,806
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,310
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,798
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,309
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,312
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,807
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,386
; PRIOR FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 267
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-730-267

Query Match 69.6%; Score 16; DB 10; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 2 FGTSW 6

RESULT 27

US-10-046-922-48
; Sequence 48, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 7
; TYPE: PRT
; ORGANISM: peptide
US-10-046-922-48

Query Match 69.6%; Score 16; DB 13; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 3 FEAAM 7

RESULT 28

US-10-621-363-267
; Sequence 267, Application US/10621363
; Publication No. US20040023283A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/621,363
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 267
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-621-363-267

Query Match 69.6%; Score 16; DB 15; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
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Db 2 FGTSW 6

RESULT 29

US-10-072-419-4
; Sequence 4, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Schistocerca gregaria
US-10-072-419-4

Query Match 69.6%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |

Db

4 FSTGW 8

RESULT 30

US-10-072-419-11
; Sequence 11, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Locusta migratoria
US-10-072-419-11

Query Match 69.6%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 4 FSAGW 8

RESULT 31

US-10-072-419-15
; Sequence 15, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Phymateus leprosus
US-10-072-419-15

Query Match 69.6%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 4 FSTGW 8

RESULT 32

US-10-072-419-24
; Sequence 24, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24

; LENGTH: 8
; TYPE: PRT
; ORGANISM: Gryllobates sigillatus
US-10-072-419-24

Query Match 69.6%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 4 FSTGW 8

RESULT 33

US-10-072-419-25
; Sequence 25, Application US/10072419
; Publication No. US20030162717A1

; GENERAL INFORMATION:

; APPLICANT: Schacter, Bernice

; APPLICANT: Schacter, Lee

; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human

; FILE REFERENCE: 10739-1

; CURRENT APPLICATION NUMBER: US/10/072,419

; CURRENT FILING DATE: 2002-02-07

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 25

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Libanasisidus vittatus

US-10-072-419-25

Query Match 69.6%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 4 FSTGW 8

RESULT 34

US-10-072-419-30
; Sequence 30, Application US/10072419
; Publication No. US20030162717A1

; GENERAL INFORMATION:

; APPLICANT: Schacter, Bernice

; APPLICANT: Schacter, Lee

; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human

; FILE REFERENCE: 10739-1

; CURRENT APPLICATION NUMBER: US/10/072,419

; CURRENT FILING DATE: 2002-02-07

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 30

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Onitis sp.

US-10-072-419-30

Query Match 69.6%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 4 FSTGW 8

RESULT 35

US-10-367-580-260
; Sequence 260, Application US/10367580

; Publication No. US20040071720A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461061
; CURRENT APPLICATION NUMBER: US/10/367,580
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,832
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 260
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-580-260

Query Match 69.6%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 2 FLSSW 6

RESULT 36

US-10-367-580-264

; Sequence 264, Application US/10367580
; Publication No. US20040071720A1

; GENERAL INFORMATION:

; APPLICANT: Rothman, James E.

; APPLICANT: Hartl, F. Ulrich

; APPLICANT: Hoe, Mee H.

; APPLICANT: Houghton, Alan

; APPLICANT: Takechi, Yoshizumi

; APPLICANT: Mayhew, Mark

; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

; FILE REFERENCE: 11746/461061

; CURRENT APPLICATION NUMBER: US/10/367,580

; CURRENT FILING DATE: 2003-02-14

; PRIOR APPLICATION NUMBER: US 09/794,832

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: US 09/011,645

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: PCT/US96/13363

; PRIOR FILING DATE: 1996-08-16

; PRIOR APPLICATION NUMBER: US 60/002,490

; PRIOR FILING DATE: 1995-08-18

; PRIOR APPLICATION NUMBER: US 60/002,479

; PRIOR FILING DATE: 1995-08-18

; NUMBER OF SEQ ID NOS: 349

; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 264

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide
US-10-367-580-264

Query Match 69.6%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 2 FLSSW 6

RESULT 37

US-10-367-593-260
; Sequence 260, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR FILING DATE: 1995-08-18
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 260
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-593-260

Query Match 69.6%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 2 FLSSW 6

RESULT 38

US-10-367-593-264
; Sequence 264, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR FILING DATE: 1995-08-18
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16

; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 264
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-593-264

Query Match 69.6%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 2 FLSSW 6

RESULT 39

US-10-367-594-260
; Sequence 260, Application US/10367594
; Publication No. US20040071722A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461041
; CURRENT APPLICATION NUMBER: US/10/367,594
; CURRENT FILING DATE: 2003-02-14
; PRIOR FILING DATE: 1995-08-18
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 260
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-594-260

Query Match 69.6%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 2 FLSSW 6

RESULT 40

US-10-367-594-264
; Sequence 264, Application US/10367594
; Publication No. US20040071722A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.

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/ APPLICANT: Hartl, F. Ulrich
/ APPLICANT: Hoe, Mee H.
/ APPLICANT: Houghton, Alan
/ APPLICANT: Takechi, Yoshizumi
/ APPLICANT: Mayhew, Mark
/ TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
/ FILE REFERENCE: 11746/461041
/ CURRENT APPLICATION NUMBER: US/10/367,594
/ CURRENT FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: US 09/680,806
/ PRIOR FILING DATE: 2000-10-05
/ PRIOR APPLICATION NUMBER: US 09/011,645
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: PCT/US96/13363
/ PRIOR FILING DATE: 1996-08-16
/ PRIOR APPLICATION NUMBER: US 60/002,490
/ PRIOR FILING DATE: 1995-08-18
/ PRIOR APPLICATION NUMBER: US 60/002,479
/ PRIOR FILING DATE: 1995-08-18
/ NUMBER OF SEQ ID NOS: 349
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 264
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-367-594-264
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Query Match          69.6%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 FXXW 5
         |
Db       2 FLSSW 6
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Job time : 110.588 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:46:49 ; Search time 27.7647 Seconds
(without alignments)
21.509 Million cell updates/sec

Title: US-09-214-371-10
Perfect score: 23
Sequence: 1 FXXXXXXX 8

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 196327

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	17	73.9	13	3	US-09-085-072-7
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3	17	73.9	15	4	US-09-142-524D-88
4	16	69.6	6	1	US-07-920-519-10
5	16	69.6	6	1	US-08-086-410-7
6	16	69.6	6	1	US-08-314-586-10
7	16	69.6	7	4	US-09-774-639-284
8	16	69.6	9	4	US-09-702-114A-28
9	16	69.6	10	1	US-08-208-886C-87
10	16	69.6	10	1	US-08-704-744-89
11	16	69.6	10	1	US-08-469-557-68
12	16	69.6	10	2	US-08-290-793B-68
13	16	69.6	11	1	US-08-277-660A-16
14	16	69.6	11	1	US-08-277-660A-17
15	16	69.6	11	1	US-08-424-957-29
16	16	69.6	11	1	US-08-424-957-30
17	16	69.6	11	3	US-09-035-686-29
18	16	69.6	11	3	US-09-035-686-30
19	16	69.6	12	2	US-08-406-330-32
20	16	69.6	12	2	US-08-556-597-32
21	16	69.6	13	1	US-08-305-871A-23
22	16	69.6	13	3	US-08-912-560-11
23	16	69.6	13	4	US-08-788-822A-27
24	16	69.6	13	4	US-09-543-608A-27
25	16	69.6	13	4	US-09-556-818-65
26	16	69.6	13	6	5185431-25
27	16	69.6	13	6	5185431-25

101	15	65.2	9	1	US-08-638-911A-12	Sequence 12, Appl	174	15	65.2	11	3	US-09-035-686-42	Sequence 42, Appl
102	15	65.2	9	1	US-08-638-911A-15	Sequence 15, Appl	175	15	65.2	11	3	US-09-035-686-43	Sequence 43, Appl
103	15	65.2	9	1	US-08-638-911A-18	Sequence 18, Appl	176	15	65.2	11	3	US-09-035-686-44	Sequence 44, Appl
104	15	65.2	9	1	US-08-638-911A-21	Sequence 21, Appl	177	15	65.2	11	3	US-09-035-686-45	Sequence 45, Appl
105	15	65.2	9	2	US-08-709-177-5	Sequence 5, Appl	178	15	65.2	11	3	US-09-035-686-46	Sequence 46, Appl
106	15	65.2	9	2	US-08-709-177-8	Sequence 8, Appl	179	15	65.2	11	4	US-09-603-052-5	Sequence 5, Appl
107	15	65.2	9	2	US-08-709-177-11	Sequence 11, Appl	180	15	65.2	11	4	US-09-069-827A-46	Sequence 46, Appl
108	15	65.2	9	2	US-08-709-177-14	Sequence 14, Appl	181	15	65.2	11	4	US-09-069-827A-172	Sequence 172, App
109	15	65.2	9	3	US-08-396-385-7	Sequence 7, Appl	182	15	65.2	11	4	US-09-620-091-444	Sequence 444, App
110	15	65.2	9	3	US-09-249-272-3	Sequence 3, Appl	183	15	65.2	11	5	PCT-US96-09473-2	Sequence 2, Appl
111	15	65.2	9	3	US-09-287-221-7	Sequence 7, Appl	184	15	65.2	12	1	US-08-439-114-4	Sequence 4, Appl
112	15	65.2	9	4	US-09-225-322B-12	Sequence 12, Appl	185	15	65.2	12	1	US-08-200-011-5	Sequence 5, Appl
113	15	65.2	9	4	US-09-764-304-12	Sequence 12, Appl	186	15	65.2	12	1	US-08-665-643A-6	Sequence 6, Appl
114	15	65.2	9	4	US-08-634-332A-71	Sequence 71, Appl	187	15	65.2	12	4	US-08-634-332A-70	Sequence 70, Appl
115	15	65.2	9	4	US-09-555-790A-7	Sequence 7, Appl	188	15	65.2	12	4	US-09-428-082B-131	Sequence 131, App
116	15	65.2	9	4	US-09-555-790A-9	Sequence 9, Appl	189	15	65.2	12	4	US-09-428-082B-132	Sequence 132, App
117	15	65.2	9	4	US-09-771-415-16	Sequence 16, Appl	190	15	65.2	12	4	US-09-428-082B-133	Sequence 133, App
118	15	65.2	9	4	US-09-239-043D-2374	Sequence 2374, Ap	191	15	65.2	12	4	US-09-428-082B-134	Sequence 134, App
119	15	65.2	10	1	US-08-221-580-2	Sequence 2, Appl	192	15	65.2	12	4	US-09-428-082B-137	Sequence 137, App
120	15	65.2	10	1	US-08-208-886C-83	Sequence 83, Appl	193	15	65.2	12	4	US-09-428-082B-143	Sequence 143, App
121	15	65.2	10	1	US-08-277-660A-7	Sequence 7, Appl	194	15	65.2	12	4	US-09-428-082B-144	Sequence 144, App
122	15	65.2	10	1	US-08-277-660A-8	Sequence 8, Appl	195	15	65.2	12	4	US-09-428-082B-145	Sequence 145, App
123	15	65.2	10	1	US-08-704-744-85	Sequence 85, Appl	196	15	65.2	12	4	US-09-428-082B-146	Sequence 146, App
124	15	65.2	10	1	US-08-424-957-11	Sequence 11, Appl	197	15	65.2	13	1	US-08-463-115-102	Sequence 102, App
125	15	65.2	10	1	US-08-424-957-12	Sequence 12, Appl	198	15	65.2	13	1	US-08-465-388-102	Sequence 102, App
126	15	65.2	10	1	US-08-424-957-18	Sequence 18, Appl	199	15	65.2	13	2	US-08-480-190-26	Sequence 26, Appl
127	15	65.2	10	2	US-08-469-557-64	Sequence 64, Appl	200	15	65.2	13	2	US-08-488-379-26	Sequence 26, Appl
128	15	65.2	10	2	US-08-290-793B-64	Sequence 64, Appl	201	15	65.2	13	4	US-08-475-399A-26	Sequence 26, Appl
129	15	65.2	10	2	US-08-556-597-93	Sequence 93, Appl	202	15	65.2	13	4	US-08-077-255A-26	Sequence 26, Appl
130	15	65.2	10	2	US-08-713-636-4	Sequence 4, Appl	203	15	65.2	13	4	US-09-695-437A-19	Sequence 19, Appl
131	15	65.2	10	3	US-08-974-899-10	Sequence 10, Appl	204	15	65.2	13	4	US-09-695-437A-23	Sequence 23, Appl
132	15	65.2	10	3	US-09-035-686-11	Sequence 11, Appl	205	15	65.2	13	4	US-09-695-437A-24	Sequence 24, Appl
133	15	65.2	10	3	US-09-035-686-12	Sequence 12, Appl	206	15	65.2	13	5	PCT-US93-07545-26	Sequence 26, Appl
134	15	65.2	10	3	US-09-035-686-18	Sequence 18, Appl	207	15	65.2	14	2	US-08-764-640-33	Sequence 33, Appl
135	15	65.2	10	4	US-09-490-702B-53	Sequence 53, Appl	208	15	65.2	14	3	US-08-973-225-33	Sequence 33, Appl
136	15	65.2	10	4	US-09-490-702B-72	Sequence 72, Appl	209	15	65.2	14	3	US-08-973-225-213	Sequence 213, App
137	15	65.2	10	4	US-09-795-798-10	Sequence 10, Appl	210	15	65.2	14	3	US-09-244-298A-33	Sequence 33, Appl
138	15	65.2	10	5	PCT-US95-04018-64	Sequence 64, Appl	211	15	65.2	14	3	US-09-516-704-33	Sequence 33, Appl
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140	15	65.2	11	1	US-08-277-660A-10	Sequence 10, Appl	213	15	65.2	14	4	US-09-549-090-213	Sequence 213, App
141	15	65.2	11	1	US-08-277-660A-11	Sequence 11, Appl	214	15	65.2	14	4	US-09-832-230A-33	Sequence 33, Appl
142	15	65.2	11	1	US-08-277-660A-12	Sequence 12, Appl	215	15	65.2	14	4	US-09-428-082B-68	Sequence 68, Appl
143	15	65.2	11	1	US-08-277-660A-13	Sequence 13, Appl	216	15	65.2	14	4	US-09-695-437A-18	Sequence 18, Appl
144	15	65.2	11	1	US-08-277-660A-15	Sequence 15, Appl	217	15	65.2	14	4	US-09-695-437A-24	Sequence 24, Appl
145	15	65.2	11	1	US-08-277-660A-19	Sequence 19, Appl	218	15	65.2	14	4	US-09-695-437A-25	Sequence 25, Appl
146	15	65.2	11	1	US-08-277-660A-20	Sequence 20, Appl	219	15	65.2	14	4	US-09-695-437A-26	Sequence 26, Appl
147	15	65.2	11	1	US-08-424-957-17	Sequence 17, Appl	220	15	65.2	15	1	US-08-277-660A-4	Sequence 4, Appl
148	15	65.2	11	1	US-08-424-957-23	Sequence 23, Appl	221	15	65.2	15	1	US-08-277-660A-5	Sequence 5, Appl
149	15	65.2	11	1	US-08-424-957-24	Sequence 24, Appl	222	15	65.2	15	1	US-08-277-660A-6	Sequence 6, Appl
150	15	65.2	11	1	US-08-424-957-25	Sequence 25, Appl	223	15	65.2	15	1	US-08-277-660A-6	Sequence 6, Appl
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152	15	65.2	11	1	US-08-424-957-28	Sequence 28, Appl	225	15	65.2	15	1	US-08-424-957-20	Sequence 20, Appl
153	15	65.2	11	1	US-08-424-957-32	Sequence 32, Appl	226	15	65.2	15	1	US-08-424-957-21	Sequence 21, Appl
154	15	65.2	11	1	US-08-424-957-33	Sequence 33, Appl	227	15	65.2	15	1	US-08-424-957-22	Sequence 22, Appl
155	15	65.2	11	1	US-08-424-957-34	Sequence 34, Appl	228	15	65.2	15	2	US-08-553-257A-52	Sequence 52, Appl
156	15	65.2	11	1	US-08-424-957-36	Sequence 36, Appl	229	15	65.2	15	3	US-09-280-047-6	Sequence 6, Appl
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158	15	65.2	11	1	US-08-424-957-42	Sequence 42, Appl	231	15	65.2	15	3	US-09-035-686-1	Sequence 1, Appl
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161	15	65.2	11	1	US-08-424-957-46	Sequence 46, Appl	234	15	65.2	15	3	US-09-035-686-22	Sequence 22, Appl
162	15	65.2	11	3	US-08-424-957-46	Sequence 46, Appl	235	15	65.2	15	3	US-08-208-573B-6	Sequence 6, Appl
163	15	65.2	11	3	US-09-035-686-17	Sequence 17, Appl	236	15	65.2	15	4	US-09-914-259-155	Sequence 165, App
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165	15	65.2	11	3	US-09-035-686-24	Sequence 24, Appl	238	15	65.2	15	4	US-08-634-332A-69	Sequence 69, Appl
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171	15	65.2	11	3	US-09-035-686-34	Sequence 34, Appl	244	15	65.2	15	4	US-09-428-082B-140	Sequence 140, App
172	15	65.2	11	3	US-09-035-686-36	Sequence 36, Appl	245	15	65.2	15	4	US-09-428-082B-141	Sequence 141, App
173	15	65.2	11	3	US-09-035-686-40	Sequence 40, Appl	246	15	65.2	15	4	US-09-511-204B-3	Sequence 3, Appl

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254	15	65.2	15	4	US-09-695-437A-17	Sequence 17, Appli	327	14	60.9	5	4	US-10-122-246A-101	Sequence 101, App
255	15	65.2	15	4	US-09-695-437A-20	Sequence 20, Appli	328	14	60.9	5	4	US-10-122-246A-102	Sequence 102, App
256	15	65.2	15	4	US-09-695-437A-21	Sequence 21, Appli	329	14	60.9	5	4	US-10-122-246A-103	Sequence 103, App
257	15	65.2	15	4	US-09-695-437A-22	Sequence 22, Appli	330	14	60.9	5	4	US-10-122-246A-104	Sequence 104, App
258	15	65.2	15	4	US-09-695-437A-32	Sequence 32, Appli	331	14	60.9	5	4	US-10-122-246A-105	Sequence 105, App
259	15	65.2	15	4	US-09-695-437A-33	Sequence 33, Appli	332	14	60.9	5	4	US-10-122-246A-106	Sequence 106, App
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263	15	65.2	15	4	US-09-732-384-6	Sequence 6, Appli	336	14	60.9	6	1	US-08-269-257-7	Sequence 7, Appli
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269	15	65.2	16	4	US-09-406-640-19	Sequence 19, Appli	342	14	60.9	6	1	US-08-321-625-27	Sequence 27, Appli
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273	15	65.2	16	6	5208144-11	Patent No. 5208144	346	14	60.9	6	1	US-08-476-000-30	Sequence 30, Appli
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275	15	65.2	17	2	US-08-637-759B-238	Sequence 238, App	348	14	60.9	6	1	US-08-472-840-30	Sequence 30, Appli
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278	15	65.2	18	2	US-08-248-839C-166	Sequence 166, App	351	14	60.9	6	2	US-08-672-805-4	Sequence 4, Appli
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286	15	65.2	18	4	US-08-634-332A-63	Sequence 63, Appli	359	14	60.9	6	3	US-09-181-083-27	Sequence 27, Appli
287	15	65.2	18	4	US-09-695-437A-63	Sequence 63, Appli	360	14	60.9	6	3	US-09-181-083-28	Sequence 28, Appli
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292	15	65.2	19	4	US-09-774-639-342	Sequence 342, App	365	14	60.9	6	3	US-09-166-205B-28	Sequence 28, Appli
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299	15	65.2	20	3	US-08-871-355A-458	Sequence 458, App	372	14	60.9	6	4	US-09-750-754-29	Sequence 29, Appli
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301	15	65.2	20	3	US-08-630-052-11	Sequence 11, Appli	374	14	60.9	6	4	US-09-692-945-10	Sequence 10, Appli
302	15	65.2	20	4	US-09-643-597-234	Sequence 234, App	375	14	60.9	6	4	US-09-446-109A-20	Sequence 20, Appli
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304	15	65.2	20	4	US-09-081-975-10	Sequence 10, Appli	377	14	60.9	6	5	PCT-US94-02639-28	Sequence 28, Appli
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314	15	65.2	20	4	US-09-342-673-31	Sequence 31, Appli	387	14	60.9	7	1	US-08-321-625-79	Sequence 79, Appli
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316	15	65.2	20	4	US-09-476-496A-234	Sequence 234, App	389	14	60.9	7	1	US-08-087-219-4	Sequence 4, Appli
317	15	65.2	20	4	US-09-630-940B-234	Sequence 234, App	390	14	60.9	7	1	US-08-476-537-71	Sequence 71, Appli
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319	15	65.2	20	5	PCT-US95-09307-11	Sequence 11, Appli	392	14	60.9	7	1	US-08-485-607-71	Sequence 71, Appli

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394	14	60.9	7	3	US-09-258-754-402	Sequence 402, App	467	14	60.9	10	2	US-08-751-300-97	Sequence 97, Appl
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397	14	60.9	7	3	US-09-181-083-79	Sequence 79, Appl	470	14	60.9	10	3	US-08-485-324-16	Sequence 16, Appl
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408	14	60.9	8	3	US-09-063-893A-8	Sequence 8, Appl	481	14	60.9	10	4	US-09-239-043D-2392	Sequence 2392, Ap
409	14	60.9	8	3	US-08-444-818-323	Sequence 323, App	482	14	60.9	10	4	US-09-620-091-46	Sequence 46, Appl
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418	14	60.9	8	4	US-09-601-729-168	Sequence 168, App	491	14	60.9	10	4	US-09-043-813-26	Sequence 26, Appl
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424	14	60.9	9	3	US-09-407-549-16	Sequence 16, Appl	497	14	60.9	10	4	US-09-043-813-44	Sequence 44, Appl
425	14	60.9	9	4	US-09-402-641-5	Sequence 5, Appl	498	14	60.9	10	4	US-09-043-813-57	Sequence 57, Appl
426	14	60.9	9	4	US-09-073-138-77	Sequence 77, Appl	499	14	60.9	10	4	US-09-043-813-59	Sequence 59, Appl
427	14	60.9	9	4	US-09-870-089B-3	Sequence 3, Appl	500	14	60.9	10	4	US-09-043-813-63	Sequence 63, Appl
428	14	60.9	9	4	US-09-870-089B-7	Sequence 7, Appl	501	14	60.9	10	4	US-09-043-813-65	Sequence 65, Appl
429	14	60.9	9	4	US-09-870-089B-9	Sequence 9, Appl	502	14	60.9	10	4	US-09-043-813-76	Sequence 76, Appl
430	14	60.9	10	1	US-08-321-623-74	Sequence 74, Appl	503	14	60.9	10	4	US-09-756-247-16	Sequence 16, Appl
431	14	60.9	10	1	US-08-242-678D-5	Sequence 5, Appl	504	14	60.9	10	4	US-09-756-247-36	Sequence 36, Appl
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433	14	60.9	10	2	US-08-370-909-16	Sequence 16, Appl	506	14	60.9	11	1	US-08-321-625-10	Sequence 10, Appl
434	14	60.9	10	2	US-08-370-909-17	Sequence 17, Appl	507	14	60.9	11	1	US-08-424-957-35	Sequence 35, Appl
435	14	60.9	10	2	US-08-556-597-120	Sequence 120, App	508	14	60.9	11	2	US-08-486-839-9	Sequence 9, Appl
436	14	60.9	10	2	US-08-902-623-37	Sequence 37, Appl	509	14	60.9	11	3	US-08-485-324-14	Sequence 14, Appl
437	14	60.9	10	2	US-08-902-623-40	Sequence 40, Appl	510	14	60.9	11	3	US-09-151-011-9	Sequence 9, Appl
438	14	60.9	10	2	US-08-902-623-72	Sequence 72, Appl	511	14	60.9	11	3	US-08-447-506-14	Sequence 14, Appl
439	14	60.9	10	2	US-08-747-137-122	Sequence 122, App	512	14	60.9	11	3	US-08-235-437-14	Sequence 14, Appl
440	14	60.9	10	2	US-08-751-300-2	Sequence 2, Appl	513	14	60.9	11	3	US-09-035-686-35	Sequence 35, Appl
441	14	60.9	10	2	US-08-751-300-5	Sequence 5, Appl	514	14	60.9	11	3	US-08-447-515-14	Sequence 14, Appl
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443	14	60.9	10	2	US-08-751-300-11	Sequence 11, Appl	516	14	60.9	11	3	US-09-224-785-5	Sequence 5, Appl
444	14	60.9	10	2	US-08-751-300-14	Sequence 14, Appl	517	14	60.9	11	3	US-09-186-958-5	Sequence 5, Appl
445	14	60.9	10	2	US-08-751-300-17	Sequence 17, Appl	518	14	60.9	11	3	US-09-186-958-8	Sequence 8, Appl
446	14	60.9	10	2	US-08-751-300-20	Sequence 20, Appl	519	14	60.9	11	3	US-09-186-958-8	Sequence 8, Appl
447	14	60.9	10	2	US-08-751-300-23	Sequence 23, Appl	520	14	60.9	11	3	US-09-186-958-9	Sequence 9, Appl
448	14	60.9	10	2	US-08-751-300-26	Sequence 26, Appl	521	14	60.9	11	3	US-09-669-271A-5	Sequence 5, Appl
449	14	60.9	10	2	US-08-751-300-29	Sequence 29, Appl	522	14	60.9	11	3	US-09-669-271A-6	Sequence 6, Appl
450	14	60.9	10	2	US-08-751-300-32	Sequence 32, Appl	523	14	60.9	11	3	US-09-669-271A-8	Sequence 8, Appl
451	14	60.9	10	2	US-08-751-300-35	Sequence 35, Appl	524	14	60.9	11	3	US-09-669-271A-9	Sequence 9, Appl
452	14	60.9	10	2	US-08-751-300-38	Sequence 38, Appl	525	14	60.9	11	3	US-09-343-623-9	Sequence 9, Appl
453	14	60.9	10	2	US-08-751-300-41	Sequence 41, Appl	526	14	60.9	11	4	US-09-081-975-21	Sequence 21, Appl
454	14	60.9	10	2	US-08-751-300-44	Sequence 44, Appl	527	14	60.9	11	4	US-09-461-325-504	Sequence 504, App
455	14	60.9	10	2	US-08-751-300-57	Sequence 57, Appl	528	14	60.9	11	4	US-09-881-276-5	Sequence 5, Appl
456	14	60.9	10	2	US-08-751-300-59	Sequence 59, Appl	529	14	60.9	11	4	US-09-881-276-6	Sequence 6, Appl
457	14	60.9	10	2	US-08-751-300-65	Sequence 63, Appl	530	14	60.9	11	4	US-09-881-276-9	Sequence 8, Appl
458	14	60.9	10	2	US-08-751-300-66	Sequence 65, Appl	531	14	60.9	11	4	US-09-881-276-9	Sequence 9, Appl
459	14	60.9	10	2	US-08-751-300-77	Sequence 77, Appl	532	14	60.9	11	4	US-09-756-594-5	Sequence 5, Appl
460	14	60.9	10	2	US-08-751-300-90	Sequence 90, Appl	533	14	60.9	11	4	US-09-069-827A-43	Sequence 43, Appl
461	14	60.9	10	2	US-08-751-300-91	Sequence 91, Appl	534	14	60.9	11	4	US-09-069-827A-44	Sequence 44, Appl
462	14	60.9	10	2	US-08-751-300-92	Sequence 92, Appl	535	14	60.9	11	4	US-09-069-827A-47	Sequence 47, Appl
463	14	60.9	10	2	US-08-751-300-93	Sequence 93, Appl	536	14	60.9	11	4	US-10-012-542-504	Sequence 504, App
464	14	60.9	10	2	US-08-751-300-94	Sequence 94, Appl	537	14	60.9	11	4	US-09-750-754-10	Sequence 10, Appl
465	14	60.9	10	2	US-08-751-300-95	Sequence 95, Appl	538	14	60.9	11	4	US-09-428-082B-325	Sequence 325, App

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542	14	60.9	12	3	US-09-115-444-45	Sequence 45, App	615	14	60.9	15	4	US-09-441-992-51	Sequence 51, App
543	14	60.9	12	3	US-08-186-958-13	Sequence 13, App	616	14	60.9	15	4	US-09-574-749B-54	Sequence 54, App
544	14	60.9	12	3	US-09-669-271A-13	Sequence 13, App	617	14	60.9	15	4	US-09-644-442-7	Sequence 7, App
545	14	60.9	12	4	US-09-721-362-45	Sequence 45, App	618	14	60.9	15	4	US-09-072-967-57	Sequence 57, App
546	14	60.9	12	4	US-09-752-165-65	Sequence 65, App	619	14	60.9	15	4	US-09-072-967-123	Sequence 123, App
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550	14	60.9	12	4	US-09-428-082B-135	Sequence 135, App	623	14	60.9	15	5	PCT-US94-02465-51	Sequence 51, App
551	14	60.9	12	4	US-09-428-082B-136	Sequence 136, App	624	14	60.9	15	5	PCT-US94-10356-2	Sequence 2, App
552	14	60.9	13	1	US-08-487-568-87	Sequence 87, App	625	14	60.9	15	5	PCT-US94-10356-3	Sequence 3, App
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554	14	60.9	13	3	US-09-236-415-5	Sequence 5, App	627	14	60.9	15	5	PCT-US94-10358-7	Sequence 7, App
555	14	60.9	13	4	US-09-081-975-9	Sequence 9, App	628	14	60.9	15	5	PCT-US94-10358-20	Sequence 20, App
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557	14	60.9	13	5	PCT-US94-01234-47	Sequence 47, App	630	14	60.9	15	5	PCT-US95-00498-51	Sequence 51, App
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560	14	60.9	14	2	US-08-392-816-12	Sequence 12, App	633	14	60.9	16	1	US-08-321-625-18	Sequence 18, App
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566	14	60.9	14	3	US-09-247-154-10	Sequence 10, App	639	14	60.9	16	1	US-08-321-625-25	Sequence 25, App
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571	14	60.9	14	4	US-09-461-325-508	Sequence 508, App	644	14	60.9	16	1	US-08-321-625-68	Sequence 68, App
572	14	60.9	14	4	US-09-610-833-10	Sequence 10, App	645	14	60.9	16	1	US-08-321-625-80	Sequence 80, App
573	14	60.9	14	4	US-08-329-855A-10	Sequence 10, App	646	14	60.9	16	1	US-08-077-797A-43	Sequence 43, App
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575	14	60.9	14	4	US-10-115-123-508	Sequence 508, App	648	14	60.9	16	1	US-08-333-577-5	Sequence 5, App
576	14	60.9	15	1	US-08-311-611A-51	Sequence 51, App	649	14	60.9	16	3	US-09-181-083-18	Sequence 18, App
577	14	60.9	15	1	US-08-372-783-51	Sequence 51, App	650	14	60.9	16	3	US-09-181-083-20	Sequence 20, App
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580	14	60.9	15	1	US-08-306-473A-51	Sequence 51, App	653	14	60.9	16	3	US-09-181-083-23	Sequence 23, App
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582	14	60.9	15	1	US-08-625-691-10	Sequence 10, App	655	14	60.9	16	3	US-09-181-083-25	Sequence 25, App
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585	14	60.9	15	2	US-08-485-445A-51	Sequence 51, App	658	14	60.9	16	3	US-09-181-083-64	Sequence 64, App
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587	14	60.9	15	2	US-08-553-257A-51	Sequence 51, App	660	14	60.9	16	3	US-09-181-083-68	Sequence 68, App
588	14	60.9	15	3	US-09-119-263-51	Sequence 51, App	661	14	60.9	16	3	US-09-181-083-80	Sequence 80, App
589	14	60.9	15	3	US-08-657-162-51	Sequence 51, App	662	14	60.9	16	3	US-09-093-539-51	Sequence 51, App
590	14	60.9	15	3	US-09-224-480-51	Sequence 9, App	663	14	60.9	16	4	US-09-009-953-39	Sequence 39, App
591	14	60.9	15	3	US-09-217-352-9	Sequence 9, App	664	14	60.9	16	4	US-09-009-953-230	Sequence 230, App
592	14	60.9	15	3	US-08-818-112-57	Sequence 57, App	665	14	60.9	16	4	US-09-081-975-23	Sequence 23, App
593	14	60.9	15	3	US-08-818-112-123	Sequence 123, App	666	14	60.9	16	4	US-09-790-230-51	Sequence 51, App
594	14	60.9	15	3	US-08-818-111-57	Sequence 57, App	667	14	60.9	16	4	US-09-311-784A-308	Sequence 308, App
595	14	60.9	15	3	US-08-818-111-118	Sequence 118, App	668	14	60.9	16	4	US-09-546-013-72	Sequence 72, App
596	14	60.9	15	3	US-09-056-556-57	Sequence 57, App	669	14	60.9	16	4	US-09-750-754-18	Sequence 18, App
597	14	60.9	15	3	US-09-056-556-123	Sequence 123, App	670	14	60.9	16	4	US-09-750-754-20	Sequence 20, App
598	14	60.9	15	3	US-09-663-733A-28	Sequence 28, App	671	14	60.9	16	4	US-09-750-754-21	Sequence 21, App
599	14	60.9	15	4	US-09-009-953-247	Sequence 247, App	672	14	60.9	16	4	US-09-750-754-22	Sequence 22, App
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603	14	60.9	15	4	US-08-487-795A-17	Sequence 17, App	676	14	60.9	16	4	US-09-750-754-53	Sequence 53, App
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606	14	60.9	15	4	US-08-121-105B-3	Sequence 3, App	679	14	60.9	16	4	US-09-750-754-65	Sequence 65, App
607	14	60.9	15	4	US-08-121-105B-16	Sequence 16, App	680	14	60.9	16	4	US-09-750-754-68	Sequence 68, App
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610	14	60.9	15	4	US-09-061-975-24	Sequence 24, App	683	14	60.9	16	4	US-09-541-345-4	Sequence 4, App
611	14	60.9	15	4	US-09-072-596-118	Sequence 57, App	684	14	60.9	16	4	US-09-541-345-20	Sequence 20, App

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686	14	60.9	16	4	US-09-541-345-37	Sequence 37, Appl	759	14	60.9	17	4	US-09-428-082B-209	Sequence 209, App
687	14	60.9	16	4	US-09-541-345-38	Sequence 38, Appl	760	14	60.9	17	4	US-08-077-255A-123	Sequence 123, App
688	14	60.9	16	4	US-09-541-345-39	Sequence 39, Appl	761	14	60.9	17	4	US-09-490-070A-222	Sequence 222, App
689	14	60.9	16	4	US-09-541-345-40	Sequence 40, Appl	762	14	60.9	17	4	US-09-490-070A-228	Sequence 228, App
690	14	60.9	16	4	US-09-541-345-41	Sequence 41, Appl	763	14	60.9	17	4	US-09-490-070A-254	Sequence 254, App
691	14	60.9	16	4	US-09-541-345-42	Sequence 42, Appl	764	14	60.9	17	4	US-09-490-070A-262	Sequence 262, App
692	14	60.9	16	4	US-09-541-345-43	Sequence 43, Appl	765	14	60.9	17	4	US-09-490-153-222	Sequence 222, App
693	14	60.9	16	4	US-09-541-345-44	Sequence 44, Appl	766	14	60.9	17	4	US-09-490-153-228	Sequence 228, App
694	14	60.9	16	4	US-09-541-345-45	Sequence 45, Appl	767	14	60.9	17	4	US-09-490-153-254	Sequence 254, App
695	14	60.9	16	4	US-09-541-345-46	Sequence 46, Appl	768	14	60.9	17	4	US-09-490-153-262	Sequence 262, App
696	14	60.9	16	4	US-09-541-345-47	Sequence 47, Appl	769	14	60.9	17	4	US-09-350-841A-814	Sequence 814, App
697	14	60.9	16	4	US-09-541-345-48	Sequence 48, Appl	770	14	60.9	17	4	US-09-695-437A-40	Sequence 40, Appl
698	14	60.9	16	4	US-09-541-345-50	Sequence 50, Appl	771	14	60.9	17	4	US-09-490-324-222	Sequence 222, App
699	14	60.9	16	4	US-09-541-345-51	Sequence 51, Appl	772	14	60.9	17	4	US-09-490-324-228	Sequence 228, App
700	14	60.9	16	4	US-09-541-345-52	Sequence 52, Appl	773	14	60.9	17	4	US-09-490-324-254	Sequence 254, App
701	14	60.9	16	4	US-09-541-345-53	Sequence 53, Appl	774	14	60.9	17	4	US-09-490-324-262	Sequence 262, App
702	14	60.9	16	4	US-09-541-345-55	Sequence 55, Appl	775	14	60.9	17	5	PCT-US93-07545-123	Sequence 123, App
703	14	60.9	16	4	US-09-541-345-57	Sequence 57, Appl	776	14	60.9	17	5	PCT-US94-05684-7	Sequence 7, Appl
704	14	60.9	16	4	US-09-541-345-58	Sequence 58, Appl	777	14	60.9	17	5	PCT-US94-10356-19	Sequence 19, Appl
705	14	60.9	16	4	US-09-541-345-59	Sequence 59, Appl	778	14	60.9	17	5	PCT-US94-10356-21	Sequence 21, Appl
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707	14	60.9	16	4	US-09-541-345-62	Sequence 62, Appl	780	14	60.9	18	1	US-08-375-100-3	Sequence 3, Appl
708	14	60.9	16	4	US-09-541-345-63	Sequence 63, Appl	781	14	60.9	18	2	US-08-448-603A-24	Sequence 24, Appl
709	14	60.9	16	4	US-09-541-345-64	Sequence 64, Appl	782	14	60.9	18	2	US-08-484-905-36	Sequence 36, Appl
710	14	60.9	16	4	US-09-541-345-66	Sequence 66, Appl	783	14	60.9	18	3	US-08-940-095-139	Sequence 139, App
711	14	60.9	16	4	US-09-541-345-69	Sequence 69, Appl	784	14	60.9	18	3	US-08-940-095-224	Sequence 224, App
712	14	60.9	16	4	US-09-541-345-71	Sequence 71, Appl	785	14	60.9	18	3	US-08-481-985B-36	Sequence 36, Appl
713	14	60.9	16	4	US-09-541-345-73	Sequence 73, Appl	786	14	60.9	18	3	US-08-940-093-199	Sequence 199, App
714	14	60.9	16	4	US-09-541-345-74	Sequence 74, Appl	787	14	60.9	18	3	US-08-940-093-224	Sequence 224, App
715	14	60.9	16	4	US-09-541-345-75	Sequence 75, Appl	788	14	60.9	18	3	US-09-134-075-24	Sequence 24, Appl
716	14	60.9	16	4	US-09-541-345-76	Sequence 76, Appl	789	14	60.9	18	3	US-08-940-096-199	Sequence 199, App
717	14	60.9	16	4	US-09-541-345-77	Sequence 77, Appl	790	14	60.9	18	3	US-08-940-096-224	Sequence 224, App
718	14	60.9	16	4	US-09-541-345-79	Sequence 79, Appl	791	14	60.9	18	3	US-08-370-476-36	Sequence 36, Appl
719	14	60.9	16	4	US-09-541-345-81	Sequence 81, Appl	792	14	60.9	18	3	US-09-082-279B-1147	Sequence 1147, Ap
720	14	60.9	16	4	US-09-541-345-83	Sequence 83, Appl	793	14	60.9	18	3	US-09-465-719-199	Sequence 199, App
721	14	60.9	16	4	US-09-541-345-84	Sequence 84, Appl	794	14	60.9	18	3	US-09-465-719-224	Sequence 224, App
722	14	60.9	16	4	US-09-541-345-85	Sequence 85, Appl	795	14	60.9	18	3	US-09-453-605-199	Sequence 199, App
723	14	60.9	16	4	US-09-541-345-86	Sequence 86, Appl	796	14	60.9	18	3	US-09-453-605-224	Sequence 224, App
724	14	60.9	16	4	US-09-541-345-88	Sequence 88, Appl	797	14	60.9	18	3	US-09-492-739-24	Sequence 24, Appl
725	14	60.9	16	4	US-09-541-345-91	Sequence 91, Appl	798	14	60.9	18	3	US-08-993-877-16	Sequence 16, Appl
726	14	60.9	16	4	US-09-541-345-92	Sequence 92, Appl	799	14	60.9	18	3	US-09-315-304B-1147	Sequence 1147, Ap
727	14	60.9	16	4	US-09-541-345-96	Sequence 96, Appl	800	14	60.9	18	3	US-09-453-838-199	Sequence 199, App
728	14	60.9	16	4	US-09-541-345-98	Sequence 98, Appl	801	14	60.9	18	3	US-09-453-838-224	Sequence 224, App
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730	14	60.9	16	4	US-09-541-345-106	Sequence 106, App	803	14	60.9	18	4	US-08-940-136-199	Sequence 199, App
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732	14	60.9	16	5	PCT-US94-01238-43	Sequence 43, Appl	805	14	60.9	18	4	US-08-634-332A-12	Sequence 12, Appl
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734	14	60.9	17	1	US-08-370-567-7	Sequence 7, Appl	807	14	60.9	18	4	US-09-834-784-1147	Sequence 1147, Ap
735	14	60.9	17	1	US-08-438-759-7	Sequence 7, Appl	808	14	60.9	18	4	US-09-453-841-199	Sequence 199, App
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737	14	60.9	17	2	US-08-488-379-123	Sequence 123, App	810	14	60.9	18	4	US-10-158-847-78	Sequence 78, Appl
738	14	60.9	17	3	US-09-181-083-35	Sequence 35, Appl	811	14	60.9	18	4	US-09-453-833-199	Sequence 199, App
739	14	60.9	17	3	US-08-990-823-88	Sequence 88, Appl	812	14	60.9	18	4	US-09-453-833-224	Sequence 224, App
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745	14	60.9	17	3	US-09-025-769B-262	Sequence 262, App	818	14	60.9	18	4	US-09-620-091-195	Sequence 195, App
746	14	60.9	17	3	US-09-315-304B-814	Sequence 814, App	819	14	60.9	18	4	US-09-453-840-199	Sequence 199, App
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751	14	60.9	17	4	US-08-475-399A-123	Sequence 123, App	824	14	60.9	18	4	US-09-453-834-199	Sequence 199, App
752	14	60.9	17	4	US-09-205-258-363	Sequence 363, App	825	14	60.9	18	4	US-09-453-834-224	Sequence 224, App
753	14	60.9	17	4	US-09-834-784-814	Sequence 814, App	826	14	60.9	18	4	US-09-966-931A-24	Sequence 24, Appl
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755	14	60.9	17	4	US-09-477-135A-89	Sequence 89, Appl	828	14	60.9	19	4	US-09-489-847-359	Sequence 359, App
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832	14	60.9	19	4	US-09-620-091-382	Sequence 382, App	905	14	60.9	20	3	US-09-119-263-57	Sequence 57, Appl
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842	14	60.9	20	1	US-08-311-611A-152	Sequence 152, App	915	14	60.9	20	3	US-08-658-136-27	Sequence 27, Appl
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844	14	60.9	20	1	US-08-311-611A-160	Sequence 160, App	917	14	60.9	20	3	US-08-657-162-57	Sequence 57, Appl
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866	14	60.9	20	1	US-08-321-625-50	Sequence 50, Appl	939	14	60.9	20	3	US-09-181-083-36	Sequence 36, Appl
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868	14	60.9	20	1	US-08-306-473A-57	Sequence 57, Appl	941	14	60.9	20	3	US-09-093-539-54	Sequence 54, Appl
869	14	60.9	20	1	US-08-306-473A-58	Sequence 58, Appl	942	14	60.9	20	3	US-08-927-597-76	Sequence 76, Appl
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871	14	60.9	20	1	US-08-306-473A-101	Sequence 101, App	944	14	60.9	20	3	US-08-927-597-83	Sequence 83, Appl
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878	14	60.9	20	1	US-08-209-762-57	Sequence 57, Appl	951	14	60.9	20	3	US-09-217-352-148	Sequence 148, App
879	14	60.9	20	1	US-08-209-762-58	Sequence 58, Appl	952	14	60.9	20	3	US-08-860-656B-12	Sequence 12, Appl
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883	14	60.9	20	2	US-08-621-803-7	Sequence 7, Appl	956	14	60.9	20	4	US-09-155-613A-6	Sequence 6, Appl
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ALIGNMENTS

RESULT 1
US-09-085-072-7
; Sequence 7, Application US/09085072
; Patent No. 6285150
; GENERAL INFORMATION:
; APPLICANT: L. Terstappen et al.
; TITLE OF INVENTION: PHAGE ANTIBODIES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,072
; FILING DATE: 26-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: 890-2 FWC/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-085-072-7

Query Match 73.9%; Score 17; DB 3; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Sequence 147, App
Sequence 148, App
Sequence 149, App
Sequence 156, App
Sequence 157, App
Sequence 32, Appl
Sequence 33, Appl
Sequence 39, Appl
Sequence 459, App
Sequence 1, Appl
Sequence 45, Appl
Sequence 61, Appl
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Sequence 57, Appl
Sequence 58, Appl
Sequence 59, Appl
Sequence 101, App
Sequence 150, App
Sequence 151, App

QY 1 FXXW 5
DB 6 FASSW 10

RESULT 2

US-09-142-524D-87
; Sequence 87, Application US/09142524D
; Patent No. 6719976
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103
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; CURRENT FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 87
; LENGTH: 15
; TYPE: PPT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4
US-09-142-524D-87

Query Match 73.9%; Score 17; DB 4; Length 15;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 9 FSTAW 13

RESULT 3

US-09-142-524D-88
; Sequence 88, Application US/09142524D
; Patent No. 6719976
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103
; CURRENT APPLICATION NUMBER: US/09/142,524D
; CURRENT FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 88
; LENGTH: 15
; TYPE: PPT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5
US-09-142-524D-88

Query Match 73.9%; Score 17; DB 4; Length 15;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 4 FSTAW 8

RESULT 4

US-07-920-519-10
; Sequence 10, Application US/07920519
; Patent No. 5382518
; GENERAL INFORMATION:
; APPLICANT: CAPUT, DANIEL
; APPLICANT: FERRARA, PASCUAL
; APPLICANT: GUILLEMOT, JEAN-CLAUDE
; APPLICANT: KAGHAD, MOURAD
; APPLICANT: LEGOUX, RICHARD
; APPLICANT: LOISON, GERARD
; APPLICANT: LARBRE, ELIZABETH
; APPLICANT: LUPKER, JOHANNES
; APPLICANT: LEPLATOIS, PASCUAL
; APPLICANT: SALOME, MARK
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN.
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR.
; TITLE OF INVENTION: MICRO-ORGANISMS AND TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/920,519
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/659,408
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16781/276 BEDL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: Hydrolysis product T 23

US-07-920-519-10

Query Match 69.6%; Score 16; DB 1; Length 6;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 1 FDATW 5

RESULT 5

US-08-086-410-7
; Sequence 7, Application US/08086410
; Patent No. 5407822
; GENERAL INFORMATION:
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: LOISON, Gerard
; APPLICANT: PESSEGUE, Bernard
; APPLICANT: SHIRE, David
; TITLE OF INVENTION: Artificial promoter for the expression
; TITLE OF INVENTION: of proteins in yeast
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: King Street Station, Suite 500, 1800 Diagonal
; STREET: Road, PO Box 299
; CITY: ALEXANDRIA
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,410
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,083
; FILING DATE: 02-OCT-1991
; APPLICATION NUMBER: FR 89 17467
; FILING DATE: 29-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/318
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: hydrolysis product T23

US-08-086-410-7
Query Match 69.6%; Score 16; DB 1; Length 6;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 1 FDATW 5

RESULT 6

US-08-314-586-10
; Sequence 10, Application US/08314586
; Patent No. 5541098
; GENERAL INFORMATION:
; APPLICANT: CAPUT, DANIEL
; APPLICANT: FERRARA, PASCUAL
; APPLICANT: GUILLEMOT, JEAN-CLAUDE
; APPLICANT: KAGHAD, MOURAD
; APPLICANT: LEGOUX, RICHARD
; APPLICANT: LOISON, GERARD
; APPLICANT: LARBRE, ELIZABETH

```
; APPLICANT: LUPKER, JOHANNES
; APPLICANT: LEPLATOIS, PASCUAL
; APPLICANT: SALOME, MARK
; APPLICANT: LAURENT, PATRICK
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
; TITLE OF INVENTION: MICROORGANISMS AND TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,586
; FILING DATE: 28-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/659,408
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16781/509/BEDL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: Hydrolysis product T 23
;
US-08-314-586-10

Query Match 69.6%; Score 16; DB 1; Length 6;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 1 FDATW 5

RESULT 7
US-09-774-639-284
; Sequence 284, Application US/09774639
; Patent No. 6806351
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 7
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-774-639-284

Query Match 69.6%; Score 16; DB 4; Length 7;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 2 FGTW 6

RESULT 8
US-09-702-114A-28
; Sequence 28, Application US/09702114A
; Patent No. 6566078
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Paris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: 36P6D5: SECRETED TUMOR ANTIGEN
; FILE REFERENCE: 129,22-US-U1
; CURRENT APPLICATION NUMBER: US/09/702,114A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/162,417
; PRIOR FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-702-114A-28

Query Match 69.6%; Score 16; DB 4; Length 9;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 4 FRSSW 8

RESULT 9
US-08-208-886C-87
; Sequence 87, Application US/08208886C
; Patent No. 5597710
; GENERAL INFORMATION:
; APPLICANT: Dalié, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,886C
; FILING DATE: March 10, 1994
; CLASSIFICATION: 424
```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Foulke, Cynthia L.
;; REGISTRATION NUMBER: 32,364
;; REFERENCE/DOCKET NUMBER: JB0429
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 908 298 2987
;; TELEFAX: 908 298 5388
;; INFORMATION FOR SEQ ID NO: 87:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-208-886C-87

Query Match 69.6%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 4 FSSW 8

RESULT 10
US-08-704-744-89
; Sequence 89, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-704-744-89

Query Match 69.6%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 4 FSSW 8

RESULT 11
US-08-469-557-68
; Sequence 68, Application US/08469557
; Patent No. 5770403
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Le, Hung
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Nguyen, Hanh
; APPLICANT: Tindall, Stephen
; APPLICANT: Zavodny, Paul
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; TITLE OF INVENTION: Against Human Interleukin-4
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,557
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290,793
; FILING DATE: August 16, 1994
; APPLICATION NUMBER: PCT/US93/01301
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/841,659
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/782,784
; FILING DATE: 24-OCT-1991
; APPLICATION NUMBER: US 07/499,327
; FILING DATE: 21-MAY-1990
; APPLICATION NUMBER: PCT/US88/03631
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: US 07/655,966
; FILING DATE: 14-FEB-1991
; APPLICATION NUMBER: US 07/113,623
; FILING DATE: 26-OCT-1987
; APPLICATION NUMBER: US 06/881,553
; FILING DATE: 03-JUL-1986
; APPLICATION NUMBER: US 06/843,958
; FILING DATE: 25-MAR-1986
; APPLICATION NUMBER: US 06/799,668
; FILING DATE: 19-NOV-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: 2409K7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908 298-2987
; TELEFAX: 908-298-5388

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; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; US-08-469-557-68
;
Query Match          69.6%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
Db      4 FSSW 8

RESULT 12
US-08-290-793B-68
; Sequence 68, Application US/08290793B
; Patent No. 5863537
; GENERAL INFORMATION:
; APPLICANT: Dali, Barbara
; APPLICANT: Le, Hung
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Nguyen, Hanh
; APPLICANT: Tindall, Stephen
; APPLICANT: Zavodny, Paul
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,793B
; FILING DATE: August 16, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01301
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/841,659
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/782,784
; FILING DATE: 24-OCT-1991
; APPLICATION NUMBER: US 07/499,327
; FILING DATE: 21-MAY-1990
; APPLICATION NUMBER: PCT/US88/03631
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: US 07/655,966
; FILING DATE: 14-FEB-1991
; APPLICATION NUMBER: US 07/113,623
; FILING DATE: 26-OCT-1987
; APPLICATION NUMBER: US 06/881,553
; FILING DATE: 03-JUL-1986
; APPLICATION NUMBER: US 06/843,958
; FILING DATE: 25-MAR-1986
; APPLICATION NUMBER: US 06/799,668
; FILING DATE: 19-NOV-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: 2409K7

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908 298-2987
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; US-08-290-793B-68
;
Query Match          69.6%; Score 16; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
Db      4 FSSW 8

RESULT 13
US-08-277-660A-16
; Sequence 16, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Pickesley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MD2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
; US-08-277-660A-16
;
Query Match          69.6%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
Db      5 FSALW 9

RESULT 14
US-08-277-660A-17
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; Sequence 17, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 398-3249
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-277-660A-17

Query Match 69.6%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 5 FSDAW 9

RESULT 15
US-08-424-957-29
; Sequence 29, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957

; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/277,660
; APPLICATION NUMBER: 20-JUL-1994
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-29

Query Match 69.6%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 5 FSALW 9

RESULT 16
US-08-424-957-30
; Sequence 30, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/277,660
; APPLICATION NUMBER: 20-JUL-1994
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown

US-08-424-957-30

Query Match 69.6%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0;

QY 1 FXXW 5
DB 5 FSDAW 9

RESULT 17

US-09-035-686-29
; Sequence 29, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Pickesley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-09-035-686-29

Query Match 69.6%; Score 16; DB 3; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0;

QY 1 FXXW 5
DB 5 FSALW 9

RESULT 18

US-09-035-686-30
; Sequence 30, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Pickesley, Steven M.

APPLICANT: Lane, David P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
TITLE OF INVENTION: Protein and Therapeutic Application Thereof
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,686
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/424,957
FILING DATE: 19-APR-1995
APPLICATION NUMBER: US 08/277,660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-61228/WH/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-09-035-686-30

Query Match 69.6%; Score 16; DB 3; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0;

QY 1 FXXW 5
DB 5 FSDAW 9

RESULT 19

US-08-406-330-32
; Sequence 32, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/406,330
FILING DATE: 530
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/100
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-32

Query Match 69.6%; Score 16; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 3 FSSW 7

RESULT 20

US-08-556-597-32
Sequence 32, Application US/08556597
Patent No. 5877155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyte, Vicki A.
TITLE OF INVENTION: MINOTOPES AND ANTI-MINOTOPES OF
HUMAN PLATELET GLYCOPROTEIN IB/IX
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/556,597
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-32

Query Match 69.6%; Score 16; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 3 FSSW 7

RESULT 21

US-08-305-871A-23
Sequence 23, Application US/09305871A
Patent No. 5736142
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Gaeta, Federico
APPLICANT: Grey, Howard M.
APPLICANT: Sidney, John
TITLE OF INVENTION: Alteration of Immune Response Using Pan
DR-Binding Peptides
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/305,871A
FILING DATE: 14-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,101
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-0062-10
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..13
OTHER INFORMATION: /note= "Peptide wherein X is
tyrosine or phenylalanine."
US-08-305-871A-23

Query Match 69.6%; Score 16; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 3 FVAW 7

RESULT 22

US-08-912-560-11


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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-218-025A-139

Query Match 69.6%; Score 16; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 1 FNSTW 5

RESULT 29
US-08-847-844A-22
; Sequence 22, Application US/08847844A
; Patent No. 6150160
; GENERAL INFORMATION:
; APPLICANT: KAZAZIAN JR., HAIG H.
; APPLICANT: BOEKE, JEF D.
; APPLICANT: MORAN, JOHN V.
; APPLICANT: DOMBOSKI, BETH A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,844A
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/749,805
; FILING DATE: 16-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,831
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-23U2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-218-025A-139

Query Match 69.6%; Score 16; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 1 FNSTW 5

RESULT 29
US-08-847-844A-22
; Sequence 22, Application US/08847844A
; Patent No. 6150160
; GENERAL INFORMATION:
; APPLICANT: KAZAZIAN JR., HAIG H.
; APPLICANT: BOEKE, JEF D.
; APPLICANT: MORAN, JOHN V.
; APPLICANT: DOMBOSKI, BETH A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,844A
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/749,805
; FILING DATE: 16-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,831
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-23U2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-218-025A-139

Query Match 69.6%; Score 16; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 5 FSQAW 9

RESULT 26
US-08-218-025A-139
; Patent No. 5185431
; APPLICANT: YOSHIMATSU, KENTARO; SHIKATA, YASUSHI; TANAKA, ISAO;
; HASEGAWA, YOSHIKAZU; SETO, TOSHIO; OSAWA, TOSHIO
; TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392,841
; FILING DATE: 11-AUG-1989
; SEQ ID NO: 25;
; LENGTH: 13
; US-08-218-025A-139

Query Match 69.6%; Score 16; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 5 FSQAW 9

RESULT 27
US-08-218-025A-139
; Patent No. 5185431
; APPLICANT: YOSHIMATSU, KENTARO; SHIKATA, YASUSHI; TANAKA, ISAO;
; HASEGAWA, YOSHIKAZU; SETO, TOSHIO; OSAWA, TOSHIO
; TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392,841
; FILING DATE: 11-AUG-1989
; SEQ ID NO: 25;
; LENGTH: 13
; US-08-218-025A-139

Query Match 69.6%; Score 16; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 5 FSQAW 9

RESULT 28
US-08-218-025A-139
; Sequence 139, Application US/08218025A
; Patent No. 5556744
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Ugen, Kenneth E.
; APPLICANT: Williams, William V.
; TITLE OF INVENTION: Methods and Compositions for Diagnosing
; and Treating Certain HIV Infected Patients
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: P.O. Box 457, 321 No. 5556744ristown Road
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-847-844A-22

Query Match 69.6%; Score 16; DB 3; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 6 FIATW 10

RESULT 30
PCT-US93-08699-1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON & JOHNSON and GEORGETOWN UNIVERSITY
; TITLE OF INVENTION: IMMUNOREACTIVE PEPTIDES FROM
; TITLE OF INVENTION: EPSTEIN-BARR VIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08699
; FILING DATE: 15-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD-3033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
PCT-US93-08699-1

Query Match 69.6%; Score 16; DB 5; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 3 FTETW 7

RESULT 31
US-09-330-914A-11

; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-847-844A-22

Query Match 69.6%; Score 16; DB 3; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 6 FIATW 10

RESULT 30
PCT-US93-08699-1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON & JOHNSON and GEORGETOWN UNIVERSITY
; TITLE OF INVENTION: IMMUNOREACTIVE PEPTIDES FROM
; TITLE OF INVENTION: EPSTEIN-BARR VIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08699
; FILING DATE: 15-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD-3033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
PCT-US93-08699-1

Query Match 69.6%; Score 16; DB 5; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 3 FTETW 7

RESULT 31
US-09-330-914A-11

; Sequence 11, Application US/09330914A
; Patent No. 6432671
; GENERAL INFORMATION:
; APPLICANT: Flöhe, Leopold
; No. 6432671ecke, Everson
; Kalisz, Henryk
; Montemartini, Marisa
; TITLE OF INVENTION: TRYPARADOXIN, EXPRESSION PLASMID, PROCESS OF
; PRODUCTION, METHOD OF USE, TEST KIT, AND
; PHARMACEUTICAL COMPOSITION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: Unites States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,914A
; FILING DATE: 11-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/06983
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, James P.
; REGISTRATION NUMBER: 28,491
; REFERENCE/DOCKET NUMBER: 29473/35678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-330-914A-11

Query Match 69.6%; Score 16; DB 4; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 8 FQSW 12

RESULT 32
US-08-413-233-3
; Sequence 3, Application US/08413233
; Patent No. 6506553
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard S.
; APPLICANT: Parks, D. Ello
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS OF EPSTEIN-BARR
; TITLE OF INVENTION: VIRUS ASSOCIATED DISEASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOEB AND LOEB
; STREET: 1880 Century Park East, 5th Floor
; CITY: Los Angeles
; STATE: California
```

; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,233
; FILING DATE: 30-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Yang, Wei-ning
; REGISTRATION NUMBER: 38,690
; REFERENCE/DOCKET NUMBER: 7586D.4007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 553-5050
; TELEFAX: (310) 553-4619
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..16
; US-08-413-233-3

Query Match 69.6%; Score 16; DB 4; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
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DB 3 FTETW 7

RESULT 33
US-09-690-454-88
; Sequence 88, Application US/09690454
; Patent No. 6531447
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/09/690,454
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 16

; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-690-454-88

Query Match 69.8%; Score 16; DB 4; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
DB 8 FRSAW 12

RESULT 34

US-09-170-496D-285
; Sequence 285, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 285
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6555339el Sequence
; US-09-170-496D-285

Query Match 69.6%; Score 16; DB 4; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
DB 5 FMSTW 9

RESULT 35

US-08-218-025A-115
; Sequence 115, Application US/08218025A
; Patent No. 5556744
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Ugen, Kenneth E.
; APPLICANT: Williams, William V.
; TITLE OF INVENTION: Methods and Compositions for Diagnosing
; TITLE OF INVENTION: and Treating Certain HIV Infected Patients
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: P.O. Box 457, 321 No. 5556744ristown Road
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-218-025A-115

Query Match          69.6%; Score 16; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
DB      13 FNSTW 17

RESULT 36
US-08-746-283-7
; Sequence 7, Application US/08746283
; Patent No. 5834280
; GENERAL INFORMATION:
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Si, Joan Q.
; APPLICANT: Aagaard, Jesper
; TITLE OF INVENTION: Glucose Oxidases
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5834280 No. 5834280disk of No. 5834280th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,283
; FILING DATE: 07-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Agtis, Dr. Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4158.214-US
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5834280e
US-08-746-283-7

Query Match          69.6%; Score 16; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
DB      13 FNSTW 17
```

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DB      3 FTSVW 7

RESULT 37
US-08-746-257A-5
; Sequence 5, Application US/08746257A
; Patent No. 5879921
; GENERAL INFORMATION:
; APPLICANT: Cherry, Joel
; APPLICANT: Berka, Randy
; APPLICANT: Halkier, Torben
; TITLE OF INVENTION: Glucose Oxidases
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5879921 No. 5879921disk of No. 5879921th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,257A
; FILING DATE: 07-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Starnes, Robert L.
; REGISTRATION NUMBER: 41,324
; REFERENCE/DOCKET NUMBER: 4700.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5879921e
US-08-746-257A-5

Query Match          69.6%; Score 16; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
DB      3 FTSVW 7

RESULT 38
US-08-987-743-11
; Sequence 11, Application US/08987743
; Patent No. 6123938
; GENERAL INFORMATION:
; APPLICANT: Stern, Robert
; APPLICANT: Csoka, Anthony
; APPLICANT: Frost, Gregory I.
; APPLICANT: Wong, Tim M.
; TITLE OF INVENTION: Purification and Microsequencing of
; FILE REFERENCE: 9076/088CIP2
; CURRENT APPLICATION NUMBER: US/08/987,743
; CURRENT FILING DATE: 1997-12-09
; EARLIER APPLICATION NUMBER: 08/733,360
; EARLIER FILING DATE: 1996-10-17
; NUMBER OF SEQ ID NOS: 16
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: H. sapiens
US-08-987-743-11

Query Match
Best Local Similarity 69.6%; Score 16; DB 3; Length 17;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 11 FTTW 15

RESULT 39
US-09-170-496D-286
; Sequence 286, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 286
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6555339el Sequence
US-09-170-496D-286

Query Match
Best Local Similarity 69.6%; Score 16; DB 4; Length 17;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 5 FMSTW 9

RESULT 40
US-08-934-915-125
; Sequence 125, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-125

Query Match
Best Local Similarity 69.6%; Score 16; DB 2; Length 18;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 7 FSRTW 11

Search completed: October 18, 2005, 16:00:25
Job time : 35.7647 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2005, 15:17:40 ; Search time 109.647 Seconds
(without alignments)
37.362 Million cell updates/sec

Title: US-09-214-371-10

Perfect score: 23

Sequence: 1 FXXWXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	17	73.9	9	1 AKH HELZE	P67787 heliothis z
2	17	73.9	13	2 Q9XLI2	Q9XLI2 bemisia tab
3	17	73.9	26	2 Q9S880	Q9S880 spinacia ol
4	17	73.9	29	2 Q7RQ81	Q7RQ81 plasmodium
5	17	73.9	32	2 Q05602	Q05602 pseudomonas
6	17	73.9	35	2 Q72FN9	Q72FN9 desulfovibr
7	17	73.9	36	2 Q9PV61	Q9PV61 mola mola (
8	17	73.9	38	1 P9AI PROMA	Q87786 prochloroco
9	17	73.9	38	2 Q7U4F1	Q7U4F1 synechococc
10	17	73.9	38	2 Q7V513	Q7V513 prochloroco
11	17	73.9	38	2 Q9PV63	Q9PV63 pseudopleur
12	17	73.9	40	2 Q9PT24	Q9PT24 oncorhynch
13	17	73.9	40	2 Q9PT28	Q9PT28 salarias sp
14	17	73.9	40	2 Q9PT29	Q9PT29 epinephelus
15	17	73.9	40	2 Q9PU00	Q9PU00 dicentrarch
16	17	73.9	40	2 Q9PU01	Q9PU01 dendrochiru
17	17	73.9	40	2 Q9PU02	Q9PU02 zeus faber
18	17	73.9	40	2 Q9PU03	Q9PU03 sargocentro
19	17	73.9	40	2 Q9PU04	Q9PU04 fundulus he
20	17	73.9	40	2 Q9PU05	Q9PU05 hemiramphus
21	17	73.9	40	2 Q9PU06	Q9PU06 lampiris sp.
22	17	73.9	40	2 Q9PV62	Q9PV62 ostracion s
23	17	73.9	40	2 Q9PV64	Q9PV64 channa sp.
24	17	73.9	40	2 Q9PV65	Q9PV65 colisa lai
25	17	73.9	40	2 Q9PV66	Q9PV66 stromateus
26	17	73.9	40	2 Q9PV68	Q9PV68 acanthurus
27	17	73.9	40	2 Q9PV69	Q9PV69 cryptocentr
28	17	73.9	40	2 Q9PV70	Q9PV70 disostichu
29	17	73.9	40	2 Q9PV71	Q9PV71 mullus sp.
30	17	73.9	40	2 Q9PV72	Q9PV72 lates calca
31	17	73.9	40	2 Q9PV73	Q9PV73 mastacembel

32	17	73.9	40	2 Q9PV74	Q9PV74 hippocampus
33	17	73.9	40	2 Q9PV75	Q9PV75 poecilia la
34	17	73.9	40	2 Q9PV77	Q9PV77 mugil cepha
35	17	73.9	40	2 Q9PV78	Q9PV78 lophius sp.
36	17	73.9	40	2 Q9PV79	Q9PV79 galaxias ma
37	17	73.9	40	2 Q9PV80	Q9PV80 plecoglossu
38	17	73.9	40	2 Q9PV81	Q9PV81 esox lucius
39	17	73.9	40	2 Q9PV82	Q9PV82 barbus tetr
40	17	73.9	40	2 Q9PV84	Q9PV84 anguilla sp
41	17	73.9	40	2 Q9PV85	Q9PV85 osteoglossu
42	17	73.9	40	2 Q9PV88	Q9PV88 torpedo cal
43	17	73.9	40	2 Q9PV89	Q9PV89 triakis sp.
44	17	73.9	41	2 Q9PV02	Q9PV02 polypterus
45	17	73.9	44	2 Q8XPJ4	Q8XPJ4 raietonia s
46	17	73.9	48	2 Q6H9V4	Q6H9V4 phage phi 4
47	17	73.9	49	2 Q8EF00	Q8EF00 shewanella
48	17	73.9	53	2 Q80077	Q80077 staphylococ
49	17	73.9	53	2 Q8SDM7	Q8SDM7 staphylococ
50	17	73.9	53	2 Q6R847	Q6R847 bacterioph
51	17	73.9	53	2 Q9B0G7	Q9B0G7 staphylococ
52	17	73.9	53	2 Q9G031	Q9G031 bacterioph
53	17	73.9	53	2 Q8NVN8	Q8NVN8 staphylococ
54	17	73.9	53	2 Q8NWC8	Q8NWC8 staphylococ
55	17	73.9	53	2 Q931J8	Q931J8 staphylococ
56	17	73.9	53	2 Q99SQ2	Q99SQ2 staphylococ
57	17	73.9	53	2 Q6G7V0	Q6G7V0 staphylococ
58	17	73.9	53	2 Q6GAP3	Q6GAP3 staphylococ
59	17	73.9	53	2 Q6GF65	Q6GF65 staphylococ
60	17	73.9	53	2 Q6GGM4	Q6GGM4 staphylococ
61	17	73.9	54	2 Q645F8	Q645F8 stereochilu
62	17	73.9	54	2 Q8VSJ2	Q8VSJ2 shigella fl
63	17	73.9	54	2 Q6AQ08	Q6AQ08 desulfotale
64	17	73.9	55	2 Q644C2	Q644C2 hydromantes
65	17	73.9	55	2 Q9MBS6	Q9MBS6 staphylococ
66	17	73.9	55	2 Q8FPA2	Q8FPA2 corynebacte
67	17	73.9	57	2 Q8WYF2	Q8WYF2 homo sapien
68	17	73.9	65	1 AKH_MANSE	P67788 manduca sex
69	17	73.9	67	2 Q64109	Q64109 bacterioph
70	17	73.9	67	2 Q34509	Q34509 bacillus su
71	17	73.9	68	2 Q97736	Q97736 human immun
72	17	73.9	69	2 Q6YZN9	Q6YZN9 oryza sativ
73	17	73.9	69	2 Q84NA8	Q84NA8 arabidopsis
74	17	73.9	70	2 Q68124	Q68124 gasteroste
75	17	73.9	70	2 Q68127	Q68127 gasteroste
76	17	73.9	70	2 Q9MJL9	Q9MJL9 scenedesmus
77	17	73.9	70	2 Q69587	Q69587 mycobacteri
78	17	73.9	72	2 Q88601	Q88601 tobaccos mos
79	17	73.9	77	1 PUFQ_RHOSH	P16069 rhodobacter
80	17	73.9	78	2 Q678B4	Q678B4 lymphocyati
81	17	73.9	79	2 Q82YT7	Q82YT7 enterococcu
82	17	73.9	81	2 Q984H4	Q984H4 rhizobium l
83	17	73.9	82	2 Q7EY23	Q7EY23 oryza sativ
84	17	73.9	84	1 Y149_ARCFU	Y149_ARCFU archaeoglob
85	17	73.9	84	2 Q60744	Q60744 homo sapien
86	17	73.9	84	2 Q42015	Q42015 arabidopsis
87	17	73.9	85	2 Q6ZLK9	Q6ZLK9 oryza sativ
88	17	73.9	86	2 Q7PP04	Q7PP04 anopheles g
89	17	73.9	87	2 Q8U3P7	Q8U3P7 pyrococcus
90	17	73.9	87	2 Q6YVF4	Q6YVF4 oryza sativ
91	17	73.9	88	1 TH12_DICDI	P29446 dictyostell
92	17	73.9	88	2 Q8PZQ6	Q8PZQ6 methanosarc
93	17	73.9	89	2 Q6IG64	Q6IG64 drosophila
94	17	73.9	89	2 Q9B049	Q9B049 mycobacteri
95	17	73.9	89	2 Q7P017	Q7P017 chromobacte
96	17	73.9	92	2 Q9F1H3	Q9F1H3 enterococcu
97	17	73.9	92	2 Q9LCU1	Q9LCU1 thermotoga
98	17	73.9	93	1 CD06_HUMAN	Q99440 homo sapien
99	17	73.9	93	2 Q8TL30	Q8TL30 methanosarc
100	17	73.9	95	2 Q7YX88	Q7YX88 caenorhabdi

ALIGNMENTS

```

RESULT 1
AKH HELZE
ID AKH HELZE STANDARD; PRT; 9 AA.
AC P67787; P08901;
DT 01-NOV-1988 (Rel. 09, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adipokine hormone (Hes-AKH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helioverpa.
OX NCBI_TaxID=7113;
RN [1]
RP SEQUENCE.
RX MEDLINE=06186794; PubMed=3964263;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Holman G.M.,
RA Wagner R.M., Ridgway R.L., Hayes D.K.;
RT "Isolation and primary structure of a peptide from the corpora
RT cardaca of Heliothis zea with adipokinetic activity.";
RL Biochem. Biophys. Res. Commun. 135:622-628(1986).
CC -1- FUNCTION: This hormone, released from cells in the corpora
CC cardaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A24244; A24244.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
DR Amidation; Direct protein sequencing; Flight; Neuropeptide;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 Pyroglutamate carboxylic acid.
FT MOD_RES 9 9 Glycine amide.
SQ SEQUENCE 9 AA; 1026 MW; 403665A5A1A9D1A7 CRC64;

Query Match 73.9%; Score 17; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 4 FTSSW 8

RESULT 2
Q9XLI2
ID Q9XLI2 PRELIMINARY; PRT; 13 AA.
AC Q9XLI2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase I (Fragment).
OS Bemisia tabaci (Sweetpotato whitefly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleyrodiformes;
OC Aleyrodoidae; Aleyrodidae; Aleyrodinae; Bemisia.
OX NCBI_TaxID=7038;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10583831;
RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,
RA Brown J.K.;
RT "A phylogeographical analysis of the Bemisia tabaci species complex
RT based on mitochondrial DNA markers.";
RL Mol. Ecol. 8:1683-1691(1999).
DR EMBL; AF10703; AAD28415.1;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;

Query Match 73.9%; Score 17; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 4 FTSSW 8

RESULT 3
Q9S880
ID Q9S880 PRELIMINARY; PRT; 26 AA.
AC Q9S880;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thioresoxin H2 (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX MEDLINE=91378382; PubMed=1897989;
RA Marcus F., Chamberlain S.H., Chu C., Masiarz F.R., Shin S., Yee B.C.,
RA Buchanan B.B.;
RT "Plant thioresoxin h: an animal-like thioresoxin occurring in multiple
RT cell compartments.";
RL Arch. Biochem. Biophys. 287:195-198(1991).
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioresoxin.
DR InterPro; IPR006663; Thioresoxin_dom2.
DR Pfam; PF00085; Thioresoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Redox-active center.
FT NON_TER 1 1
FT NON_TER 26 26
SQ SEQUENCE 26 AA; 2880 MW; A5317FC47DDB8863 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 26;
Best Local Similarity 40.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 6 FTASW 10

RESULT 4
Q7RQ81
ID Q7RQ81 PRELIMINARY; PRT; 29 AA.
AC Q7RQ81;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Names:PY01221;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteaux M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,

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RA Florens L., Yates F.R. III, Raine J.D., Sindén R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.,
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite *Plasmodium yoelii* yoelii.",
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL: AABL01000318; EAA20511.1; --
 DR Hypothetical protein.
 KW Desulfococcus proteobacteriae; Desulfococcus proteobacteriae;
 SQ SEQUENCE 29 AA; 3408 MW; F36142D3148EE117 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 29;
 Best Local Similarity 40.0%; Pred. No. 5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

Qy 1 FXXXW 5
 |
 Db 11 FSASW 15

RESULT 5

ID O05602 PRELIMINARY; PRT; 32 AA.
 AC O05602;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Transposon Tn5041 DNA (Fragment).
 OS Pseudomonas sp.
 OC Bacteria; Proteobacteria.
 OX NCBI_TaxID=306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KHP41;
 RX MEDLINE=97419493; PubMed=9274008;
 RA Kholidi G.Y., Yurieva O.V., Gorlenko Z.M., Mindlin S.Z., Bass I.A.,
 RA Lomovskaya O.L., Kopteva A.V., Nikiforov V.G.;
 RT "Tn5041: a chimeric mercury resistance transposon closely related to
 RT the toluene degradative transposon Tn4651.";
 RL Microbiology 143:2549-2556(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KHP41;
 RA Kholidi G.Y., Mindlin S.Z., Gorlenko Z.M., Bass I.A., Kalyaeva E.S.,
 RA Nikiforov V.;
 RT "Host-dependent transposition of Tn5041.";
 RL Russ. J. Genet. 36:365-373(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KHP41;
 RX MEDLINE=22315381; PubMed=12427948;
 RA Kholidi G., Gorlenko Z., Mindlin S., Hobman J., Nikiforov V.;
 RT "Tn5041-like transposons: molecular diversity, evolutionary
 RT relationships and distribution of distinct variants in environmental
 RT bacteria.";
 RL Microbiology 148:3569-3582(2002).
 DR EMBL: X98999; CAA67458.1; --
 FT NON TER 1 1
 FT NON TER 32 32
 SQ SEQUENCE 32 AA; 3298 MW; AF42B5EEF917077A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 32;
 Best Local Similarity 40.0%; Pred. No. 5.4e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 |
 Db 11 FSSSW 15

RESULT 6

Q72FN9 PRELIMINARY; PRT; 35 AA.
 AC Q72FN9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=DVU0174;
 OS Desulfococcus proteobacteriae (strain Hildenborough / ATCC 29579 / NCIMB 8303).
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfococcinales;
 OC Desulfococcaceae; Desulfococcus.
 OX NCBI_TaxID=882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15077118; DOI=10.1038/nbt959;
 RA Heidelberg J.F., Seshadri R., Haveman S.A., Henne C.L., Paulsen I.T.,
 RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
 RA Dougherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
 RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
 RA Peterson J.D., Daviden T.M., Zafar N., Zhou L., Radune D.,
 RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
 RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
 RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
 RT Desulfococcus proteobacteriae Hildenborough.";
 RL Nat. Biotechnol. 22:554-559(2004).
 DR EMBL: AE017309; AAS94658.1; --
 DR TIGR: DVU0174; --
 KW Complete proteome.
 SQ SEQUENCE 35 AA; 3907 MW; CD423DA7D1422A7E CRC64;

Query Match 73.9%; Score 17; DB 2; Length 35;
 Best Local Similarity 40.0%; Pred. No. 5.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 |
 Db 15 FATAW 19

RESULT 7

Q9PV61 PRELIMINARY; PRT; 36 AA.
 AC Q9PV61;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Dystrophin (Fragment).
 GN Name=Dyst;
 OS Mola mola (ocean sunfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Molidae; Mola.
 OX NCBI_TaxID=94237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
 RA Venkatesh B., Ning Y., Brenner S.;
 RT "Late changes in spliceosomal introns define clades in vertebrate
 RT evolution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
 DR EMBL: AF137130; AAD54215.1; --
 DR HSSP: P11532; 1DXX.
 DR InterPro; IPR001715; Calponin-like.
 FT NON TER 1 1
 FT NON TER 36 36
 SQ SEQUENCE 36 AA; 4181 MW; DE01642A8CAAFCL8 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 36;
 Best Local Similarity 40.0%; Pred. No. 5.9e+03;

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Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 32 FSSSW 36

RESULT 8
PSAI_PROMA STANDARD; PRT; 38 AA.
AC 087786;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 08-JUL-2004 (Rel. 44, Last annotation update)
DE Photosystem I reaction center subunit VIII.
GN Name=psai; OrderedLocNames=Pro1678;
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1219;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SARG / CMP 1375 / SS120;
RA van der Staay G.W.M., Moon-van der Staay S.Y., Garczarek L.,
RA Partensky F.;
RT "Characterization of the photosystem I subunits Psai and Psal from two
RT strains of the marine cyanobacterium Prochlorococcus."
RL Photosyn. Res. 57:183-191(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SARG / CMP 1375 / SS120;
RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
RA Wolf Y.I., Hess W.R.;
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT a nearly minimal phototrophic genome."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
CC -!- FUNCTION: May help in the organization of the psal subunit.
CC -!- SIMILARITY: Belongs to the psal family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z98594; CAB11178.1; ALT INIT.
DR EMBL; AE017166; AAQ00722.1; -.
DR HAMAP; MF 00431; atypical; 1.
DR InterPro; IPR001302; PSI_8.
DR Pfam; PF00796; PSI_8; 1.
KW Complete proteome; Photosynthesis; Photosystem I; Transmembrane.
FT TRANSMEM 12 32 Potential.
SQ SEQUENCE 38 AA; 4081 MW; 19DCDABA650A2F2 CRC64;

Query Match 73.9%; Score 17; DB 1; Length 38;
Best Local Similarity 40.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 5 FAATW 9

RESULT 9
Q7U4F1 PRELIMINARY; PRT; 38 AA.
ID Q7U4F1
AC Q7U4F1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Photosystem I subunit VIII (Psal).
GN Name=psai; OrderedLocNames=SYNW2117;
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahmeha B., Larimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarran J.,
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus."
RL Nature 424:1037-1042(2003).
RL EMBL; BX569694; CAB08632.1; -.
KW Complete proteome.
SQ SEQUENCE 38 AA; 3975 MW; 75BEAB4500A52503 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 38;
Best Local Similarity 40.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 5 FAATW 9

RESULT 10
Q7V513 PRELIMINARY; PRT; 38 AA.
ID Q7V513
AC Q7V513;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Photosystem I subunit VIII (Psal).
GN Name=psai; OrderedLocNames=PMT1767;
OS Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation."
RL Nature 424:1042-1047(2003).
RL EMBL; BX572100; CAB21942.1; -.
KW Complete proteome.
SQ SEQUENCE 38 AA; 4097 MW; 017DCC1CD4C3F4E2 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 38;
Best Local Similarity 40.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db 5 FAATW 9

RESULT 11
Q9PV63 PRELIMINARY; PRT; 38 AA.
ID Q9PV63
AC Q9PV63;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE Dystrophin (Fragment).
GN Name=Dyst;
OS Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
OS americanus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
OX NCBI_TaxID=8265;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137128; AAD54213.1; -.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
FT NON_TER 1
FT NON_TER 38
FT NON_TER 38
SQ SEQUENCE 38 AA; 4424 MW; 41C67E01642A8CB0 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 38;
Best Local Similarity 40.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 32 FSSW 36

RESULT 12
Q9PT24
ID Q9PT24 PRELIMINARY; PRT; 40 AA.
AC Q9PT24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137093; AAD54187.1; -.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4551 MW; B485AA19BDB4B17 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 32 FSSW 36

RESULT 13
Q9PT28
ID Q9PT28 PRELIMINARY; PRT; 40 AA.

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AC Q9PT28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Salarias sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Blennioidei;
OC Blenniidae; Salarias.
OX NCBI_TaxID=94312;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137121; AAD54206.1; -.
DR EMBL; AF137120; AAD54206.1; JOINED.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 32 FSSW 36

RESULT 14
Q9PT29
ID Q9PT29 PRELIMINARY; PRT; 40 AA.
AC Q9PT29;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Epinephelus coioides (Orange-spotted grouper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Serranidae; Epinephelinae; Epinephelus.
OX NCBI_TaxID=94232;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137117; AAD54203.1; -.
DR EMBL; AF137116; AAD54203.1; JOINED.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

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Db          32 FSSW 36

RESULT 15
Q9PU00
ID Q9PU00 PRELIMINARY; PRT; 40 AA.
AC Q9PU00;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Dicertrachus labrax (European sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Dicertrachus.
OX NCBI_TaxID=13489;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137115; AAD54202.1; -.
DR EMBL; AF137114; AAD54202.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db          32 FSSW 36

RESULT 16
Q9PU01
ID Q9PU01 PRELIMINARY; PRT; 40 AA.
AC Q9PU01;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Dendrochirus zebra (Zebra turkeyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Scorpaenidae; Scorpaenidae; Pteroinae; Dendrochirus.
OX NCBI_TaxID=94308;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137112; AAD54200.1; -.
DR EMBL; AF137111; AAD54200.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40

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SQ SEQUENCE 40 AA; 4638 MW; B49D49A67E0167B5 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db          32 FSSW 36

RESULT 17
Q9PU02
ID Q9PU02 PRELIMINARY; PRT; 40 AA.
AC Q9PU02;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Zeus faber (John Dory).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Zeiformes; Zeidae; Zeus.
OX NCBI_TaxID=64108;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137108; AAD55460.1; -.
DR EMBL; AF137107; AAD55460.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4645 MW; BA7D49A676A3642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db          32 FSSW 36

RESULT 18
Q9PU03
ID Q9PU03 PRELIMINARY; PRT; 40 AA.
AC Q9PU03;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Sargocentron sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Beryciformes; Holocentridae;
OC Sargocentron.
OX NCBI_TaxID=94226;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137106; AAD54196.1; -.

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DR EMBL; AF137105; AAD54196.1; JOINED.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4579 MW; B49C92D67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5
Db 32 FSSW 36

RESULT 19
Q9PU04 PRELIMINARY; PRT; 40 AA.
AC Q9PU04;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137103; AAD54194.1; -.
DR EMBL; AF137102; AAD54194.1; JOINED.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5
Db 32 FSSW 36

RESULT 20
Q9PU05 PRELIMINARY; PRT; 40 AA.
AC Q9PU05;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Hemiramphus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Hemiramphidae; Hemiramphus.
OX NCBI_TaxID=94223;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=93398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137101; AAD54193.1; -.
DR EMBL; AF137100; AAD54193.1; JOINED.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5
Db 32 FSSW 36

RESULT 21
Q9PU06 PRELIMINARY; PRT; 40 AA.
AC Q9PU06;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Lampiris sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Lampridiformes; Lamprididae; Lampiris.
OX NCBI_TaxID=94303;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137096; AAD54189.1; -.
DR EMBL; AF137095; AAD54189.1; JOINED.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5
Db 32 FSSW 36

RESULT 22
Q9PV62 PRELIMINARY; PRT; 40 AA.
AC Q9PV62;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Ostracion sp. IMCB-2002.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Ostraciidae; Ostreacion; unclassified Ostreacion.
OX NCBI_TaxID=188530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137129; AAD54214.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4582 MW; B49D4BCBE01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 32 FSSW 36

RESULT 23
Q9PV64 PRELIMINARY; PRT; 40 AA.
AC Q9PV64;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Channa sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Channoidei;
OC Channidae; Channa.
OX NCBI_TaxID=94222;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137127; AAD54212.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 32 FSSW 36

RESULT 24
Q9PV65 PRELIMINARY; PRT; 40 AA.
AC Q9PV65;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Colisa lalia (dwarf gourami).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Anabantoidei; Belontiidae; Colisa.
OX NCBI_TaxID=50373;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137126; AAD54211.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 32 FSSW 36

RESULT 25
Q9PV66 PRELIMINARY; PRT; 40 AA.
AC Q9PV66;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Stromateus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Stromateoidei; Stromateidae; Stromateus.
OX NCBI_TaxID=94245;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137125; AAD54210.1; -.
DR HSSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 32 FSSW 36

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RESULT 26
Q9PV68      PRELIMINARY;      PRT;      40 AA.
AC Q9PV68;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Acanthureus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Acanthuroidei; Acanthuridae; Acanthurus.
OX NCBI_TaxID=94220;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137123; AAD54208.1; -.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4592 MW; B48FES66BDB542A CRC64;

Query Match      73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 32 FSSW 36

RESULT 27
Q9PV69      PRELIMINARY;      PRT;      40 AA.
AC Q9PV69;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Cryptocentrus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidi;
OC Gobiidae; Cryptocentrus.
OX NCBI_TaxID=94314;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137122; AAD54207.1; -.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT PROSITE; PS50021; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4611 MW; B49D4A67E01756E CRC64;

Query Match      73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 32 FSSW 36

RESULT 28
Q9PV70      PRELIMINARY;      PRT;      40 AA.
AC Q9PV70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Dissostichus mawsoni (Antarctic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidi; Nototheniidae; Dissostichus.
OX NCBI_TaxID=36200;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137119; AAD54205.1; -.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D4A67E01642A CRC64;

Query Match      73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 32 FSSW 36

RESULT 29
Q9PV71      PRELIMINARY;      PRT;      40 AA.
AC Q9PV71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Mullus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidi;
OC Mullidae; Mullus.
OX NCBI_TaxID=94224;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137118; AAD54204.1; -.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40

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SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;
Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSSW 36

RESULT 30
Q9PV72 PRELIMINARY; PRT; 40 AA.
AC Q9PV72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Lates calcarifer (Barramundi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Centropomidae; Lates.
OC NCBI_TaxID=8187;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137113; AAD54201.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSSW 36

RESULT 31
Q9PV73 PRELIMINARY; PRT; 40 AA.
AC Q9PV73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Mastacembelus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Synbranchiiformes;
OC Mastacembelidae; Mastacembelus.
OC NCBI_TaxID=94235;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137110; AAD54199.1; -.

SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;
Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSSW 36

RESULT 32
Q9PV74 PRELIMINARY; PRT; 40 AA.
AC Q9PV74;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Hippocampus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
OC Syngnathidae; Hippocampus.
OC NCBI_TaxID=72047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137109; AAD54198.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
DR PROSITE; PS50021; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4541 MW; B49D487D0E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSSW 36

RESULT 33
Q9PV75 PRELIMINARY; PRT; 40 AA.
AC Q9PV75;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Poecilia latipinna.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Poecilia.
OC NCBI_TaxID=48699;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137104; AAD54191.1; -.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 32 FSSSW 36

RESULT 34
Q9PV77 ID Q9PV77 PRELIMINARY; PRT; 40 AA.
AC Q9PV77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Mugil cephalus (Flathead mullet) (Mugil japonicus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Mugilomorpha; Mugilidae;
OC Mugil
OX NCBI_TaxID=48193;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137098; AAD54191.1; -.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 32 FSSSW 36

RESULT 35
Q9PV78 ID Q9PV78 PRELIMINARY; PRT; 40 AA.
AC Q9PV78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Lophius sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

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OC Acanthomorpha; Paracanthopterygii; Lophiiformes; Lophiidae; Lophius.
OX NCBI_TaxID=30791;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137097; AAD54190.1; -.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 32 FSSSW 36

RESULT 36
Q9PV79 ID Q9PV79 PRELIMINARY; PRT; 40 AA.
AC Q9PV79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Galaxias maculatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Galaxiidae; Galaxias.
OX NCBI_TaxID=61620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137094; AAD54188.1; -.
DR HSP; P11532; IDXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4613 MW; BA7C92D67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 32 FSSSW 36

RESULT 37
Q9PV80 ID Q9PV80 PRELIMINARY; PRT; 40 AA.
AC Q9PV80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;

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OS Plecoglossus altivelis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Osmeridae; Plecoglossus.
OX NCBI_TaxID=61084;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137092; AAD54186.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4512 MW; B4931BF59BDB542A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 32 FSSSW 36

RESULT 38
Q9PV81 ID Q9PV81 PRELIMINARY; PRT; 40 AA.
AC Q9PV81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Eox lucius (Northern pike).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Esociformes;
OC Esocidae; Eox.
OX NCBI_TaxID=8010;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137091; AAD54185.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4542 MW; 09165AA193794B14 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 32 FSSSW 36

RESULT 39
Q9PV82 ID Q9PV82 PRELIMINARY; PRT; 40 AA.
AC Q9PV82;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Barbus tetrazona.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Barbus.
OX NCBI_TaxID=94221;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137090; AAD54184.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4573 MW; 459B37C19BC3E736 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 32 FSSSW 36

RESULT 40
Q9PV84 ID Q9PV84 PRELIMINARY; PRT; 40 AA.
AC Q9PV84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Anguilla sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=62126;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137088; AAD54182.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
DR PROSITE; PS50021; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT NON_TER 40
SQ SEQUENCE 40 AA; 4574 MW; 557846E66BDB5437 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 32 FSSSW 36

Search completed: October 18, 2005, 15:30:09
Job time : 113.647 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:31:13 ; Search time 109.176 Seconds
(without alignments)
28.340 Million cell updates/sec

Title: US-09-214-371-10

Perfect score: 23

Sequence: 1 FXXWXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 716780

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	73.9	9	7	Adc07129 Honeybee
2	17	73.9	9	7	Adc07134 Painted 1
3	17	73.9	10	3	Aab10010 H. pylori
4	17	73.9	10	4	Aab86090 H. pylori
5	17	73.9	10	4	Aab86058 H. pylori
6	17	73.9	11	7	Adc07163 Painted 1
7	17	73.9	13	4	Aae05735 Complemen
8	17	73.9	13	6	Abg75574 CDR3 pept
9	17	73.9	14	4	Aam98088 Human pep
10	17	73.9	15	2	Aar97874 Japan ced
11	17	73.9	15	2	Aar97875 Japan ced
12	17	73.9	15	2	Aaw57758 Residues
13	17	73.9	19	5	Aae23038 Human thi
14	17	73.9	20	2	Aaw42165 T-cell ep
15	17	73.9	20	4	Aag62999 Complemen
16	16	69.6	5	8	Adr68284 Androgen
17	16	69.6	6	2	Aaw76953 Fusion im
18	16	69.6	6	6	AbR46309 Staphyloc
19	16	69.6	6	6	AbR46270 Staphyloc
20	16	69.6	6	6	AbR46702 Staphyloc
21	16	69.6	6	6	AbR47093 Staphyloc
22	16	69.6	6	6	AbR45149 Staphyloc
23	16	69.6	6	6	AbR45486 Staphyloc
24	16	69.6	6	6	AbR45878 Staphyloc
25	16	69.6	6	6	AbR46661 Staphyloc

26	16	69.6	6	6	ABR47053 Staphyloc
27	16	69.6	6	6	ABR45190 Staphyloc
28	16	69.6	6	6	ABR45877 Staphyloc
29	16	69.6	6	6	ABR46310 Staphyloc
30	16	69.6	6	6	ABR47094 Staphyloc
31	16	69.6	6	6	ABR46701 Staphyloc
32	16	69.6	6	6	ABR47054 Staphyloc
33	16	69.6	6	6	ABR45525 Staphyloc
34	16	69.6	6	6	ABR45918 Staphyloc
35	16	69.6	6	6	ABR45189 Staphyloc
36	16	69.6	6	6	ABR45485 Staphyloc
37	16	69.6	6	6	ABR45150 Staphyloc
38	16	69.6	6	6	ABR45526 Staphyloc
39	16	69.6	6	6	ABR46269 Staphyloc
40	16	69.6	6	6	ABR46662 Staphyloc
41	16	69.6	6	6	ABR45917 Staphyloc
42	16	69.6	6	7	ADL17086 Phase-dis
43	16	69.6	7	5	ABP53945 VEGFR-3 b
44	16	69.6	7	7	ADb47984 Novel hum
45	16	69.6	7	8	ADJ55339 Novel hum
46	16	69.6	8	2	AAV18082 Histamine
47	16	69.6	8	6	ABR53957 Beta-secr
48	16	69.6	8	6	ABR54100 Beta-secr
49	16	69.6	8	6	ABR54133 Beta-secr
50	16	69.6	8	6	ABR54102 Beta-secr
51	16	69.6	8	6	ABR54137 Beta-secr
52	16	69.6	8	6	ABR54108 Beta-secr
53	16	69.6	8	6	ABR54106 Beta-secr
54	16	69.6	8	6	ABR54135 Beta-secr
55	16	69.6	8	6	ABR53955 Beta-secr
56	16	69.6	8	6	ABR54129 Beta-secr
57	16	69.6	8	6	ABR54139 Beta-secr
58	16	69.6	8	6	ABR54104 Beta-secr
59	16	69.6	8	6	ABR54131 Beta-secr
60	16	69.6	8	6	ABR53953 Beta-secr
61	16	69.6	8	6	ABR54127 Beta-secr
62	16	69.6	8	6	ABR54141 Beta-secr
63	16	69.6	8	7	ADC07151 Libanaseid
64	16	69.6	8	7	ADC07141 Phymateus
65	16	69.6	8	7	ADC07150 Cricket A
66	16	69.6	8	7	ADC07130 Desert lo
67	16	69.6	8	7	ADC07137 Migratory
68	16	69.6	8	7	ADC07156 Onitis AK
69	16	69.6	8	8	ADR69591 Novel hyb
70	16	69.6	8	8	ADL27410 Amino aci
71	16	69.6	9	2	AAV48085 Immunogen
72	16	69.6	9	4	AAE01057 Human sec
73	16	69.6	9	5	ABP53956 VEGFR-3 b
74	16	69.6	9	5	ABP47522 N. mening
75	16	69.6	9	5	ABG97262 Human leu
76	16	69.6	9	5	AAE31347 Human tyr
77	16	69.6	9	8	ADH41183 Human rar
78	16	69.6	9	8	ADH41163 Human rar
79	16	69.6	9	8	ADH41153 Human pap
80	16	69.6	9	8	ADK09130 Human pap
81	16	69.6	9	8	ADN65877 HLA bindi
82	16	69.6	9	8	ADQ71598 Cancer re
83	16	69.6	9	8	ADQ72073 Cancer re
84	16	69.6	9	8	ADQ68606 Cancer re
85	16	69.6	9	8	ADQ72380 Cancer re
86	16	69.6	9	8	ADQ69652 Cancer re
87	16	69.6	9	8	ADQ72453 Cancer re
88	16	69.6	9	8	ADQ69664 Cancer re
89	16	69.6	9	8	ADQ71463 Cancer re
90	16	69.6	9	8	ADQ72148 Cancer re
91	16	69.6	9	8	ADQ72239 Cancer re
92	16	69.6	9	8	ADQ69952 Cancer re
93	16	69.6	9	8	ADQ70871 Cancer re
94	16	69.6	9	8	ADQ72479 Cancer re
95	16	69.6	9	8	ADQ70635 Cancer re
96	16	69.6	9	8	ADQ68180 Cancer re
97	16	69.6	9	8	ADQ70322 Cancer re
98	16	69.6	9	8	ADQ72207 Cancer re

99	16	69.6	9	8	ADP26276	Adp26276 Plasmodi	172	16	69.6	13	4	AAB73644	Aab73644 Pan-DR bi
100	16	69.6	10	1	AA50792	Aap50792 Sequence	173	16	69.6	13	4	AAB20154	Aab20154 PADRE pep
101	16	69.6	10	1	AA82754	Aap82754 Example o	174	16	69.6	13	5	AAU80293	Aau80293 Pan DR ep
102	16	69.6	10	3	AA826399	Aab26399 Human CAS	175	16	69.6	13	5	ABG31776	Abg31776 Pan DR ep
103	16	69.6	10	3	AA826393	Aab26393 Human CAS	176	16	69.6	13	5	AAE26369	Aae26369 PADRE pep
104	16	69.6	10	4	AA887239	Aab87239 Breat-ca	177	16	69.6	13	6	ABP72696	Abp72696 T cell ep
105	16	69.6	10	4	AB852440	Abbs2440 Human API	178	16	69.6	13	6	AAO30456	Aao30456 Pan DR ep
106	16	69.6	10	4	AB835295	Aab35295 Murine PS	179	16	69.6	13	6	AAO30463	Aao30463 Pan DR ep
107	16	69.6	10	5	ABG93457	Abg93457 AlclR amin	180	16	69.6	13	7	ABR82484	Abr82484 Universal
108	16	69.6	10	5	AAU72831	Aau72831 Anti-NG2	181	16	69.6	13	7	ADC81611	Adc81611 Universal
109	16	69.6	10	5	ABG78903	Abg78903 Multiple	182	16	69.6	13	8	ADM06893	Adm06893 Pan DR bi
110	16	69.6	10	6	ABR01558	Abr01558 Human ant	183	16	69.6	13	8	ADP73620	Adp73620 PADRE T c
111	16	69.6	10	6	AB858766	Abr58766 Alzheimer	184	16	69.6	13	8	ADP48563	Adp48563 Pan DR ep
112	16	69.6	10	6	AAO31089	Aao31089 Human DS -	185	16	69.6	13	8	ADP79777	Adp79777 H1A epico
113	16	69.6	10	7	ADB79048	Adb79048 Human ant	186	16	69.6	14	2	AA72636	Aar72636 Cladospor
114	16	69.6	10	7	ADC07160	Adc07160 Corn earw	187	16	69.6	14	4	AA98495	Aam98495 Human pep
115	16	69.6	10	7	ADC07162	Adc07162 Tenthredo	188	16	69.6	14	4	AA98808	Aam98808 Human pep
116	16	69.6	10	8	AD885702	Ades5702 Human Eph	189	16	69.6	14	5	AA49498	Aam49498 Ophiostom
117	16	69.6	10	8	ADH17813	Adh17813 AbM softw	190	16	69.6	14	8	ADS54226	Ads54226 Anti-huma
118	16	69.6	10	8	ADK09671	Adk09671 Human pap	191	16	69.6	15	2	AA51379	Aar51379 Antigenic
119	16	69.6	10	8	ADK09188	Adk09188 Human pap	192	16	69.6	15	2	AAW07992	Aaw07992 gp120 pep
120	16	69.6	10	8	ADN31802	Adn31802 Human Alz	193	16	69.6	15	2	AAW76978	Aaw76978 Fuston im
121	16	69.6	10	8	ADM78084	Adm78084 Human SJB	194	16	69.6	15	3	AA829726	Aab29726 Gangliosi
122	16	69.6	10	8	ADP47006	Adp47006 Murine he	195	16	69.6	15	3	AA833247	Aay83247 CVB5RP fa
123	16	69.6	10	8	ADP47009	Adp47009 Murine he	196	16	69.6	15	3	AA813300	Aab13300 Caenorhab
124	16	69.6	10	8	ADQ72837	Adq72837 Cancer re	197	16	69.6	15	3	AA829164	Aab29164 Peptide #
125	16	69.6	10	8	ADQ73638	Adq73638 Cancer re	198	16	69.6	15	4	AA857714	Aab57714 D.melanog
126	16	69.6	10	8	ADQ69470	Adq69470 Cancer re	199	16	69.6	15	5	AA847919	Aam47919 Human cla
127	16	69.6	10	8	ADQ72592	Adq72592 Cancer re	200	16	69.6	15	5	AAO20307	Aao20307 Human ple
128	16	69.6	10	8	ADQ73094	Adq73094 Cancer re	201	16	69.6	15	5	AAO20896	Aao20896 N-termina
129	16	69.6	10	8	ADQ69764	Adq69764 Cancer re	202	16	69.6	15	5	AA47805	Aam47805 Miniature
130	16	69.6	10	8	ADQ73285	Adq73285 Cancer re	203	16	69.6	15	5	AB877835	Abb77835 Peptide u
131	16	69.6	10	8	ADQ73425	Adq73425 Cancer re	204	16	69.6	15	6	ABR44352	Abx44352 N-termina
132	16	69.6	10	8	ADQ72862	Adq72862 Cancer re	205	16	69.6	15	6	ABP58627	Abp58627 Human end
133	16	69.6	10	8	ADQ73694	Adq73694 Cancer re	206	16	69.6	15	7	ADF12276	Adf12276 Drosophil
134	16	69.6	10	8	ADQ70508	Adq70508 Cancer re	207	16	69.6	15	8	ADQ74628	Adq74628 Cancer re
135	16	69.6	10	8	ADQ68354	Adq68354 Cancer re	208	16	69.6	15	8	ADQ74366	Adq74366 Cancer re
136	16	69.6	10	8	ADQ73492	Adq73492 Cancer re	209	16	69.6	15	8	ADQ73948	Adq73948 Cancer re
137	16	69.6	10	8	ADQ73555	Adq73555 Cancer re	210	16	69.6	15	8	ADQ74000	Adq74000 Cancer re
138	16	69.6	10	8	ADQ69105	Adq69105 Cancer re	211	16	69.6	15	8	ADQ74469	Adq74469 Cancer re
139	16	69.6	10	8	ADQ68777	Adq68777 Cancer re	212	16	69.6	15	8	ADQ74001	Adq74001 Cancer re
140	16	69.6	10	8	ADP47172	Adp47172 Human pho	213	16	69.6	15	8	ADQ74122	Adq74122 Cancer re
141	16	69.6	10	8	ADP47157	Adp47157 Human pho	214	16	69.6	15	8	ADQ74177	Adq74177 Cancer re
142	16	69.6	10	8	ADP47152	Adp47152 Human pho	215	16	69.6	15	8	ADQ74313	Adq74313 Cancer re
143	16	69.6	10	8	ADP47139	Adp47139 Human pho	216	16	69.6	15	8	ADQ74213	Adq74213 Cancer re
144	16	69.6	10	8	ADP47175	Adp47175 Human pho	217	16	69.6	15	8	ADR68288	Adr68288 Androgen
145	16	69.6	10	8	ADRO3387	Adro3387 Humanised	218	16	69.6	16	2	AAW73469	Aaw73469 Human sec
146	16	69.6	10	8	ADRO3386	Adro3386 Humanised	219	16	69.6	16	7	ADC22804	Aac22804 Human G p
147	16	69.6	10	8	ADRO3383	Adro3383 Humanised	220	16	69.6	16	7	AAE39001	Aae39001 Human RAT
148	16	69.6	10	8	ADR19445	Adr19445 TPPI deri	221	16	69.6	16	7	ADH14277	Adh14277 Mutated e
149	16	69.6	10	8	ADR89805	Adr89805 Anti-CD70	222	16	69.6	17	2	AAW05080	Aaw05080 Generic e
150	16	69.6	11	5	ABP47662	Abp47662 N. mening	223	16	69.6	17	2	AAW07949	Aaw07949 gp120 pep
151	16	69.6	11	6	AAE31825	Aae31825 Androgen	224	16	69.6	17	2	AAW60595	Aaw60595 Cladospor
152	16	69.6	11	6	AAE31805	Adg15913 Synthetic	225	16	69.6	17	2	AAW22119	Aay22119 Human uri
153	16	69.6	11	8	ADG15913	Adg15913 Synthetic	226	16	69.6	17	3	AA97262	Aay97262 Calycin c
154	16	69.6	11	8	ADG15912	Adg15912 Synthetic	227	16	69.6	17	5	ABG70457	Abg70457 CDR3 regi
155	16	69.6	11	8	ADG15911	Adg15911 Synthetic	228	16	69.6	17	5	AAU82493	Aau82493 Llama CDR
156	16	69.6	12	8	ADW82020	Adw82020 Camelidae	229	16	69.6	17	5	ABO24493	Abo24493 Yeast eno
157	16	69.6	12	2	AAW32654	Aaw32654 Human pla	230	16	69.6	17	6	ABO27485	Abo27485 Anti-Rh(D
158	16	69.6	12	2	AAW71784	Aaw71784 Mimotope	231	16	69.6	17	6	ABO27486	Abo27486 Anti-Rh(D
159	16	69.6	12	4	AA660021	Aae60021 Internali	232	16	69.6	17	7	ADC22805	Adc22805 Human G p
160	16	69.6	12	5	AAE29104	Aae29104 Human DBH	233	16	69.6	17	7	ADP71551	Adp71551 Human uri
161	16	69.6	12	5	AAE29118	Aae29118 Human DBH	234	16	69.6	17	7	ADH14278	Adh14278 Mutated e
162	16	69.6	12	6	AAE30883	Aae30883 p300-bind	235	16	69.6	17	8	ABO57902	Abo57902 Human gen
163	16	69.6	12	7	ADA88856	Ada88856 Internali	236	16	69.6	17	8	ABO56359	Abo56359 Human gen
164	16	69.6	12	7	ADC28198	Adc28198 Synthetic	237	16	69.6	18	2	AAW18153	Aaw18153 Cationic,
165	16	69.6	12	8	ADL23639	Adl23639 RAD51C pr	238	16	69.6	18	3	AB13301	Aab13301 Caenorhab
166	16	69.6	13	2	AA870250	Aar70250 Pan-DR-bi	239	16	69.6	18	3	AA813299	Aab13299 Caenorhab
167	16	69.6	13	2	AAW22121	Aaw22121 Padre (pa	240	16	69.6	18	5	AAU91098	Aau91098 Human sec
168	16	69.6	13	3	AAW64575	Aay64575 Human Fac	241	16	69.6	18	5	AAU91081	Aau91081 Human alb
169	16	69.6	13	3	AAV52558	Aay52558 Universal	242	16	69.6	18	5	ABG65209	Abg65209 Human alb
170	16	69.6	13	3	AA836289	Aab36289 Promiscuo	243	16	69.6	18	5	ABG65210	Abg65210 Human alb
171	16	69.6	13	4	AA899710	Aab99710 Pan-DR-bi	244	16	69.6	18	8	ADL18453	Adl18453 Antimicro

245	16	69.6	18	8	ADL78477	Adl78477 Albumin f	318	15	65.2	6	ABR46423	AbR46423 Staphyloc
246	16	69.6	18	8	ADL78476	Adl78476 Albumin f	319	15	65.2	6	ABR46659	AbR46659 Staphyloc
247	16	69.6	19	3	AAB52193	Aab52193 Human ant	320	15	65.2	6	ABR46719	AbR46719 Staphyloc
248	16	69.6	19	4	AAM21012	Aam21012 Peptide #	321	15	65.2	6	ABR46759	AbR46759 Staphyloc
249	16	69.6	19	4	ABBA3110	Abb31110 Peptide #	322	15	65.2	6	ABR45182	AbR45182 Staphyloc
250	16	69.6	19	4	AAM36940	Aam36940 Peptide #	323	15	65.2	6	ABR45517	AbR45517 Staphyloc
251	16	69.6	19	4	ABB26248	Abb26248 Protein #	324	15	65.2	6	ABR45518	AbR45518 Staphyloc
252	16	69.6	19	4	AAM76834	Aam76834 Human bon	325	15	65.2	6	ABR46301	AbR46301 Staphyloc
253	16	69.6	19	4	AAM64011	Aam64011 Human bra	326	15	65.2	6	ABR46379	AbR46379 Staphyloc
254	16	69.6	19	4	ABGS58507	Abg58507 Human liv	327	15	65.2	6	ABR46439	AbR46439 Staphyloc
255	16	69.6	19	5	ABGA5977	Abg45977 Human pep	328	15	65.2	6	ABR46475	AbR46475 Staphyloc
256	16	69.6	19	8	ADR68329	Adr68329 Androgen	329	15	65.2	6	ABR46495	AbR46495 Staphyloc
257	16	69.6	20	2	AAR63841	Aar63841 HIV-1 gp1	330	15	65.2	6	ABR46531	AbR46531 Staphyloc
258	16	69.6	20	2	AAW08045	Aaw08045 HIV pepti	331	15	65.2	6	ABR46694	AbR46694 Staphyloc
259	16	69.6	20	2	AAW08044	Aaw08044 HIV pepti	332	15	65.2	6	ABR45501	AbR45501 Staphyloc
260	16	69.6	20	2	AAR88352	Aar88352 Adenomat	333	15	65.2	6	ABR45510	AbR45510 Staphyloc
261	16	69.6	20	2	AAW02155	Aay02155 Peptide u	334	15	65.2	6	ABR45901	AbR45901 Staphyloc
262	16	69.6	20	3	AAW70799	Aay70799 Murine an	335	15	65.2	6	ABR45915	AbR45915 Staphyloc
263	16	69.6	20	3	AAB10376	Aab10376 HBV core	336	15	65.2	6	ABR46268	AbR46268 Staphyloc
264	16	69.6	20	4	ABBS0791	Abb50791 Human sec	337	15	65.2	6	ABR45894	AbR45894 Staphyloc
265	16	69.6	20	5	AAE20323	Aae20323 Human B7-	338	15	65.2	6	ABR46308	AbR46308 Staphyloc
266	16	69.6	20	5	ABP30920	Abp30920 O8E antib	339	15	65.2	6	ABR46435	AbR46435 Staphyloc
267	16	69.6	20	5	ABP30919	Abp30919 O8E antib	340	15	65.2	6	ABR46535	AbR46535 Staphyloc
268	16	69.6	20	6	ABO45048	Abob45048 Novel hum	341	15	65.2	6	ABR46678	AbR46678 Staphyloc
269	16	69.6	20	7	ABO26528	Abob26528 Protein a	342	15	65.2	6	ABR45166	AbR45166 Staphyloc
270	16	69.6	20	7	ADA08565	Ada08565 Human O8E	343	15	65.2	6	ABR45181	AbR45181 Staphyloc
271	16	69.6	20	7	ADA08564	Ada08564 Human O8E	344	15	65.2	6	ABR46293	AbR46293 Staphyloc
272	16	69.6	20	7	ADC99562	Adc99562 Cancer-re	345	15	65.2	6	ABR46647	AbR46647 Staphyloc
273	16	69.6	20	7	ABW01365	Abw01365 Human HEA	346	15	65.2	6	ABR46693	AbR46693 Staphyloc
274	16	69.6	20	7	ADF08907	Adf08907 Secreted	347	15	65.2	6	ABR46699	AbR46699 Staphyloc
275	16	69.6	20	7	ADF08908	Adf08908 Secreted	348	15	65.2	6	ABR47077	AbR47077 Staphyloc
276	16	69.6	20	7	ADF09113	Adf09113 Secreted	349	15	65.2	6	ABR47092	AbR47092 Staphyloc
277	16	69.6	20	7	ADG09114	Adg09114 Secreted	350	15	65.2	6	ABR45147	AbR45147 Staphyloc
278	16	69.6	20	7	ADG46195	Adg46195 O8E antib	351	15	65.2	6	ABR45187	AbR45187 Staphyloc
279	16	69.6	20	7	ADG46194	Adg46194 O8E antib	352	15	65.2	6	ABR45484	AbR45484 Staphyloc
280	16	69.6	20	8	ADR05597	Adr05597 Novel s8d	353	15	65.2	6	ABR45509	AbR45509 Staphyloc
281	15	65.2	5	2	AAW17807	Aaw17807 Cyclic pe	354	15	65.2	6	ABR46267	AbR46267 Staphyloc
282	15	65.2	5	2	AAW17812	Aaw17812 Cyclic pe	355	15	65.2	6	ABR45909	AbR45909 Staphyloc
283	15	65.2	5	2	AAW17806	Aaw17806 Cyclic pe	356	15	65.2	6	ABR46383	AbR46383 Staphyloc
284	15	65.2	5	3	AAW33038	Aay33038 Carbohydr	357	15	65.2	6	ABR46715	AbR46715 Staphyloc
285	15	65.2	5	3	AAW07280	Abw07280 Motif bin	358	15	65.2	6	ABR46755	AbR46755 Staphyloc
286	15	65.2	5	5	ABP67371	Abp67371 Human CD6	359	15	65.2	6	ABR47070	AbR47070 Staphyloc
287	15	65.2	5	6	ABU87123	Abu87123 Carbohydr	360	15	65.2	6	ABR47085	AbR47085 Staphyloc
288	15	65.2	5	8	ADR68292	Adr68292 Androgen	361	15	65.2	6	ABR45502	AbR45502 Staphyloc
289	15	65.2	5	8	ADP68294	Adp68294 Androgen	362	15	65.2	6	ABR45876	AbR45876 Staphyloc
290	15	65.2	6	1	AAP50709	Aap50709 Hexapepti	363	15	65.2	6	ABR46294	AbR46294 Staphyloc
291	15	65.2	6	2	AAR54182	Aar54182 CHA255 li	364	15	65.2	6	ABR46419	AbR46419 Staphyloc
292	15	65.2	6	2	AAR89913	Aar89913 p53/MDM2	365	15	65.2	6	ABR46660	AbR46660 Staphyloc
293	15	65.2	6	2	AAR89915	Aar89915 p53 minim	366	15	65.2	6	ABR47052	AbR47052 Staphyloc
294	15	65.2	6	2	AAW13606	Aaw13606 p53 prote	367	15	65.2	6	ABR47078	AbR47078 Staphyloc
295	15	65.2	6	2	AAW04677	Aay04677 Peptide #	368	15	65.2	6	ABR45165	AbR45165 Staphyloc
296	15	65.2	6	3	AAW17074	Aab17074 Mdm/hdm a	369	15	65.2	6	ABR45483	AbR45483 Staphyloc
297	15	65.2	6	3	ABW73169	Abw73169 Mdm/hdm a	370	15	65.2	6	ABR45524	AbR45524 Staphyloc
298	15	65.2	6	5	ABP67361	Abp67361 Human CD6	371	15	65.2	6	ABR45910	AbR45910 Staphyloc
299	15	65.2	6	6	ABR46285	AbR46285 Staphyloc	372	15	65.2	6	ABR46685	AbR46685 Staphyloc
300	15	65.2	6	6	ABR46643	AbR46643 Staphyloc	373	15	65.2	6	ABR46686	AbR46686 Staphyloc
301	15	65.2	6	6	ABR45148	AbR45148 Staphyloc	374	15	65.2	6	ABR47091	AbR47091 Staphyloc
302	15	65.2	6	6	ABR46479	AbR46479 Staphyloc	375	15	65.2	6	ABR45916	AbR45916 Staphyloc
303	15	65.2	6	6	ABR47051	AbR47051 Staphyloc	376	15	65.2	6	ABR46302	AbR46302 Staphyloc
304	15	65.2	6	6	ABR47069	AbR47069 Staphyloc	377	15	65.2	6	ABR46603	AbR46603 Staphyloc
305	15	65.2	6	6	ABR45893	AbR45893 Staphyloc	378	15	65.2	6	ABR46677	AbR46677 Staphyloc
306	15	65.2	6	6	ABR46491	AbR46491 Staphyloc	379	15	65.2	6	ABG73432	Abg73432 Human p53
307	15	65.2	6	6	ABR46607	AbR46607 Staphyloc	380	15	65.2	6	ABG73433	Abg73433 Human p53
308	15	65.2	6	6	ABR46700	AbR46700 Staphyloc	381	15	65.2	6	ABR82526	AbR82526 Human apy
309	15	65.2	6	6	ABR45188	AbR45188 Staphyloc	382	15	65.2	6	ADJ73323	Adj73323 Mdm/hdm a
310	15	65.2	6	6	ABR45173	AbR45173 Staphyloc	383	15	65.2	6	ADJ52957	Adj52957 CHI delet
311	15	65.2	6	6	ABR45523	AbR45523 Staphyloc	384	15	65.2	7	ADJ51918	Adj51918 CHI delet
312	15	65.2	6	6	ABR45875	AbR45875 Staphyloc	385	15	65.2	7	AAP93327	Aap93327 Sequence
313	15	65.2	6	6	ABR45902	AbR45902 Staphyloc	386	15	65.2	7	AAR32880	Aar32880 Antibody
314	15	65.2	6	6	ABR46286	AbR46286 Staphyloc	387	15	65.2	7	AAR89921	Aar89921 Tryptic p
315	15	65.2	6	6	ABR46307	AbR46307 Staphyloc	388	15	65.2	7	AAR89925	AbR89925 p53 bindi
316	15	65.2	6	6	ABR47086	AbR47086 Staphyloc	389	15	65.2	7	AAW34151	Aay34151 Angiopoie
317	15	65.2	6	6	ABR45174	AbR45174 Staphyloc	390	15	65.2	7	AAW94141	Aaw94141 FG loop s

391	15	65.2	7	3	AAV82380	Hepta-pept	464	15	65.2	8	6	ABR54070	Beta-secr
392	15	65.2	7	3	AAV57789	IRAM-inte	465	15	65.2	8	6	ABR54078	Beta-secr
393	15	65.2	7	3	AB23205	Hep47-bin	466	15	65.2	8	6	ABR54080	Beta-secr
394	15	65.2	7	3	AA01512	Peptide w	467	15	65.2	8	6	ABR53951	Beta-secr
395	15	65.2	7	4	AAAB73050	Luteinisi	468	15	65.2	8	6	ABR54049	Beta-secr
396	15	65.2	7	4	AAAM47040	H11 bindi	469	15	65.2	8	6	ABR53996	Beta-secr
397	15	65.2	7	4	AAAM46975	H11 bindi	470	15	65.2	8	6	ABR54000	Beta-secr
398	15	65.2	7	4	AAAM46990	H11 bindi	471	15	65.2	8	6	ABR54047	Beta-secr
399	15	65.2	7	4	AAAM46970	H11 bindi	472	15	65.2	8	6	ABR54025	Beta-secr
400	15	65.2	7	5	AB994332	Ubiquitin	473	15	65.2	8	6	ABR53994	Beta-secr
401	15	65.2	7	5	ABP67352	Human CD6	474	15	65.2	8	6	ABR54023	Beta-secr
402	15	65.2	7	5	ABP67752	Human CD6	475	15	65.2	8	6	ABR54017	Beta-secr
403	15	65.2	7	5	ABG77724	Targettin	476	15	65.2	8	6	AD44112	Beta-secr
404	15	65.2	7	7	ADL17146	Phage-dis	477	15	65.2	8	6	ABP71906	R. erythr
405	15	65.2	7	7	ADL17080	Phage-dis	478	15	65.2	8	7	ADC20439	Human sec
406	15	65.2	7	7	ADL17130	Phage-dis	479	15	65.2	8	7	ADC07142	Golden-wi
407	15	65.2	7	7	ADL17176	Phage-dis	480	15	65.2	8	7	ADC07143	Emperor d
408	15	65.2	7	7	ADL17077	Phage-dis	481	15	65.2	8	7	ADP10743	Human sec
409	15	65.2	7	7	ADL17227	Phage-dis	482	15	65.2	8	7	ADL17302	DENSIN-18
410	15	65.2	7	8	ADH08433	IGS produ	483	15	65.2	8	8	ADK01990	Hepatit
411	15	65.2	7	8	ADJ32411	PG loop p	484	15	65.2	8	8	ADK10578	Human pap
412	15	65.2	7	8	ADRE68302	Androgen	485	15	65.2	8	8	ADQ28799	Human cel
413	15	65.2	8	2	AAW61038	Dynorphin	486	15	65.2	8	8	ADQ28800	Human cel
414	15	65.2	8	2	AAW94606	Human ins	487	15	65.2	8	8	ADP69714	Novel hyb
415	15	65.2	8	2	AAV21268	Human sem	488	15	65.2	8	8	ADSO0534	Human Apo
416	15	65.2	8	2	AAW37209	Human sem	489	15	65.2	8	8	ADSO0532	Human Apo
417	15	65.2	8	2	AAW37186	Human onc	490	15	65.2	8	8	ADSO0533	Human Apo
418	15	65.2	8	2	AAW37176	Human onc	491	15	65.2	8	8	ADSO0535	Human Apo
419	15	65.2	8	2	AAW37185	Human onc	492	15	65.2	8	8	ADR99992	Human apo
420	15	65.2	8	2	AAW37206	Human MDM	493	15	65.2	8	8	ADR99995	Human apo
421	15	65.2	8	2	AAW37177	Human onc	494	15	65.2	8	8	ADR99994	Human apo
422	15	65.2	8	2	AAW37207	Human MDM	495	15	65.2	8	8	ADR99993	Human apo
423	15	65.2	8	2	AAV25556	Human MHC	496	15	65.2	8	8	ADS54215	Human apo
424	15	65.2	8	3	AAV85386	IL-2 deri	497	15	65.2	8	8	ADS54216	Human apo
425	15	65.2	8	3	AAV85387	IL-2 deri	498	15	65.2	8	8	ADS54215	Human apo
426	15	65.2	8	3	AAV85388	IL-2 deri	499	15	65.2	8	8	ADS54214	Human apo
427	15	65.2	8	3	AA09130	Hepatit	500	15	65.2	9	2	AAV53342	Chimeric
428	15	65.2	8	4	AB62220	Glycine m	501	15	65.2	9	2	AAW00686	Peptide c
429	15	65.2	8	5	ABP67745	Human CD6	502	15	65.2	9	2	AAW45692	HBV env 3
430	15	65.2	8	5	ABP67344	Human CD6	503	15	65.2	9	2	AAW39724	Human car
431	15	65.2	8	6	ABP99660	Human sec	504	15	65.2	9	2	AAW43849	Specific
432	15	65.2	8	6	ABP98083	Amino aci	505	15	65.2	9	2	AAW43845	Specific
433	15	65.2	8	6	ABP98084	Amino aci	506	15	65.2	9	2	AAW81310	Human INO
434	15	65.2	8	6	ABP98081	Amino aci	507	15	65.2	9	2	AAW81250	Human INO
435	15	65.2	8	6	ABP98082	Amino aci	508	15	65.2	9	2	AAW72493	Dengue vi
436	15	65.2	8	6	ABR01140	Human gen	509	15	65.2	9	2	AAW46351	Amino aci
437	15	65.2	8	6	ABP68159	Bacillus	510	15	65.2	9	2	AAW46349	Amino aci
438	15	65.2	8	6	ABP68159	Bacillus	511	15	65.2	9	2	AAW46348	Amino aci
439	15	65.2	8	6	ABP68163	Bacillus	512	15	65.2	9	2	AAW46350	Amino aci
440	15	65.2	8	6	ABP68181	Bacillus	513	15	65.2	9	2	AAW37199	Human onc
441	15	65.2	8	6	ABP68158	Bacillus	514	15	65.2	9	2	AAV46725	Immunogen
442	15	65.2	8	6	ABP68166	Bacillus	515	15	65.2	9	2	AAV25555	Human MHC
443	15	65.2	8	6	ABP68160	Bacillus	516	15	65.2	9	2	AAV27259	Human tum
444	15	65.2	8	6	ABR54027	Beta-secr	517	15	65.2	9	3	AAV84757	Antigenic
445	15	65.2	8	6	ABR54059	Beta-secr	518	15	65.2	9	3	AAV84765	Antigenic
446	15	65.2	8	6	ABR53990	Beta-secr	519	15	65.2	9	3	AAV84756	Antigenic
447	15	65.2	8	6	ABR54021	Beta-secr	520	15	65.2	9	3	AAV84758	Antigenic
448	15	65.2	8	6	ABR54074	Beta-secr	521	15	65.2	9	3	AAV84759	Antigenic
449	15	65.2	8	6	ABR53998	Beta-secr	522	15	65.2	9	3	AAV71328	Rat neur
450	15	65.2	8	6	ABR54015	Beta-secr	523	15	65.2	9	3	AAAB23806	Phage dis
451	15	65.2	8	6	ABR53986	Beta-secr	524	15	65.2	9	3	AAAB34807	Human sec
452	15	65.2	8	6	ABR54072	Beta-secr	525	15	65.2	9	3	AAAB01629	Chimeric
453	15	65.2	8	6	ABR54045	Beta-secr	526	15	65.2	9	4	AAAB46945	Human SAR
454	15	65.2	8	6	ABR54068	Beta-secr	527	15	65.2	9	4	ABM00050	Savinas a
455	15	65.2	8	6	ABR53988	Beta-secr	528	15	65.2	9	4	ABM00058	Savinas a
456	15	65.2	8	6	ABR54053	Beta-secr	529	15	65.2	9	4	ABM00059	Savinas a
457	15	65.2	8	6	ABR54055	Beta-secr	530	15	65.2	9	4	AAAB75691	HIA class
458	15	65.2	8	6	ABR54057	Beta-secr	531	15	65.2	9	4	AAAG63257	Complem
459	15	65.2	8	6	ABR54076	Beta-secr	532	15	65.2	9	4	AAAM24637	Human MHC
460	15	65.2	8	6	ABR54082	Beta-secr	533	15	65.2	9	5	ABG79074	Human CEA
461	15	65.2	8	6	ABR54051	Beta-secr	534	15	65.2	9	5	ABG35129	Pancreat
462	15	65.2	8	6	ABR53992	Beta-secr	535	15	65.2	9	5	ABP47446	N. mening
463	15	65.2	8	6	ABR54019	Beta-secr	536	15	65.2	9	5	ABG97340	Human leu

537	15	65.2	9	5	ABG97341	Human leu	610	15	65.2	9	6	ABJ61113	184P1E2-r
538	15	65.2	9	5	AAO18872	Human CEA	611	15	65.2	9	6	ABJ61402	184P1E2-r
539	15	65.2	9	5	ABP67738	Human CD6	612	15	65.2	9	6	ABJ58361	184P1E2-r
540	15	65.2	9	5	ABP67337	Human CD6	613	15	65.2	9	6	ABJ60622	184P1E2-r
541	15	65.2	9	5	ABJ11741	Human CD6	614	15	65.2	9	6	ABJ63441	184P1E2-r
542	15	65.2	9	5	ABJ12589	Human 125	615	15	65.2	9	6	ABJ63923	184P1E2-r
543	15	65.2	9	5	ABJ12352	Human 125	616	15	65.2	9	6	ABJ63965	184P1E2-r
544	15	65.2	9	5	ABJ11603	Human 125	617	15	65.2	9	6	ABJ57333	184P1E2-r
545	15	65.2	9	5	ABJ11833	Human 125	618	15	65.2	9	6	ABJ58971	184P1E2-r
546	15	65.2	9	5	ABJ12880	Human 125	619	15	65.2	9	6	ABJ60509	184P1E2-r
547	15	65.2	9	5	ABJ113175	Human 125	620	15	65.2	9	6	ABJ62494	184P1E2-r
548	15	65.2	9	5	ABJ12444	Human 125	621	15	65.2	9	6	ABJ64062	184P1E2-r
549	15	65.2	9	5	ABJ12211	Human 125	622	15	65.2	9	6	ABJ64839	184P1E2-r
550	15	65.2	9	5	ABJ09544	Hepatitits	623	15	65.2	9	6	ABJ65025	184P1E2-r
551	15	65.2	9	5	ABG60517	Selective	624	15	65.2	9	6	ABJ57376	184P1E2-r
552	15	65.2	9	5	AAE31317	Human p53	625	15	65.2	9	6	ABJ63110	184P1E2-r
553	15	65.2	9	5	AAE31316	Human p53	626	15	65.2	9	6	ABJ63111	184P1E2-r
554	15	65.2	9	5	AAE31395	Human p53	627	15	65.2	9	6	ABJ62218	184P1E2-r
555	15	65.2	9	5	AAU09701	Anti-mela	628	15	65.2	9	6	ABO27023	Yellow fe
556	15	65.2	9	5	AAU96014	Carcino e	629	15	65.2	9	6	ABO27024	West nile
557	15	65.2	9	6	ABJ20021	MHC bindi	630	15	65.2	9	6	ABO27025	Murray va
558	15	65.2	9	6	ABR56915	Pancreati	631	15	65.2	9	6	ABO27026	Kunjin vi
559	15	65.2	9	6	ABR24615	Human can	632	15	65.2	9	7	ADA07879	Viral pro
560	15	65.2	9	6	ABR24590	Human can	633	15	65.2	9	7	ADA07878	Viral pro
561	15	65.2	9	6	ABR25041	Human can	634	15	65.2	9	7	ADA07881	Viral pro
562	15	65.2	9	6	ABR25394	Human can	635	15	65.2	9	7	ADA07880	Viral pro
563	15	65.2	9	6	ABR24408	Human can	636	15	65.2	9	7	ADD26353	Staphyloc
564	15	65.2	9	6	ABR24647	Human can	637	15	65.2	9	7	ADD94560	Human SIM
565	15	65.2	9	6	ABR20240	Human can	638	15	65.2	9	7	ADD94768	Human SIM
566	15	65.2	9	6	ABR25665	Human can	639	15	65.2	9	7	ADD94574	Human SIM
567	15	65.2	9	6	ABR25205	Human can	640	15	65.2	9	7	ADG38574	Human car
568	15	65.2	9	6	ABR24809	Human can	641	15	65.2	9	7	ADG38572	Human car
569	15	65.2	9	6	ABR25596	Human can	642	15	65.2	9	7	AAO24240	MHC bindi
570	15	65.2	9	6	ABR23040	Human can	643	15	65.2	9	7	AAO24239	MHC bindi
571	15	65.2	9	6	ABR21629	Human can	644	15	65.2	9	7	ADI03011	Human non
572	15	65.2	9	6	ABJ58972	184P1E2-r	645	15	65.2	9	7	ADL17217	Phage-dis
573	15	65.2	9	6	ABJ59510	184P1E2-r	646	15	65.2	9	7	ADL17251	Phage-dis
574	15	65.2	9	6	ABJ63247	184P1E2-r	647	15	65.2	9	7	ADL17455	Human SNT
575	15	65.2	9	6	ABJ65204	184P1E2-r	648	15	65.2	9	7	ADL17228	Phage-dis
576	15	65.2	9	6	ABJ61887	184P1E2-r	649	15	65.2	9	7	ADK65171	Human VEG
577	15	65.2	9	6	ABJ63999	184P1E2-r	650	15	65.2	9	7	ADK65120	Human VEG
578	15	65.2	9	6	ABJ64840	184P1E2-r	651	15	65.2	9	8	ADG89640	Class I H
579	15	65.2	9	6	ABJ60510	184P1E2-r	652	15	65.2	9	8	ADK39506	Hepatitits
580	15	65.2	9	6	ABJ62064	184P1E2-r	653	15	65.2	9	8	ADK10586	Human pap
581	15	65.2	9	6	ABJ62495	184P1E2-r	654	15	65.2	9	8	ADK03265	Hepatitits
582	15	65.2	9	6	ABJ65468	184P1E2-r	655	15	65.2	9	8	ADK05899	Hepatitits
583	15	65.2	9	6	ABJ58585	184P1E2-r	656	15	65.2	9	8	ADK10587	Human pap
584	15	65.2	9	6	ABJ59876	184P1E2-r	657	15	65.2	9	8	ADK05107	Hepatitits
585	15	65.2	9	6	ABJ59965	184P1E2-r	658	15	65.2	9	8	ADK10585	Human pap
586	15	65.2	9	6	ABJ61159	184P1E2-r	659	15	65.2	9	8	ADK05911	Hepatitits
587	15	65.2	9	6	ABJ64098	184P1E2-r	660	15	65.2	9	8	ADK10584	Human pap
588	15	65.2	9	6	ABJ64452	184P1E2-r	661	15	65.2	9	8	ADM12337	MHC Class
589	15	65.2	9	6	ABJ60738	184P1E2-r	662	15	65.2	9	8	ADL19695	125P5C8 p
590	15	65.2	9	6	ABJ65172	184P1E2-r	663	15	65.2	9	8	ADL19077	125P5C8 p
591	15	65.2	9	6	ABJ59130	184P1E2-r	664	15	65.2	9	8	ADL18847	125P5C8 p
592	15	65.2	9	6	ABJ59833	184P1E2-r	665	15	65.2	9	8	ADL19603	125P5C8 p
593	15	65.2	9	6	ABJ59945	184P1E2-r	666	15	65.2	9	8	ADL19840	125P5C8 p
594	15	65.2	9	6	ABJ60623	184P1E2-r	667	15	65.2	9	8	ADL18985	125P5C8 p
595	15	65.2	9	6	ABJ63529	184P1E2-r	668	15	65.2	9	8	ADL20131	125P5C8 p
596	15	65.2	9	6	ABJ65631	184P1E2-r	669	15	65.2	9	8	ADL20425	125P5C8 p
597	15	65.2	9	6	ABJ60467	184P1E2-r	670	15	65.2	9	8	ADL19462	125P5C8 p
598	15	65.2	9	6	ABJ61114	184P1E2-r	671	15	65.2	9	8	ADP25801	Plasmodiu
599	15	65.2	9	6	ABJ63481	184P1E2-r	672	15	65.2	9	8	ADP25807	Carcinoem
600	15	65.2	9	6	ABJ61514	184P1E2-r	673	15	65.2	9	8	ADQ28798	Human cel
601	15	65.2	9	6	ABJ61798	184P1E2-r	674	15	65.2	9	8	ADP79788	Human HLA
602	15	65.2	9	6	ABJ62063	184P1E2-r	675	15	65.2	9	8	ADP60098	Human HLA
603	15	65.2	9	6	ABJ62639	184P1E2-r	676	15	65.2	10	2	AAR89917	Human p53
604	15	65.2	9	6	ABJ58529	184P1E2-r	677	15	65.2	10	2	AAR89918	Mouse p53
605	15	65.2	9	6	ABJ63337	184P1E2-r	678	15	65.2	10	2	AAW32713	Human pla
606	15	65.2	9	6	ABJ64453	184P1E2-r	679	15	65.2	10	2	AAW13605	p53 prote
607	15	65.2	9	6	ABJ61556	184P1E2-r	680	15	65.2	10	2	AAW37961	Peptide s
608	15	65.2	9	6	ABJ62994	184P1E2-r	681	15	65.2	10	2	AAW62010	Heavy cha
609	15	65.2	9	6	ABJ61053	184P1E2-r	682	15	65.2	10	2	AAW37198	Human onc

683	15	65.2	10	2	AAY25554	Aay25554 Human MHC	756	15	65.2	10	6	ABJ67907	Abj67907 184P1E2-r
684	15	65.2	10	2	AAY40648	Aay40648 S2 deriva	757	15	65.2	10	6	ABJ68931	Abj68931 184P1E2-r
685	15	65.2	10	3	AAY82337	Aay82337 Humanised	758	15	65.2	10	6	ABJ65862	Abj65862 184P1E2-r
686	15	65.2	10	3	AAB29987	Aab29987 Scaffold	759	15	65.2	10	6	ABJ66586	Abj66586 184P1E2-r
687	15	65.2	10	4	AAM24632	Aam24632 Human MHC	760	15	65.2	10	6	ABJ67496	Abj67496 184P1E2-r
688	15	65.2	10	4	AAB76236	Aab76236 Tumour as	761	15	65.2	10	6	ABJ66002	Abj66002 184P1E2-r
689	15	65.2	10	4	AAB76069	Aab76069 Tumour as	762	15	65.2	10	6	ABJ67609	Abj67609 184P1E2-r
690	15	65.2	10	4	AAG87403	Aag87403 Saccharom	763	15	65.2	10	6	ABJ69115	Abj69115 184P1E2-r
691	15	65.2	10	4	AAG87402	Aag87402 Saccharom	764	15	65.2	10	6	ABJ65863	Abj65863 184P1E2-r
692	15	65.2	10	4	ABB52377	Abb52377 Human API	765	15	65.2	10	6	ABJ58400	Abj58400 184P1E2-r
693	15	65.2	10	4	AAB35294	Aab35294 Murine PS	766	15	65.2	10	6	ABJ68318	Abj68318 184P1E2-r
694	15	65.2	10	5	ABB06172	Abb06172 Gonadotro	767	15	65.2	10	6	ABJ68081	Abj68081 184P1E2-r
695	15	65.2	10	5	ABG70414	Abg70414 CDRI/H1 r	768	15	65.2	10	6	ABJ68082	Abj68082 184P1E2-r
696	15	65.2	10	5	AAG98467	Aag98467 Novel hum	769	15	65.2	10	6	ABJ68164	Abj68164 184P1E2-r
697	15	65.2	10	5	ABP67331	Abp67331 Human CD6	770	15	65.2	10	7	ADC07158	Adc07158 Playpleu
698	15	65.2	10	5	ABP67732	Abp67732 Human CD6	771	15	65.2	10	7	ADD94159	Add94159 Mouse HUI
699	15	65.2	10	5	ABJ13821	Abj13821 Human 125	772	15	65.2	10	7	ADD94141	Add94141 Mouse HUI
700	15	65.2	10	5	ABJ11673	Abj11673 Human 125	773	15	65.2	10	7	ADD94158	Add94158 Mouse HUI
701	15	65.2	10	5	ABJ13682	Abj13682 Human 125	774	15	65.2	10	7	ADD94162	Add94162 Mouse HUI
702	15	65.2	10	5	ABJ14107	Abj14107 Human 125	775	15	65.2	10	7	ADD94161	Add94161 Mouse HUI
703	15	65.2	10	5	ABJ13459	Abj13459 Human 125	776	15	65.2	10	7	ADD94160	Add94160 Mouse HUI
704	15	65.2	10	5	ABJ13896	Abj13896 Human 125	777	15	65.2	10	7	ADD94632	Add94632 Human SIM
705	15	65.2	10	5	ABJ11759	Abj11759 Human 125	778	15	65.2	10	7	ADF10400	Adf10400 Serum alb
706	15	65.2	10	5	ABJ14159	Abj14159 Human 125	779	15	65.2	10	7	ADL17313	Adl17313 DENSTN-18
707	15	65.2	10	5	AU82450	Aau82450 Llama CDR	780	15	65.2	10	7	ADL17226	Adl17226 Phage-dis
708	15	65.2	10	5	AAU82812	Aau82812 Human Cal	781	15	65.2	10	7	ADL17327	Adl17327 Human scr
709	15	65.2	10	5	AAU82829	Aau82829 Human Cal	782	15	65.2	10	7	ADL17218	Adl17218 Phage-dis
710	15	65.2	10	6	ABP70583	Abp70583 Hepatitis	783	15	65.2	10	7	ADL17215	Adl17215 Phage-dis
711	15	65.2	10	6	ABO10708	Abol10708 Murine J4	784	15	65.2	10	7	ADL17219	Adl17219 Phage-dis
712	15	65.2	10	6	ABR25335	Abrr25335 Human can	785	15	65.2	10	7	ADM07751	Adm07751 Canine im
713	15	65.2	10	6	ABR25737	Abrr25737 Human can	786	15	65.2	10	7	ADM07748	Adm07748 Canine im
714	15	65.2	10	6	ABR25754	Abrr25754 Human can	787	15	65.2	10	7	ADM07744	Adm07744 Canine im
715	15	65.2	10	6	ABR23106	Abrr23106 Human can	788	15	65.2	10	8	ADG38998	Adg38998 Humanised
716	15	65.2	10	6	ABR21698	Abrr21698 Human can	789	15	65.2	10	8	ADG78885	Adg78885 Human p53
717	15	65.2	10	6	ABR22470	Abrr22470 Human can	790	15	65.2	10	8	ADL82158	Adl82158 Plasma re
718	15	65.2	10	6	ABR24908	Abrr24908 Human can	791	15	65.2	10	8	ADJ50603	Adj50603 Human ser
719	15	65.2	10	6	ABR23870	Abrr23870 Human can	792	15	65.2	10	8	ADK10594	Adk10594 Human pap
720	15	65.2	10	6	ABR25307	Abrr25307 Human can	793	15	65.2	10	8	ADK03263	Adk03263 Hepatitis
721	15	65.2	10	6	ABR24723	Abrr24723 Human can	794	15	65.2	10	8	ADK03268	Adk03268 Hepatitis
722	15	65.2	10	6	ABR20303	Abrr20303 Human can	795	15	65.2	10	8	ADK10595	Adk10595 Human pap
723	15	65.2	10	6	ABR25496	Abrr25496 Human can	796	15	65.2	10	8	ADK10596	Adk10596 Human pap
724	15	65.2	10	6	ABR24681	Abrr24681 Human can	797	15	65.2	10	8	ADK05932	Adk05932 Hepatitis
725	15	65.2	10	6	ABR24520	Abrr24520 Human can	798	15	65.2	10	8	ADK10593	Adk10593 Human pap
726	15	65.2	10	6	ABR21070	Abrr21070 Human can	799	15	65.2	10	8	ADK10592	Adk10592 Human pap
727	15	65.2	10	6	ABR59148	Abrr59148 Alzheimer	800	15	65.2	10	8	ADK03267	Adk03267 Hepatitis
728	15	65.2	10	6	ABR44652	Abrr44652 Murine J4	801	15	65.2	10	8	ADL21058	Adl21058 125P5C8 p
729	15	65.2	10	6	ABR47280	Abrr47280 Staphyloc	802	15	65.2	10	8	ADL21133	Adl21133 125P5C8 p
730	15	65.2	10	6	ABJ57466	Abj57466 184P1E2-r	803	15	65.2	10	8	ADL19003	Adl19003 125P5C8 p
731	15	65.2	10	6	ABJ58687	Abj58687 184P1E2-r	804	15	65.2	10	8	ADL21344	Adl21344 125P5C8 p
732	15	65.2	10	6	ABJ66221	Abj66221 184P1E2-r	805	15	65.2	10	8	ADL21396	Adl21396 125P5C8 p
733	15	65.2	10	6	ABJ67498	Abj67498 184P1E2-r	806	15	65.2	10	8	ADL20709	Adl20709 125P5C8 p
734	15	65.2	10	6	ABJ68257	Abj68257 184P1E2-r	807	15	65.2	10	8	ADL18917	Adl18917 125P5C8 p
735	15	65.2	10	6	ABJ69492	Abj69492 184P1E2-r	808	15	65.2	10	8	ADL20919	Adl20919 125P5C8 p
736	15	65.2	10	6	ABJ66633	Abj66633 184P1E2-r	809	15	65.2	10	8	ADN32081	Adn32081 Human Alz
737	15	65.2	10	6	ABJ66805	Abj66805 184P1E2-r	810	15	65.2	10	8	ADN48959	Adn48959 Peptide #
738	15	65.2	10	6	ABJ69386	Abj69386 184P1E2-r	811	15	65.2	10	8	ADN64792	Adn64792 HLA bindi
739	15	65.2	10	6	ABJ68555	Abj68555 184P1E2-r	812	15	65.2	10	8	ADN49156	Adn49156 Human car
740	15	65.2	10	6	ABJ69580	Abj69580 184P1E2-r	813	15	65.2	10	8	ADO77933	Ado77933 Gonadotro
741	15	65.2	10	6	ABJ58245	Abj58245 184P1E2-r	814	15	65.2	10	8	ADP47005	Adp47005 Murine he
742	15	65.2	10	6	ABJ67497	Abj67497 184P1E2-r	815	15	65.2	10	8	ADP47213	Adp47213 Human pho
743	15	65.2	10	6	ABJ66765	Abj66765 184P1E2-r	816	15	65.2	10	8	ADQ92367	Adq92367 Human hul
744	15	65.2	10	6	ABJ68357	Abj68357 184P1E2-r	817	15	65.2	10	8	ADQ92369	Adq92369 Human hul
745	15	65.2	10	6	ABJ58624	Abj58624 184P1E2-r	818	15	65.2	10	8	ADQ92371	Adq92371 Human hul
746	15	65.2	10	6	ABJ57961	Abj57961 184P1E2-r	819	15	65.2	10	8	ADQ92373	Adq92373 Human hul
747	15	65.2	10	6	ABJ66841	Abj66841 184P1E2-r	820	15	65.2	10	8	ADQ80558	Adq80558 TNF-alpha
748	15	65.2	10	6	ABJ57757	Abj57757 184P1E2-r	821	15	65.2	10	8	ADQ80562	Adq80562 TNF-alpha
749	15	65.2	10	6	ABJ67608	Abj67608 184P1E2-r	822	15	65.2	10	8	ADQ80556	Adq80556 TNF-alpha
750	15	65.2	10	6	ABJ67679	Abj67679 184P1E2-r	823	15	65.2	10	8	ADQ80560	Adq80560 TNF-alpha
751	15	65.2	10	6	ABJ68752	Abj68752 184P1E2-r	824	15	65.2	10	8	ADQ90780	Adq90780 Mouse com
752	15	65.2	10	6	ABJ68831	Abj68831 184P1E2-r	825	15	65.2	10	8	ADQ90780	Adq90780 Mouse com
753	15	65.2	10	6	ABJ68832	Abj68832 184P1E2-r	826	15	65.2	10	8	ADQ90780	Adq90780 Mouse com
754	15	65.2	10	6	ABJ68968	Abj68968 184P1E2-r	827	15	65.2	10	8	ADQ90780	Adq90780 Mouse com
755	15	65.2	10	6	ABJ69385	Abj69385 184P1E2-r	828	15	65.2	10	8	ADQ90923	Adq90923 Pancreati

829	15	65.2	10	8	ADS18661	Adsi18661 Peptide s	902	15	65.2	12	5	ABB81664	Abb81664 Yellow me
830	15	65.2	10	8	ADP79877	Adp79877 Human HLA	903	15	65.2	12	6	AAB30893	Aae30893 MD2-bind
831	15	65.2	10	8	ADP80344	Adp80344 Human HLA	904	15	65.2	12	6	AAB30886	Aae30886 MD2-bind
832	15	65.2	10	8	ADT02867	Adt02867 Human p53	905	15	65.2	12	6	ABP71371	Abr71371 Anti-OPGL
833	15	65.2	10	8	ADP70840	Adp70840 Synthetic	906	15	65.2	12	6	ABR00856	Abr00856 Bioactive
834	15	65.2	11	1	AAP71510	Aap71510 Growth ho	907	15	65.2	12	7	ADC35960	Adc35960 Peptide
835	15	65.2	11	1	AAP82068	Aap82068 Polypepti	908	15	65.2	12	7	ADC36035	Adc36035 Chemokine
836	15	65.2	11	2	AAW05784	Aaw05784 Presenili	909	15	65.2	12	7	ADB78490	Adb78490 Peptide 3
837	15	65.2	11	2	AAW11231	Aaw11231 Peptide A	910	15	65.2	12	7	ADI03010	Adi03010 Human mon
838	15	65.2	11	2	AAW12288	Aaw12288 Mycobacte	911	15	65.2	12	7	ADL17289	Adl17289 DENSIN-18
839	15	65.2	11	2	AAW62114	Aaw62114 Human MDM	912	15	65.2	12	7	ADJ73326	Adj73326 Mdm/hdm a
840	15	65.2	11	2	AAW25553	Aaw25553 Human MHC	913	15	65.2	12	7	ADJ73330	Adj73330 Mdm/hdm a
841	15	65.2	11	4	AAU271152	Aau271152 Human Leu	914	15	65.2	12	7	ADJ73339	Adj73339 Mdm/hdm a
842	15	65.2	11	4	AAU26842	Aau26842 Human Leu	915	15	65.2	12	7	ADJ73324	Adj73324 Mdm/hdm a
843	15	65.2	11	5	ABP47586	Abp47586 N. mening	916	15	65.2	12	7	ADJ73336	Adj73336 Mdm/hdm a
844	15	65.2	11	5	ABP67727	Abp67727 Human CD6	917	15	65.2	12	7	ADJ73327	Adj73327 Mdm/hdm a
845	15	65.2	11	5	ABP67326	Abp67326 Human CD6	918	15	65.2	12	7	ADJ73337	Adj73337 Mdm/hdm a
846	15	65.2	11	5	AAU93631	Aau93631 Granulocy	919	15	65.2	12	7	ADJ73338	Adj73338 Mdm/hdm a
847	15	65.2	11	5	AAW52269	Aaw52269 Miniature	920	15	65.2	12	7	ADJ73325	Adj73325 Mdm/hdm a
848	15	65.2	11	5	ABG67493	Abg67493 Human ADP	921	15	65.2	12	7	ADJ73325	Adj73325 Mdm/hdm a
849	15	65.2	11	6	ABR59507	Abr59507 S. aureus	922	15	65.2	12	8	ADJ52964	Adj52964 Wild type
850	15	65.2	11	6	ADA23607	Ada23607 Alzheimer	923	15	65.2	12	8	ADJ52960	Adj52960 CH1 delet
851	15	65.2	11	8	ADG15910	Adg15910 Synthetic	924	15	65.2	12	8	ADJ52959	Adj52959 CH1 delet
852	15	65.2	11	8	ADG15914	Adg15914 Synthetic	925	15	65.2	12	8	ADJ52971	Adj52971 CH1 delet
853	15	65.2	11	8	ADJ25786	Adj25786 MD2 bind	926	15	65.2	12	8	ADJ52972	Adj52972 CH1 delet
854	15	65.2	11	8	ADJ25912	Adj25912 MD2 bind	927	15	65.2	12	8	ADJ52970	Adj52970 CH1 delet
855	15	65.2	11	8	ADN64806	Adn64806 HLA bindi	928	15	65.2	12	8	ADJ52958	Adj52958 CH1 delet
856	15	65.2	11	8	ADR20392	Adr20392 Tryptic d	929	15	65.2	12	8	ADJ52961	Adj52961 CH1 delet
857	15	65.2	11	8	ADP80368	Adp80368 Human HLA	930	15	65.2	12	8	ADJ52973	Adj52973 CH1 delet
858	15	65.2	12	1	AAP93573	Aap93573 Extracell	931	15	65.2	12	8	ADJ51921	Adj51921 CH1 delet
859	15	65.2	12	2	AAR77621	Aar77621 Ascorbate	932	15	65.2	12	8	ADJ51922	Adj51922 CH1 delet
860	15	65.2	12	2	AAR83344	Aar83344 KB-bindin	933	15	65.2	12	8	ADJ51920	Adj51920 CH1 delet
861	15	65.2	12	2	AAW29957	Aaw29957 Cysteine	934	15	65.2	12	8	ADJ51932	Adj51932 CH1 delet
862	15	65.2	12	2	AAW18715	Aaw18715 C-src exo	935	15	65.2	12	8	ADJ51931	Adj51931 CH1 delet
863	15	65.2	12	2	AAW81309	Aaw81309 Human iNO	936	15	65.2	12	8	ADJ51919	Adj51919 CH1 delet
864	15	65.2	12	2	AAW81249	Aaw81249 Human iNO	937	15	65.2	12	8	ADJ51934	Adj51934 CH1 delet
865	15	65.2	12	2	AAW371190	Aaw371190 Human onc	938	15	65.2	12	8	ADJ51925	Adj51925 CH1 delet
866	15	65.2	12	2	AAW371184	Aaw371184 Human onc	939	15	65.2	12	8	ADJ51933	Adj51933 CH1 delet
867	15	65.2	12	2	AAW371195	Aaw371195 Human onc	940	15	65.2	12	8	ADJ57768	Adj57768 Surface g
868	15	65.2	12	2	AAW371171	Aaw371171 Human onc	941	15	65.2	12	8	ADJ57296	Adj57296 Provasopr
869	15	65.2	12	2	AAW371182	Aaw371182 Human onc	942	15	65.2	12	8	ADR65746	Adr65746 HLA bindi
870	15	65.2	12	2	AAW371181	Aaw371181 Human p53	943	15	65.2	12	8	ADR42787	Adr42787 Modulator
871	15	65.2	12	2	AAW371188	Aaw371188 Human onc	944	15	65.2	13	2	AAR49316	Aar49316 Beta2m po
872	15	65.2	12	2	AAW371189	Aaw371189 Human onc	945	15	65.2	13	2	AAR59205	Aaw59205 Seg ID 10
873	15	65.2	12	2	AAW37222	Aaw37222 MD2 bind	946	15	65.2	13	2	AAR40094	Aaw40094 Seg ID 10
874	15	65.2	12	2	AAW25552	Aaw25552 Human MHC	947	15	65.2	13	2	AAW67036	Aaw67036 Polioviru
875	15	65.2	12	3	AAW66808	Aaw66808 T cell an	948	15	65.2	13	2	AAW25551	Aaw25551 Human MHC
876	15	65.2	12	3	AAW17076	Aaw17076 Mdm/hdm a	949	15	65.2	13	3	AAW57799	Aaw57799 TRAM-inte
877	15	65.2	12	3	AAW17078	Aaw17078 Mdm/hdm a	950	15	65.2	13	4	AAB20427	Aab20427 Anti-FIX/
878	15	65.2	12	3	AAW17089	Aaw17089 Mdm/hdm a	951	15	65.2	13	4	AAB20390	Aab20390 Anti-FIX/
879	15	65.2	12	3	AAW17081	Aaw17081 Mdm/hdm a	952	15	65.2	13	4	AAB86009	Aab86009 DCM-assoc
880	15	65.2	12	3	AAW17078	Aaw17078 Mdm/hdm a	953	15	65.2	13	4	AAB86007	Aab86007 DCM-assoc
881	15	65.2	12	3	AAW17090	Aaw17090 Mdm/hdm a	954	15	65.2	13	4	AAB86006	Aab86006 DCM-assoc
882	15	65.2	12	3	AAW17088	Aaw17088 Mdm/hdm a	955	15	65.2	13	5	ABP68836	Abp68836 Marine sn
883	15	65.2	12	3	AAW17075	Aaw17075 Mdm/hdm a	956	15	65.2	13	5	ABP67720	Abp67720 Human CD6
884	15	65.2	12	3	AAW17077	Aaw17077 Mdm/hdm a	957	15	65.2	13	5	ABP67319	Abp67319 Human CD6
885	15	65.2	12	3	AAW93809	Aaw93809 Reactive	958	15	65.2	13	5	ABP59059	Abp59059 Peptide #
886	15	65.2	12	3	AAW93867	Aaw93867 Reactive	959	15	65.2	13	5	ADG67226	Adg67226 Human 5G1
887	15	65.2	12	4	AAB86005	Aab86005 DCM-assoc	960	15	65.2	13	5	ADG66202	Adg66202 Human pro
888	15	65.2	12	5	ABG06167	Abg06167 Gonadotro	961	15	65.2	13	5	ADG66200	Adg66200 Human pro
889	15	65.2	12	5	ABG78401	Abg78401 Memapsin	962	15	65.2	13	5	ADG67227	Adg67227 Human 5G1
890	15	65.2	12	5	ABW73170	Abw73170 Mdm/hdm a	963	15	65.2	13	5	ADG66203	Adg66203 Human pro
891	15	65.2	12	5	ABW73172	Abw73172 Mdm/hdm a	964	15	65.2	13	5	ADG67228	Adg67228 Human 5G1
892	15	65.2	12	5	ABW73185	Abw73185 Mdm/hdm a	965	15	65.2	13	5	ADG66201	Adg66201 Human pro
893	15	65.2	12	5	ABW73184	Abw73184 Mdm/hdm a	966	15	65.2	13	5	ADG67229	Adg67229 Human 5G1
894	15	65.2	12	5	ABW73176	Abw73176 Mdm/hdm a	967	15	65.2	13	6	ABP76124	Abp76124 Human GEN
895	15	65.2	12	5	ABW73183	Abw73183 Mdm/hdm a	968	15	65.2	13	6	ABP76126	Abp76126 Human GEN
896	15	65.2	12	5	ABW73173	Abw73173 Mdm/hdm a	969	15	65.2	13	6	ABP76127	Abp76127 Human GEN
897	15	65.2	12	5	ABW73171	Abw73171 Mdm/hdm a	970	15	65.2	13	7	AAO30274	Aao30274 Human GEN
898	15	65.2	12	5	ABW73182	Abw73182 Mdm/hdm a	971	15	65.2	13	7	ADP75888	Adp75888 Trichoder
899	15	65.2	12	5	ABP67723	Abp67723 Human CD6	972	15	65.2	13	7	ADP75892	Adp75892 Interfaci
900	15	65.2	12	5	ABP67322	Abp67322 Human CD6	973	15	65.2	13	7	ADP75892	Adp75892 Antimicro
901	15	65.2	12	5	ABG60547	Abg60547 Selective	974	15	65.2	13	7	ADP75888	Adp75888 Antimicro

975 15 65.2 13 7 ADF57890 Antimicro
 976 15 65.2 13 7 ADI57984 Anti-TNF-
 977 15 65.2 13 7 ADI57985 Anti-TNF-
 978 15 65.2 13 7 ADI57983 Anti-TNF-
 979 15 65.2 13 7 ADI57986 Anti-TNF-
 980 15 65.2 13 8 ADH94540 Lecithin
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 984 15 65.2 13 8 ADOS7860 Human for
 985 15 65.2 14 2 AAW36628 Thrombopo
 986 15 65.2 14 2 AAW36628 Thrombopo
 987 15 65.2 14 2 AAW53471 P2 predom
 988 15 65.2 14 2 AAW37197 Human onc
 989 15 65.2 14 2 AAW25550 Human MHC
 990 15 65.2 14 2 AAW42867 Vpr-bind
 991 15 65.2 14 3 AAB17012 TPO-nimet
 992 15 65.2 14 3 AAB13866 L2/HNK1 c
 993 15 65.2 14 4 AAB20428 Anti-FIX/
 994 15 65.2 14 4 AAW98166 Human pep
 995 15 65.2 14 4 AAW98166 Human pep
 996 15 65.2 14 4 AAW98166 Human pep
 997 15 65.2 14 4 AAW98166 Human pep
 998 15 65.2 14 4 AAW98166 Human pep
 999 15 65.2 14 4 AAW98166 Human pep
 1000 15 65.2 14 4 AAB86012 DCM-assoc

ALIGNMENTS

RESULT 1
 ADC07129
 ID ADC07129 standard; peptide; 9 AA.
 XX
 AC ADC07129;
 DT 18-DEC-2003 (first entry)
 XX
 DE Honeybee AKH peptide.
 XX
 KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;
 KW antidiabetic; hypotensive; cardiant; antiarthritic; cyostatic;
 KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;
 KW obesity; type II diabetes; cholelithiasis; hypertension;
 KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;
 KW renal failure; liver; chronic pain; sleep apnea; stroke;
 KW urinary incontinence; honeybee.
 XX
 OS Synthetic.
 OS Apis mellifera.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label= OTHER
 FT /note= Pyroglutamic acid"
 FT Misc-difference 9 /note= "OTHER = Pyroglutamic acid"
 FT /note= "Preferably C-terminal amide"
 XX
 PN WO2003066080-A1.
 XX
 PD 14-AUG-2003.
 XX
 PF 07-FEB-2003; 2003WO-US003800.
 XX
 PR 07-FEB-2002; 2002US-00072419.
 XX
 PA (BLMB-) BLM GROUP.
 XX
 PI Schacter BZ, Schacter LP;
 XX
 DR WPI; 2003-712542/67.
 XX

PT Pharmacetical composition useful for promoting weight loss, comprises an
 PT insect adipokinetic hormone, having a pyroglutamate residue at its amino
 PT terminus.
 XX
 PS Claim 29; Page 20; 82pp; English.
 XX
 CC The invention relates to a novel method of promoting lipid mobilisation
 CC in a human which comprises administering an insect adipokinetic hormone
 CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,
 CC hypotensive, cardiant, antiarthritic, cyostatic, nephrotropic,
 CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The
 CC method of the invention may be useful for treating obesity, type II
 CC diabetes, cholelithiasis, hypertension, coronary heart disease,
 CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal
 CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary
 CC incontinence. The current sequence is that of the honeybee AKH peptide of
 CC the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 73.9%; Score 17; DB 7; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXW 5
 Db 4 FTSSW 8
 RESULT 2
 ADC07134
 ID ADC07134 standard; peptide; 9 AA.
 XX
 AC ADC07134;
 DT 18-DEC-2003 (first entry)
 XX
 DE Painted lady AKH peptide.
 XX
 KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;
 KW antidiabetic; hypotensive; cardiant; antiarthritic; cyostatic;
 KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;
 KW obesity; type II diabetes; cholelithiasis; hypertension;
 KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;
 KW renal failure; liver; chronic pain; sleep apnea; stroke;
 KW urinary incontinence; painted lady.
 XX
 OS Synthetic.
 OS Vanessa cardui.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label= OTHER
 FT /note= "OTHER = Pyroglutamic acid"
 FT Misc-difference 9 /note= "OTHER = Pyroglutamic acid"
 FT /note= "Preferably C-terminal amide"
 XX
 PN WO2003066080-A1.
 XX
 PD 14-AUG-2003.
 XX
 PF 07-FEB-2003; 2003WO-US003800.
 XX
 PR 07-FEB-2002; 2002US-00072419.
 XX
 PA (BLMB-) BLM GROUP.
 XX
 PI Schacter BZ, Schacter LP;
 XX
 DR WPI; 2003-712542/67.
 XX
 PT Pharmacetical composition useful for promoting weight loss, comprises an
 PT insect adipokinetic hormone, having a pyroglutamate residue at its amino

PT terminus.
 XX Claim 29; Page 20; 82pp; English.
 PS
 CC The invention relates to a novel method of promoting lipid mobilisation
 CC in a human which comprises administering an insect adipokinetic hormone
 CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,
 CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,
 CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The
 CC method of the invention may be useful for treating obesity, type II
 CC diabetes, cholelithiasis, hypertension, coronary heart disease,
 CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal
 CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary
 CC incontinence. The current sequence is that of the painted lady AKH
 CC peptide of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 73.9%; Score 17; DB 7; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 Db 4 FTSSW 8
 RESULT 3
 AAB10010
 ID AAB10010 standard; protein; 10 AA.
 XX
 AC AAB10010;
 XX
 DT 01-NOV-2000 (first entry)
 XX
 DE H. pylori beta-urease-binding antibody heavy chain CDR1 protein #2.
 XX
 KW Acid-resistant microorganism; detection; faecal; intestine; infection;
 KW monoclonal antibody; heavy chain; complementarity determining region;
 KW CDR; beta-urease.
 XX
 OS Unidentified.
 XX
 PN WO200026571-A1.
 XX
 PD 11-MAY-2000.
 XX
 PF 29-OCT-1999; 99WO-EP008212.
 XX
 PR 29-OCT-1998; 98EP-00120517.
 PR 06-NOV-1998; 98EP-00120687.
 XX
 PA (CONN-) CONNEX GMBH.
 XX
 PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
 PI Ringsels A;
 XX
 DR WPI: 2000-365747/31.
 DR N-PSDB; AAA40166.
 XX
 FT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
 PT pylori, comprises reacting a fecal sample with two binding reagents for
 PT antigens that survive intestinal passage.
 XX
 PS Claim 26; Page 22; 84pp; German.
 XX
 CC This invention describes a novel method for the detection of a mammalian
 CC infection by an acid-resistant microorganism (A) by treating a faecal
 CC sample with at least two different monoclonal antibodies (Mab) (or their
 CC fragments or derivatives) or aptamers (collectively (II)) and detecting
 CC formation of a complex; (C) between (I) and the corresponding antigen of
 CC (A). The first and second (I) bind to epitopes of different antigens
 CC (Ag). These epitopes are present, after passage through the intestines,
 CC
 CC in at least some mammals, and have either: (i) their native structure; or
 CC (ii) a structure against which an antibody is produced by an animal
 CC infected or immunized with (A), or its extract, lysate, derived protein
 CC or fragment, or with a synthetic peptide. Practically all mammals display
 CC at least one of the specified epitopes. The method is used to detect
 CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
 CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M.
 CC tuberculosis, C. jejuni and C. pylori. (I) may also be used
 CC therapeutically. The method is direct and non-invasive, and provides an
 CC inexpensive and easily standardizable diagnosis, despite possible
 CC degradation of antigens during passage through the intestines. This
 CC sequence represents a fragment of a H. pylori beta-urease-binding
 CC antibody heavy chain complementarity determining region CDR1 which is
 CC used to illustrate the method of the invention
 XX
 SQ Sequence 10 AA;
 Query Match 73.9%; Score 17; DB 3; Length 10;
 Best Local Similarity 40.0%; Pred. No. 3.4e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 Db 4 FTSSW 8
 RESULT 4
 AAB86090
 ID AAB86090 standard; peptide; 10 AA.
 XX
 AC AAB86090;
 XX
 DT 17-JUL-2001 (first entry)
 XX
 DE H. pylori beta-urease derived antibody light chain CDR1 #1.
 XX
 KW Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
 KW acid-resistant microorganism; complementarity determining region; CDR;
 KW feces; heavy chain; light chain.
 XX
 OS Unidentified.
 XX
 PN WO200127612-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 12-OCT-2000; 2000WO-EP010057.
 XX
 PR 12-OCT-1999; 99EP-00120351.
 PR 16-MAR-2000; 2000EP-00105592.
 PR 31-MAR-2000; 2000EP-00107028.
 PR 10-MAY-2000; 2000EP-00110110.
 XX
 PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
 XX
 PI Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;
 PI
 XX
 DR WPI: 2001-282086/29.
 DR N-PSDB; AAF88117.
 XX
 FT Detecting infections by acid-resistant microorganisms, particularly for
 PT diagnosing Helicobacter pylori, comprises immunochromatographic detection
 PT of antigen in feces.
 XX
 PS Claim 27; Page 27; 90pp; German.
 XX
 CC This invention describes a novel method for detecting infection by an
 CC acid-resistant microorganism (A), in a mammal, using
 CC immunochromatography. The method is used to diagnose infection by an acid
 CC resistant microorganism (A), in a mammal, such as Helicobacter,
 CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
 CC H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,
 CC inexpensive and non-invasive, and may indicate the stage of infection. A

CC test strip used in the method may include a filter to eliminate particles
 CC present in the sample and only a single receptor provides a reasonably
 CC secure diagnosis, with specificity and selectivity improved by detecting
 CC several epitopes, with specificity and selectivity improved by detecting
 CC several epitopes (of catalase) or different antigens (catalase and beta-
 CC urease). The method can be automated. This sequence represents a
 CC complementarity determining region (CDR) from an antibody raised against
 CC the H. pylori catalase or beta-urease antigen which is used to illustrate
 CC the method of the invention
 XX
 XX Sequence 10 AA;

Query Match 73.9%; Score 17; DB 4; Length 10;
 Best Local Similarity 40.0%; Pred. No. 3.4e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 |
 4 FSTW 8

RESULT 5

AA86058
 ID AAB86058 standard; peptide; 10 AA.

AC AAB86058;

DT 17-JUL-2001 (first entry)

XX H. pylori beta-urease derived antibody light chain CDR1 #1.

XX Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;
 KW infection; acid-resistant microorganism; fecal; antibody; diagnosis;
 KW antibacterial; complementarity determining region.

XX Unidentified.

OS WO200127613-A2.

XX 19-APR-2001.

PD 12-OCT-2000; 2000WO-EP010058.

XX 12-OCT-1999; 99EP-00120351.

PR 16-MAR-2000; 2000EP-00105592.

PR 31-MAR-2000; 2000EP-00107028.

PR 10-MAY-2000; 2000EP-00110110.

XX (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

XX Reiter C, Cullmann G, Heppner P, Ringeis A, Mueller H, Haindl B;

DR WPI; 2001-282087/29.

DR N-PSDB; AAF88060.

XX Detecting infections by acid-resistant microorganisms, particularly for
 PT diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
 PT sample.

XX Claim 23; Page 17; 89pp; German.

XX This invention describes a novel method for detecting, in a mammal,
 CC infection by an acid-resistant microorganism (A) which comprises reacting
 CC a fecal sample with: (i) a receptor (R) such that a complex is formed
 CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part
 CC complex is formed with Ag, and the formation of a complex detected. R are
 CC specific for an Ag which, after passage through the intestines, at least
 CC in some mammals, retains a native (or corresponding) structure against
 CC which the mammal produces antibodies (when immunized or infected with
 CC (A), or its extracts, lysates or derived proteins (or fragments) or
 CC synthetic peptides). The products of the invention have antibacterial
 CC activity. The method is used to diagnose infection by Helicobacter,
 CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
 CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the

CC progress of treatment. Receptors, particularly antibodies, directed
 CC against Ag can be used therapeutically for treatment of infections. The
 CC method requires only one R to provide a reasonably secure diagnosis
 CC (although use of two R improves sensitivity), so is relatively
 CC inexpensive and more easily standardized. Also it is direct, non-
 CC invasive, suitable for automation and may indicate the stage of an
 CC infection. This sequence represents a complementarity determining region
 CC (CDR) from an antibody generated against a Helicobacter pylori antigen
 CC (catalase or beta-urease) which is used to illustrate the method of the
 XX invention

XX Sequence 10 AA;

Query Match 73.9%; Score 17; DB 4; Length 10;
 Best Local Similarity 40.0%; Pred. No. 3.4e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 |
 4 FSTW 8

RESULT 6

ADC07163

ID ADC07163 standard; peptide; 11 AA.

XX ADC07163;

DT 18-DEC-2003 (first entry)

XX Painted lady AKH peptide 2.

XX lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;
 KW antidiabetic; hypotensive; cardiant; antihypertensive; cytostatic;
 KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;
 KW obesity; type II diabetes; cholelithiasis; hypertension;
 KW coronary heart disease; atherosclerosis; glycogenosis; arthritis; cancer;
 KW renal failure; liver; chronic pain; sleep apnea; stroke;
 KW urinary incontinence; painted lady.

XX Synthetic.

OS Vanessa cardui.

XX Key Location/Qualifiers

FT Modified-site 1

FT /label= OTHER

FT /note= "OTHER = Pyroglutamic acid"

FT Misc-difference 11

FT /note= "Preferably C-terminal amide"

XX WO2003066080-A1.

XX 14-AUG-2003.

XX 07-FEB-2003; 2003WO-US003800.

XX 07-FEB-2002; 2002US-00072419.

XX (BLMB-) BLM GROUP.

XX Schacter BZ, Schacter LP;

XX WPI; 2003-712542/57.

XX Pharmaceutical composition useful for promoting weight loss, comprises an
 PT insect adipokinetic hormone, having a pyroglutamate residue at its amino
 PT terminus.

XX Claim 29; Page 20; 82pp; English.

XX The invention relates to a novel method of promoting lipid mobilisation
 CC in a human which comprises administering an insect adipokinetic hormone
 CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,

CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,
 CC hepatotropic, analgesic, cerebroprotective and uteropathic activities. The
 CC method of the invention may be useful for treating obesity, type II
 CC diabetes, cholelithiasis, hypertension, coronary heart disease,
 CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal
 CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary
 CC incontinence. The current sequence is that of the painted lady AKH
 CC peptide 2 of the invention.

XX
 SQ Sequence 11 AA;

Query Match 73.9%; Score 17; DB 7; Length 11;
 Best Local Similarity 40.0%; Pred. No. 3.6e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXKW 5
 |
 Db 4 FTSSW 8

RESULT 7
 AAE05735
 ID AAE05735 standard; peptide; 13 AA.

XX
 AC AAE05735;

XX
 DT 24-SEP-2001 (first entry)

XX
 DE Complementarity-determining region 3 (CDR3) of MoPhabs #7.

XX
 KW CDR3; complementarity-determining region 3; monoclonal phage antibody;

KW MoPhabs; antigen.

XX
 OS Synthetic.

XX
 PN US6265150-B1.

XX
 PD 24-JUL-2001.

XX
 PF 26-MAY-1998; 98US-00085072.

XX
 PR 07-JUN-1995; 95US-00483633.

XX
 PR 18-SEP-1997; 97US-00932892.

XX
 PA (BECT) BECTON DICKINSON & CO.

PA (CRUC-) CRUCCELL HOLLAND BV.

XX
 PI Terstappen LW, Logtenberg T;

XX
 DR WPI; 2001-463929/50.

XX
 PT Obtaining a phage particle, useful for obtaining human antibodies against
 PT known and novel surface antigens, by incubating a phage library with
 PT target cells to allow binding of the antibody fragment to the antigen.

XX
 PS Example 6; Col 6; 6pp; English.

XX
 CC The invention relates to a method of obtaining a phage particle which has
 CC an antibody fragment directed against an antigen associated with the
 CC surface of target cells in a heterogeneous cell population. The method
 CC involves incubating a library of phage particles with the target cells to
 CC allow binding of the antibody fragment expressed on the surface of the
 CC phage particles to the antigen associated with the target cells. The
 CC method is useful for obtaining human antibodies against known and novel
 CC surface antigens in their native configuration, expressed on
 CC phenotypically defined subpopulations of cells. The present sequence is
 CC complementarity-determining region 3 (CDR3) of monoclonal phage
 CC antibodies (MoPhabs) used in the exemplification of the invention

XX
 SQ Sequence 13 AA;

Query Match 73.9%; Score 17; DB 4; Length 13;
 Best Local Similarity 40.0%; Pred. No. 4.2e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXKW 5
 |
 Db 6 FASSW 10

RESULT 8
 ABG75574
 ID ABG75574 standard; peptide; 13 AA.

XX
 AC ABG75574;

XX
 DT 22-APR-2003 (first entry)

XX
 DE CDR3 peptide sequence, #7, used in phage antibody construction.

XX
 KW Phage; antibody; antigen; target cell; phage particle;
 KW cell-type specific phage antibody library; phage antibody; Phab;
 KW monoclonal phage antibody; MoPhab; blood cell; foetal bone marrow cell;
 KW complementarity determining region 3; CDR3; human.

XX
 OS Homo sapiens.

OS Synthetic.

XX
 PN US2002132228-A1.

XX
 PD 19-SEP-2002.

XX
 PF 24-MAY-2001; 2001US-00865048.

XX
 PR 07-JUN-1995; 95US-00483633.

XX
 PR 18-SEP-1997; 97US-00932892.

XX
 PR 26-MAY-1998; 98US-00085072.

XX
 PA (TERS/) TERSTAPPEN L W M M.

PA (LOGT/) LOGTENBERG T.

XX
 PI Terstappen LWM, Logtenberg T;

XX
 DR WPI; 2003-174076/17.

XX
 PT Obtaining phage having antibody specific for cell surface antigen of
 PT target cells in heterogeneous cell population, by incubating phage
 PT antibody library with target cells, and separating phage particles bound
 PT target cells.

XX
 PS Example 6; Page 4; 5pp; English.

XX
 CC The invention discloses a method for obtaining a phage comprising an
 CC antibody, or its fragment, directed against antigens associated with a
 CC target cells surface in a heterogeneous cell population. The method
 CC comprises providing a library of antibodies, or their fragments,
 CC expressed on the surface of phage particles, incubating the phage
 CC antibody library with the target cells, separating the target cells and
 CC phage particles associated with them from the phage particles not
 CC associated with the target cells and then recovering the phage particles.
 CC Also disclosed is a cell-type specific phage antibody library and an
 CC antibody, or antibody fragment, obtained using the method. The method is
 CC useful for obtaining a selection of phage antibodies (Phabs) and
 CC monoclonal phage antibodies (MoPhabs). The method is also useful for
 CC detecting known and novel structures on various populations of blood and
 CC foetal bone marrow cells. The sequence presented is an example of the
 CC partly randomised human complementarity determining region 3 (CDR3) used
 CC in the construction of the antibodies

XX
 SQ Sequence 13 AA;

Query Match 73.9%; Score 17; DB 6; Length 13;
 Best Local Similarity 40.0%; Pred. No. 4.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXKW 5

```

Db      |-----|
        | 6 PASSW 10
RESULT 9
AAM98088
ID AAM98088 standard; peptide; 14 AA.
XX
AC AAM98088;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human peptide #1363 encoded by a SNP oligonucleotide.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PK 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Shimketa RA, Leach M;
XX
XX WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Disclosure; Page 3967; 4143pp; English.
XX
XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
XX encoding polymorphic variants of proteins related to amylases, amyloid
XX protein, angiotensin, apoptosis related proteins, cadherin, cyclin,
XX polymerase, oncogenes, histones, kinases, colony stimulating factors,
XX complement related proteins, cytochromes, kinesins, cytokines,
XX interferons, interleukins, G-protein coupled receptors and thioesterases.
XX The present sequence is a peptide encoded by one such oligonucleotide.
XX The oligonucleotides and the peptides encoded by them may be used in the
XX prevention, diagnosis and treatment of diseases associated with
XX inappropriate expression of the proteins listed above. Disorders that may
XX be prevented, diagnosed and/or treated include multifactorial diseases
XX with a genetic component, such as autoimmune diseases (e.g. rheumatoid
XX arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
XX and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
XX brain, breast, colon and kidney, leukaemia), diseases of the nervous
XX system and an infection of pathogenic organisms
XX
XX Sequence 14 AA;
Query Match 73.9%; Score 17; DB 4; Length 14;
Best Local Similarity 40.0%; Pred. No. 4.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db |-----|
6 FASTW 10
RESULT 11
AAR97875
ID AAR97875 standard; peptide; 15 AA.
XX
AC AAR97875;
XX
DT 16-AUG-1996 (first entry)
XX
DE Japan cedar pollen mature allergen Cry j II amino acids 21-35.
XX
KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
KW Sugi pollinosis; diagnosis; treatment.
XX
OS Cryptomeria japonica.
XX
PN JP08047392-A.
XX
PD 20-FEB-1996.
XX
PF 07-NOV-1994; 94JP-00297840.
XX
PR 05-NOV-1993; 93JP-00276773.
PR 26-MAY-1994; 94JP-00134868.
XX
PA (MEIP ) MEIJI MILK PROD CO LTD.
XX
XX WPI; 1996-166249/17.
XX
PT Japan cedar pollen allergen Cry j II epitope - comprises at least part of
PT specified 460 aminoacid protein.
XX
PS Claim 8; Fig 3; 17pp; Japanese.
XX
XX AAR97871-R97960 are overlapping peptides used for the epitope mapping of
XX the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
XX peptides of it are useful in the diagnosis, prevention and treatment of
XX Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant
XX regions of the allergen were identified using the overlapping peptides of
XX the full epitope derived from a Cry j II antigen-specific T cell line.
XX Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460
XX amino acid allergen are the most allergenic of the 90 peptides tested
XX
XX Sequence 15 AA;
Query Match 73.9%; Score 17; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXXW 5
Db |-----|
9 FASTW 13
RESULT 11
AAR97875
ID AAR97875 standard; peptide; 15 AA.
XX
AC AAR97875;
XX
DT 16-AUG-1996 (first entry)
XX
DE Japan cedar pollen mature allergen Cry j II amino acids 21-35.
XX
KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
KW Sugi pollinosis; diagnosis; treatment.
XX
OS Cryptomeria japonica.
XX
PN JP08047392-A.
XX
PD 20-FEB-1996.
XX

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PF 07-NOV-1994; 94JP-00297840.
 PR 05-NOV-1993; 93JP-00276773.
 PR 26-MAY-1994; 94JP-00134868.
 XX
 PA (MEIP) MEIJI MILK PROD CO LTD.
 XX
 DR WPI; 1996-166249/17.
 XX
 PT Japan cedar pollen allergen Cry j II epitope - comprises at least part of
 PT specified 460 aminoacid protein.
 XX
 PS Claim 8; Fig 3; 17pp; Japanese.
 XX
 CC AAR97871-R97960 are overlapping peptides used for the epitope mapping of
 CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
 CC peptides of it are useful in the diagnosis, prevention and treatment of
 CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant
 CC regions of the allergen were identified using the overlapping peptides of
 CC the full epitope derived from a Cry j II antigen-specific T cell line.
 CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460
 CC amino acid allergen are the most allergenic of the 90 peptides tested
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 73.9%; Score 17; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXHW 5
 Db 4 FSTAW 8
 XX
 RESULT 12
 AAW57758
 ID AAW57758 standard; peptide; 15 AA.
 XX
 AC AAW57758;
 XX
 DT 17-SEP-1998 (first entry)
 XX
 DE Residues 16-30 of Cry j 2.
 XX
 CC Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;
 KW HLA class II molecule.
 XX
 OS Cryptomeria japonica.
 XX
 PN WO9820902-A1.
 XX
 PD 22-MAY-1998.
 XX
 PF 12-NOV-1997; 97WO-JP004129.
 XX
 PR 13-NOV-1996; 96JP-00302053.
 XX
 PA (MEIP) MEIJI MILK PROD CO LTD.
 XX
 PI Sone T, Kume A, Dairiki K, Kino K;
 XX
 DR WPI; 1998-297617/26.
 XX
 PT Peptides derived from Japanese cedar pollen antigens are
 PT immunotherapeutic agents - useful for allergy treatment and typing HLA
 PT class II molecules in allergy sufferers.
 XX
 PS Claim 12; Page 29; 50pp; Japanese.
 XX
 CC This sequence represents residues 16-30 of the Cry j 2 protein, and is a
 CC peptide of the invention. The peptides are derived from Japanese cedar
 CC pollen antigens, and are used as immunotherapeutic agents in the
 CC treatment of allergy. The peptides can be used for identification and

CC typing of the particular HLA class II molecules in an allergy sufferer,
 CC and also for peptide immunotherapy of an allergy. Using these peptides
 CC the immunotherapy can be targeted more specifically to the requirements
 CC of the individual patient, allowing more effective treatment of an
 CC allergy, including those patients for whom treatment with a conventional
 CC immunotherapeutic agent is ineffective
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 73.9%; Score 17; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXHW 5
 Db 9 FSTAW 13
 XX
 RESULT 13
 AAE23038
 ID AAE23038 standard; peptide; 19 AA.
 XX
 AC AAE23038;
 XX
 DT 21-AUG-2002 (first entry)
 XX
 DE Human thioredoxin, 47916 peptide.
 XX
 KW Human; thioredoxin; 22108; 47916; haematopoietic disorder; leukaemia;
 KW cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;
 KW cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;
 KW brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;
 KW cytostatic; carcinoma; cardiac; neuroprotective; antiinflammatory;
 KW gene therapy; nootropic.
 XX
 OS Homo sapiens.
 XX
 PN WO200226803-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 25-SEP-2001; 2001WO-US029967.
 XX
 PR 25-SEP-2000; 2000US-0235049P.
 XX
 PA (MILL-) MILLENIUM PHARM INC.
 XX
 PI Bandaru R, Kapeller-Libermann R;
 XX
 DR WPI; 2002-416475/44.
 XX
 PT New human thioredoxin nucleic acid and polypeptide molecules, designated
 PT 22108 and 47916, useful for diagnosing, preventing or treating cancer
 PT (e.g. carcinoma), cardiovascular diseases (e.g. heart failure) or brain
 PT disorders.
 XX
 PS Disclosure; Page 11; 124pp; English.
 XX
 CC The invention relates to human thioredoxin nucleic acid and polypeptide
 CC molecules, designated 22108 and 47916. The compound that modulates the
 CC activity or expression of 22108 and 47916 nucleic acid is useful for
 CC treating or preventing a disorder characterised by aberrant activity of
 CC 22108 and 47916-expressing cell, specifically for reducing or inhibiting
 CC the aberrant activity of the 22108 and 47916-expressing cancer cell. The
 CC 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,
 CC preventing or treating cancer in a subject (e.g. carcinoma, sarcoma,
 CC metastatic or haematopoietic disorders (e.g. leukaemia), or cancers of the
 CC lung, breast, thyroid, head neck, prostate or genito-urinary tract),
 CC cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart
 CC failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's
 CC diseases). The thioredoxin DNA is also useful in gene therapy. The
 CC present sequence is human thioredoxin, 47916 peptide
 XX

SQ Sequence 19 AA;

Query Match 73.9%; Score 17; DB 5; Length 19;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 4 FSATW 8

RESULT 14
AAW42165
ID AAW42165 standard; peptide; 20 AA.
XX
AC AAW42165;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-JUN-1998 (first entry)
XX
DE T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.
XX
KW Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;
KW diagnosis; allergy; spring tree pollen disease; pollinosis.
XX
OS Chamaecypariss obtusa.
XX
PN WO9747648-A1.
XX
PD 18-DEC-1997.
XX
PF 12-JUN-1997; 97WO-JP002031.
PR 14-JUN-1996; 96JP-00153527.
XX
PA (MEIP) MEIJI MILK PROD CO LTD.
XX
PI Kino K, Dairiri K;
XX
DR WPI; 1998-052242/05.
XX
T-cell epitope peptide portion of Japanese cypress pollen antigens Chao1
and Chao2 - used for diagnosis and treatment of spring tree pollen
disease.
XX
PS Claim 2; Page 36; 71pp; Japanese.
XX
CC The present sequence represents a T-cell epitope peptide from Japanese
cypress pollen antigen Chao2. The present invention describes peptides
which correspond to the T-cell epitope sites on Japanese cypress pollen
antigens Chao1 and Chao2. The peptides can be used as a reagent for the
diagnosis of allergy to Japanese cypress pollen, and as an antigen in the
treatment and prevention of spring tree pollen disease in which the
pollinosis involves reactivity to Japanese cypress pollen. (Updated on 25
-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
field.)
XX
SQ Sequence 20 AA;

Query Match 73.9%; Score 17; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 8 FATTW 12

RESULT 15
AAG62999
ID AAG62999 standard; peptide; 20 AA.
XX

AC AAG62999;
XX
DT 01-OCT-2001 (first entry)
XX
DE Complementarity determining region 3 (CDR3) of VH chain of clone G101.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB004501.
XX
PR 13-DEC-1999; 99US-0170599P.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases.
XX
PS Claim 1; Page 76; 109pp; English.
XX
CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC of VL and VH chains of antibodies of the invention. The specification
CC describes a mixture or panel of 5 different specific binding members,
CC each comprising an antibody VH and/or VL variable domain and capable,
CC when displayed on the surface of filamentous bacteriophage particles or
CC in the case of a specific binding member comprising the D5 VH and/or VL
CC variable domain when bound to human serum amyloid protein, to pass
CC through a mammalian blood brain barrier (BBB). The panel is useful for
CC the selection of specific binding members with a desired property such as
CC ability to cross BBB, ability to bind endothelial cells or other brain
CC cell antigen, ability to bind areas of inflammation in the brain or BBB
CC breakdown or ability to bind intracellular adhesion molecules and to bind
CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC and treatment of human or animal body, including neurological diseases,
CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC epilepsy and traumatic brain injury and any diseases involving
CC inflammation occurring within the brain or central nervous system
XX
SQ Sequence 20 AA;

Query Match 73.9%; Score 17; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 4 FSSSW 8

RESULT 16
ADR68284
ID ADR68284 standard; peptide; 5 AA.
XX
AC ADR68284;
XX
DT 02-DEC-2004 (first entry)
XX
DE Androgen receptor interacting peptide SEQ ID NO:2.
XX
KW androgen receptor binding peptide; androgen receptor interacting peptide;

KW androgen receptor; cytostatic; gene therapy; prostate cancer.
 OS Mammalia.
 OS Synthetic.
 XX
 PN WO2004076473-A2.
 XX
 PD 10-SEP-2004.
 XX
 XX 10-FEB-2004; 2004WO-US003774.
 PF
 XX
 XX 12-FEB-2003; 2003US-0446955P.
 PR
 XX (KARO-) KARO BIO AB.
 PA
 XX Buehrer BM, Barnett TR;
 PI
 XX WPI; 2004-653365/63.
 DR
 XX New polypeptides that bind to the androgen receptor, useful for
 PT diagnosing or treating diseases associated with abnormal levels of
 PT activation of androgen receptor, e.g. prostate cancer, or in biological
 PT research.
 PT
 XX Disclosure; SEQ ID NO 2; 46pp; English.
 PS
 XX The present invention describes a polypeptide that binds to the androgen
 CC receptor, or a polypeptide that comprises at least 50% amino acid
 CC sequence identity to the polypeptide. Also described: (1) methods of
 CC analysing the surface conformation of a protein using one or more of the
 CC polypeptide sequences mentioned above; (2) methods of identifying
 CC modulators of protein function using one or more of the polypeptide
 CC sequences mentioned above; (3) a pharmaceutical composition comprising a
 CC pharmaceutical carrier and one or more of the polypeptide sequences
 CC described above; (4) a peptide that binds to the androgen receptor, the
 CC binding being competitively inhibited by the polypeptide described above;
 CC (5) a chimeric protein comprising the above polypeptide and at least a
 CC portion of a filamentous phage protein, the portion of the filamentous
 CC phage protein being sufficient for integration of the chimeric protein
 CC into the coat of phage particles to display the polypeptide; (6) a
 CC filamentous phage displaying the above polypeptide; (7) a method of
 CC diagnosing a disease in a patient characterised by abnormal levels of
 CC activation of androgen receptor, comprising providing a sample of body
 CC fluid or tissue of the patient, administering a diagnostic amount of the
 CC pharmaceutical composition described above, and assaying the amount of
 CC activated androgen receptor in the body fluid or tissue of the patient;
 CC and (8) a method of treating a patient suffering from a disease
 CC characterised by abnormal levels of activation of androgen receptor,
 CC comprising administering to the patient a therapeutic amount of the
 CC pharmaceutical composition described above. The androgen receptor
 CC interacting polypeptide has cytostatic activity, and can be used in gene
 CC therapy. The composition and methods are useful for diagnosing or
 CC treating patients suffering from diseases characterised by abnormal
 CC levels of activation of androgen receptor, such as prostate cancer. They
 CC may also be used in biological research, as therapeutics or for in vitro
 CC or in vivo classification of compounds. The present sequence represents
 CC an androgen receptor interacting peptide, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 5 AA;
 Query Match 69.6%; Score 16; DB 8; Length 5;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXX 5
 |
 Db 1 FAALW 5
 RESULT 17
 AAW76953
 ID AAW76953 standard; peptide; 6 AA.

XX AAW76953;
 AC 25-JAN-1999 (first entry)
 XX
 DT Fusion immunoglobulin heavy chain HIV gp120 B cell epitope #93.
 XX
 DE B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IgH;
 XX human immune deficiency virus; HIV; tolerance; treatment; therapy;
 KW prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;
 KW microbial infection; autoimmune disease; antibody; apoptosis;
 KW antiviral T cell immunity.
 XX
 OS Mus sp.
 OS Homo sapiens.
 XX
 XX WO9836087-A1.
 PN
 XX 20-AUG-1998.
 PD
 XX 13-FEB-1998; 98WO-US002766.
 PF
 XX 13-FEB-1997; 97US-0040581P.
 PR
 XX (AMNA-) AMERICAN NAT RED CROSS.
 PA
 XX Scott D, Zambidis E;
 PI
 XX WPI; 1998-506315/43.
 DR
 XX New fusion immunoglobulin heavy chain including gp120 epitopes and
 PT related complete antibodies - DNA, vectors and transformed cells, used to
 PT induce tolerance to the epitopes for treatment of human immune deficiency
 PT virus infection.
 PT
 XX Disclosure; Page 40; 154pp; English.
 PS
 XX This sequence is an epitope used in the construction of a novel fusion
 CC immunoglobulin heavy chain (IgH) protein with a mammalian, especially
 CC human, IgH chain fused in frame at its N-terminus to one or more human
 CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or
 CC transfected cells are used to tolerate subjects to gp120 epitopes and to
 CC maintain this tolerance, particularly for treatment of HIV infection,
 CC optionally together with other therapeutic/prophylactic agents such as
 CC vaccines, chemotherapeutic agents and immune response modifiers. Such
 CC proteins can be used against other diseases where an immune response is
 CC deleterious, e.g. microbial infection, tumours or autoimmune disease.
 CC Induction of tolerance suppresses production of antibodies against gp120,
 CC so prevents or inhibits 'bystander' apoptosis of uninfected T cells that
 CC are bound to gp120 protein, maximising induction of protective antiviral
 CC T cell immunity
 CC
 XX Sequence 6 AA;
 Query Match 69.6%; Score 16; DB 2; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXX 5
 |
 Db 2 FNSTW 6
 RESULT 18
 ABR46309
 ID ABR46309 standard; peptide; 6 AA.
 XX
 XX ABR46309;
 AC
 XX 10-JUN-2003 (first entry)
 DT
 XX Staphylococcus aureus CHIPS-related peptide #1499.
 DE
 XX

KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP008004.
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 DR WPI; 2003-256333/25.
 XX
 CC Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 PS Disclosure; Page 16; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX
 PS Sequence 6 AA;
 XX
 Query Match 69.6%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 DB 1 FSFSW 5
 RESULT 19
 ABR46270
 ID ABR46270 standard; peptide; 6 AA.
 XX
 AC ABR46270;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Staphylococcus aureus CHIPS-related peptide #1460.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX

OS Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP008004.
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 PR (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 DR WPI; 2003-256333/25.
 XX
 CC Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 PS Disclosure; Page 16; 89pp; English.
 XX
 CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX
 PS Sequence 6 AA;
 XX
 Query Match 69.6%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 DB 1 FTFW 5
 RESULT 20
 ABR46702
 ID ABR46702 standard; peptide; 6 AA.
 XX
 AC ABR46702;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Staphylococcus aureus CHIPS-related peptide #1892.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 XX Disclosure; Page 17; 89pp; English.
 XX
 XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47388) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 59.6%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXW 5
 | |
 Db 1 FTFSW 5
 RESULT 21
 ABR47093
 ID ABR47093 standard; peptide; 6 AA.
 XX
 AC ABR47093;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Staphylococcus aureus CHIPS-related peptide #2283.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP008004.
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX Van Strijp JAG;
 XX
 XX WPI; 2003-256333/25.
 XX
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 XX Disclosure; Page 11; 89pp; English.

DR WPI; 2003-256333/25.
 XX
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 XX Disclosure; Page 19; 89pp; English.
 XX
 XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47388) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 59.6%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXW 5
 | |
 Db 1 FTFSW 5
 RESULT 22
 ABR45149
 ID ABR45149 standard; peptide; 6 AA.
 XX
 AC ABR45149;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Staphylococcus aureus CHIPS-related peptide #339.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2001; 2001WO-EP008004.
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 XX Van Strijp JAG;
 XX
 XX WPI; 2003-256333/25.
 XX
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX
 XX Disclosure; Page 11; 89pp; English.

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
Db 1 FTFW 5

RESULT 25

ABR46661
ID ABR46661 standard; peptide; 6 AA.

XX AC ABR46661;

DT 10-JUN-2003 (first entry)

DE Staphylococcus aureus CHIPS-related peptide #1851.

XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.

XX Staphylococcus aureus.

OS Synthetic.

XX WO2003006048-A1.

XX PD 23-JAN-2003.

XX PF 11-JUL-2001; 2001WO-EP008004.

XX PR 11-JUL-2001; 2001WO-EP008004.

XX PA (JARI-) JARI PHARM BV.

XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzter JAW;

XX PI Van Strijp JAG;

XX DR WPI; 2003-256333/25.

XX PT Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.

XX PS Disclosure; Page 17; 89pp; English.

XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection

XX SQ Sequence 6 AA;

Query Match 69.6%; Score 16; DB 6; Length 6;

Best Local Similarity 40.0%; Pred. No. 1.8e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
Db 1 FTFW 5

RESULT 26

DE Staphylococcus aureus CHIPS-related peptide #380.

ABR47053

ID ABR47053 standard; peptide; 6 AA.

XX AC ABR47053;

DT 10-JUN-2003 (first entry)

DE Staphylococcus aureus CHIPS-related peptide #2243.

XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.

XX Staphylococcus aureus.

OS Synthetic.

XX WO2003006048-A1.

XX PD 23-JAN-2003.

XX PF 11-JUL-2001; 2001WO-EP008004.

XX PR 11-JUL-2001; 2001WO-EP008004.

XX PA (JARI-) JARI PHARM BV.

XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzter JAW;

XX PI Van Strijp JAG;

XX DR WPI; 2003-256333/25.

XX PT Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.

XX PS Disclosure; Page 19; 89pp; English.

XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection

XX SQ Sequence 6 AA;

Query Match 69.6%; Score 16; DB 6; Length 6;

Best Local Similarity 40.0%; Pred. No. 1.8e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
Db 1 FTFW 5

RESULT 27

ABR45190

ID ABR45190 standard; peptide; 6 AA.

XX AC ABR45190;

DT 10-JUN-2003 (first entry)

XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; CSaR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 XX 23-JAN-2003.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 12; 89pp; English.
 XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (CSaR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 SQ Query Match 69.6%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXW 5
 Db 1 FTFSW 5
 RESULT 28
 ABR45877
 ID ABR45877 standard; peptide; 6 AA.
 AC ABR45877;
 XX 10-JUN-2003 (first entry)
 DT Staphylococcus aureus CHIPS-related peptide #1067.
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; CSaR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.

XX Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 XX 23-JAN-2003.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX 11-JUL-2001; 2001WO-EP008004.
 XX (JARI-) JARI PHARM BV.
 XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX WPI; 2003-256333/25.
 XX Combination of peptides derived from chemotaxis inhibiting protein from
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.
 XX Disclosure; Page 14; 89pp; English.
 XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (CSaR) and/or formylated peptide receptor (FPR) or neutrophils,
 CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection
 XX Sequence 6 AA;
 SQ Query Match 69.6%; Score 16; DB 6; Length 6;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXW 5
 Db 1 FSFAW 5
 RESULT 29
 ABR46310
 ID ABR46310 standard; peptide; 6 AA.
 AC ABR46310;
 XX 10-JUN-2003 (first entry)
 DT Staphylococcus aureus CHIPS-related peptide #1500.
 XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; CSaR;
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW gynecological; immunosuppressive; anti-HIV.
 XX Staphylococcus aureus.
 OS Synthetic.
 XX WO2003006048-A1.
 XX 23-JAN-2003.


```

Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 1 FFSW 5

RESULT 34
ABR45918
ID ABR45918 standard; peptide; 6 AA.
XX AC ABR45918;
XX DT 10-JUN-2003 (first entry)
XX DE Staphylococcus aureus CHIPS-related peptide #1108.
XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX PN WO2003006048-A1.
XX PD 23-JAN-2003.
XX PF 11-JUL-2001; 2001WO-EP008004.
XX PR 11-JUL-2001; 2001WO-EP008004.
XX PA (JARI-) JARI PHARM BV.
XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
XX PI Van Strijp JAG;
XX WPI; 2003-256333/25.
XX Combination of peptides derived from chemotaxis inhibiting protein from
Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
prophylaxis and treatment of inflammation, cardiovascular, skin and
kidney diseases.
XX Disclosure; Page 14; 89pp; English.
XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
Staphylococcus aureus. The peptide fragments are useful in the
prophylaxis or treatment of diseases or disorders involving the C5a-
receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
monocytes and endothelial cells or involving acute or chronic
inflammation reactions. The diseases or disorders include cardiovascular
diseases, disease of the central nervous system, gastrointestinal
diseases, skin diseases, genitourinary diseases, joint diseases,
respiratory diseases and HIV infection
XX Sequence 6 AA;
Query Match 69.6%; Score 16; DB 6; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 1 FFSW 5

RESULT 36
ABR45485
ID ABR45485 standard; peptide; 6 AA.
XX AC ABR45485;
XX DT 10-JUN-2003 (first entry)
XX
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RESULT 35
ABR45189
ID ABR45189 standard; peptide; 6 AA.
XX AC ABR45189;
XX DT 10-JUN-2003 (first entry)
XX DE Staphylococcus aureus CHIPS-related peptide #379.
XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX PN WO2003006048-A1.
XX PD 23-JAN-2003.
XX PF 11-JUL-2001; 2001WO-EP008004.
XX PR 11-JUL-2001; 2001WO-EP008004.
XX PA (JARI-) JARI PHARM BV.
XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
XX PI Van Strijp JAG;
XX WPI; 2003-256333/25.
XX Combination of peptides derived from chemotaxis inhibiting protein from
Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
prophylaxis and treatment of inflammation, cardiovascular, skin and
kidney diseases.
XX Disclosure; Page 12; 89pp; English.
XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
Staphylococcus aureus. The peptide fragments are useful in the
prophylaxis or treatment of diseases or disorders involving the C5a-
receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
monocytes and endothelial cells or involving acute or chronic
inflammation reactions. The diseases or disorders include cardiovascular
diseases, disease of the central nervous system, gastrointestinal
diseases, skin diseases, genitourinary diseases, joint diseases,
respiratory diseases and HIV infection
XX Sequence 6 AA;
Query Match 69.6%; Score 16; DB 6; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 1 FFSW 5

RESULT 36
ABR45485
ID ABR45485 standard; peptide; 6 AA.
XX AC ABR45485;
XX DT 10-JUN-2003 (first entry)
XX
```

DE Staphylococcus aureus CHIPS-related peptide #675.
XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiac; cerebroprotective; neuroprotective; nootropic; dermatological;
KW synecological; immunosuppressive; anti-HIV.
XX Staphylococcus aureus.
OS Synthetic.
OS WO2003006048-A1.
PN 23-JAN-2003.
XX 11-JUL-2001; 2001WO-EP008004.
PR 11-JUL-2001; 2001WO-EP008004.
XX (JARI-) JARI PHARM BV.
PA Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;
XX WPI; 2003-256333/25.
DR
XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.
XX Disclosure; Page 13; 89pp; English.
PS The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
XX -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection
XX Sequence 6 AA;
SQ
Query Match 69.6%; Score 16; DB 6; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXW 5
DB 1 FSPW 5
RESULT 37
ABR45150
ID ABR45150 standard; peptide; 6 AA.
XX
AC ABR45150;
XX
DT 10-JUN-2003 (first entry)
XX
DE Staphylococcus aureus CHIPS-related peptide #340.
XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiac; cerebroprotective; neuroprotective; nootropic; dermatological;
KW

KW synecological; immunosuppressive; anti-HIV.
XX Staphylococcus aureus.
OS Synthetic.
PN WO2003006048-A1.
XX 23-JAN-2003.
PD 11-JUL-2001; 2001WO-EP008004.
XX 11-JUL-2001; 2001WO-EP008004.
XX (JARI-) JARI PHARM BV.
PA Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;
XX WPI; 2003-256333/25.
DR
XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.
XX Disclosure; Page 11; 89pp; English.
PS The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
XX -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection
XX Sequence 6 AA;
SQ
Query Match 69.6%; Score 16; DB 6; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXW 5
DB 1 PTFW 5
RESULT 38
ABR45526
ID ABR45526 standard; peptide; 6 AA.
XX
AC ABR45526;
XX
DT 10-JUN-2003 (first entry)
XX
DE Staphylococcus aureus CHIPS-related peptide #716.
XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiac; cerebroprotective; neuroprotective; nootropic; dermatological;
KW synecological; immunosuppressive; anti-HIV.
XX Staphylococcus aureus.
OS Synthetic.
XX WO2003006048-A1.
PN 23-JAN-2003.
PD


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XX PF 11-JUL-2001; 2001WO-EP008004.
XX PR 11-JUL-2001; 2001WO-EP008004.
XX PA (JARI-) JARI PHARM BV.
XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
XX PI Van Strijp JAG;
XX XX WPI; 2003-256333/25.
XX XX
XX XX Combination of peptides derived from chemotaxis inhibiting protein from
XX PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
XX PT prophylaxis and treatment of inflammation, cardiovascular, skin and
XX PT kidney diseases.
XX XX
XX PS Disclosure; Page 13; 89pp; English.
XX XX
XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
XX CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
XX CC Staphylococcus aureus. The peptide fragments are useful in the
XX CC prophylaxis or treatment of diseases or disorders involving the C5a-
XX CC receptor (C5aR) and/or formulated peptide receptor (PPR) or neutrophils,
XX CC monocytes and endothelial cells or involving acute or chronic
XX CC inflammation reactions. The diseases or disorders include cardiovascular
XX CC diseases, disease of the central nervous system, gastrointestinal
XX CC diseases, skin diseases, genitourinary diseases, joint diseases,
XX CC respiratory diseases and HIV infection
XX XX
XX SQ Sequence 6 AA;
XX
XX Query Match 69.6%; Score 16; DB 6; Length 6;
XX Best Local Similarity 40.0%; Pred. No. 1.8e+06;
XX Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 FXXXX 5
XX DB 1 FFSW 5
XX
XX RESULT 39
XX ABR46269
XX ID ABR46269 standard; peptide; 6 AA.
XX AC ABR46269;
XX XX
XX DT 10-JUN-2003 (first entry)
XX DE Staphylococcus aureus CHIPS-related peptide #1459.
XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
XX KW formulated peptide receptor; PPR; neutrophil; monocyte; endothelial cell;
XX KW inflammation; cardiovascular disease; central nervous system disease;
XX KW gastrointestinal disease; skin disease; genitourinary disease;
XX KW joint disease; respiratory disease; HIV infection; antiinflammatory;
XX KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
XX KW gynecological; immunosuppressive; anti-HIV.
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX XX
XX PN WO2003006048-A1.
XX XX
XX PD 23-JAN-2003.
XX XX
XX PF 11-JUL-2001; 2001WO-EP008004.
XX XX
XX PR 11-JUL-2001; 2001WO-EP008004.
XX XX
XX PA (JARI-) JARI PHARM BV.
XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
XX PI Van Strijp JAG;
XX XX WPI; 2003-256333/25.
XX XX
XX XX Combination of peptides derived from chemotaxis inhibiting protein from
XX PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
XX PT prophylaxis and treatment of inflammation, cardiovascular, skin and
XX PT kidney diseases.
XX XX
XX PS Disclosure; Page 13; 89pp; English.
XX XX
XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
XX CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
XX CC Staphylococcus aureus. The peptide fragments are useful in the
XX CC prophylaxis or treatment of diseases or disorders involving the C5a-
XX CC receptor (C5aR) and/or formulated peptide receptor (PPR) or neutrophils,
XX CC monocytes and endothelial cells or involving acute or chronic
XX CC inflammation reactions. The diseases or disorders include cardiovascular
XX CC diseases, disease of the central nervous system, gastrointestinal
XX CC diseases, skin diseases, genitourinary diseases, joint diseases,
XX CC respiratory diseases and HIV infection
XX XX
XX SQ Sequence 6 AA;
XX
XX Query Match 69.6%; Score 16; DB 6; Length 6;
XX Best Local Similarity 40.0%; Pred. No. 1.8e+06;
XX Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 FXXXX 5
XX DB 1 FFSW 5
XX
XX RESULT 40
XX ABR46662
XX ID ABR46662 standard; peptide; 6 AA.
XX AC ABR46662;
XX XX
XX DT 10-JUN-2003 (first entry)
XX DE Staphylococcus aureus CHIPS-related peptide #1852.
XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
XX KW formulated peptide receptor; PPR; neutrophil; monocyte; endothelial cell;
XX KW inflammation; cardiovascular disease; central nervous system disease;
XX KW gastrointestinal disease; skin disease; genitourinary disease;
XX KW joint disease; respiratory disease; HIV infection; antiinflammatory;
XX KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
XX KW gynecological; immunosuppressive; anti-HIV.
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX XX
XX PN WO2003006048-A1.
XX XX
XX PD 23-JAN-2003.
XX XX
XX PF 11-JUL-2001; 2001WO-EP008004.
XX XX
XX PR 11-JUL-2001; 2001WO-EP008004.
XX XX
XX PA (JARI-) JARI PHARM BV.
XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
XX PI Van Strijp JAG;
XX XX WPI; 2003-256333/25.
XX XX
XX XX Combination of peptides derived from chemotaxis inhibiting protein from
XX PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
XX PT prophylaxis and treatment of inflammation, cardiovascular, skin and
XX PT kidney diseases.

```

XX Disclosure; Page 17; 89pp; English.
PS
XX
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection
XX
SQ Sequence 6 AA;

Query Match 69.6%; Score 16; DB 6; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 1 FTFW 5

Search completed: October 18, 2005, 15:54:56
Job time : 135.176 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:18:31 ; Search time 23.0588 Seconds
(without alignments)
33.381 Million cell updates/sec

Title: US-09-214-371-10

Perfect score: 23

Sequence: 1 FXXWXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	73.9	9	2 A24244	adipokinetic hormo
2	17	73.9	53	2 T00172	hypothetical prote
3	17	73.9	53	2 D89989	hypothetical prote
4	17	73.9	63	2 T29202	hypothetical prote
5	17	73.9	65	1 A32613	adipokinetic hormo
6	17	73.9	67	2 T12860	hypothetical prote
7	17	73.9	70	2 A86942	hypothetical prote
8	17	73.9	72	2 S15137	thioredoxin h2 - s
9	17	73.9	77	2 S18581	pufQ protein - Rho
10	17	73.9	77	2 T50756	pufQ protein [impo
11	17	73.9	84	2 E69268	hypothetical prote
12	17	73.9	88	2 B46264	thioredoxin 2 - sl
13	17	73.9	98	2 F47624	ig heavy chain V-I
14	17	73.9	99	2 S37444	gene E2 protein -
15	17	73.9	99	2 S37447	gene E2 protein -
16	17	73.9	99	2 S37441	gene E2 protein -
17	17	73.9	99	2 S37448	gene E2 protein -
18	17	73.9	99	2 S37442	gene E2 protein -
19	17	73.9	102	2 G71043	hypothetical prote
20	17	73.9	102	2 B56956	GTP-binding protei
21	17	73.9	104	1 A28086	thioredoxin - rabb
22	17	73.9	105	1 A30006	thioredoxin - chic
23	17	73.9	105	1 JH0568	thioredoxin [valid
24	17	73.9	105	1 J50667	thioredoxin - rhes
25	17	73.9	105	1 S04107	thioredoxin - mous
26	17	73.9	105	1 S04352	thioredoxin - rat
27	17	73.9	107	2 T33843	hypothetical prote
28	17	73.9	108	2 AH2101	thioredoxin [impor
29	17	73.9	112	2 PH0980	ig heavy chain V r

30	17	73.9	112	2 AF2549	hypothetical prote
31	17	73.9	113	1 S57775	thioredoxin h, cyt
32	17	73.9	114	1 JQ2242	thioredoxin h - Ar
33	17	73.9	115	1 G3HUN	ig heavy chain V-I
34	17	73.9	115	2 PL0238	ig heavy chain V r
35	17	73.9	115	2 G72642	probable surface p
36	17	73.9	116	2 T10737	thioredoxin - comm
37	17	73.9	117	2 PL0239	ig heavy chain V r
38	17	73.9	117	2 PL0234	ig heavy chain V r
39	17	73.9	117	2 PL0235	ig heavy chain V r
40	17	73.9	118	1 S34812	thioredoxin h2 - c
41	17	73.9	118	2 S58118	thioredoxin (clone
42	17	73.9	118	2 S58120	thioredoxin (clone
43	17	73.9	118	2 T10170	thioredoxin - cast
44	17	73.9	118	2 PL0231	ig heavy chain V r
45	17	73.9	118	2 F82424	diacylglycerol kin
46	17	73.9	119	2 T08142	thioredoxin h homo
47	17	73.9	119	2 D86330	F69.21 protein -
48	17	73.9	119	2 T50867	thioredoxin-like p
49	17	73.9	119	2 A24672	ig heavy chain pre
50	17	73.9	119	2 B72526	hypothetical prote
51	17	73.9	122	2 T04090	probable thioredox
52	17	73.9	123	2 S34009	ig heavy chain V r
53	17	73.9	125	2 T50866	probable thioredox
54	17	73.9	125	2 S58119	thioredoxin (clone
55	17	73.9	126	1 S16590	thioredoxin h1 - c
56	17	73.9	131	2 T50862	thioredoxin-like p
57	17	73.9	131	2 T50863	thioredoxin-like p
58	17	73.9	131	2 T50864	thioredoxin-like p
59	17	73.9	131	2 T50865	thioredoxin-like p
60	17	73.9	133	2 S58123	thioredoxin (clone
61	17	73.9	136	2 A10124	probable prelin
62	17	73.9	138	2 S03526	ig heavy chain pre
63	17	73.9	141	2 T17760	hypothetical prote
64	17	73.9	141	2 S50690	hypothetical prote
65	17	73.9	141	2 G95330	probable nucleotid
66	17	73.9	142	2 I47190	ig heavy chain var
67	17	73.9	144	2 A36324	growth arrest-spec
68	17	73.9	146	2 A11809	hypothetical prote
69	17	73.9	147	2 R87432	hypothetical prote
70	17	73.9	149	2 T23939	hypothetical prote
71	17	73.9	150	2 D69100	probable protein d
72	17	73.9	152	2 F72702	hypothetical prote
73	17	73.9	156	2 T48047	hypothetical prote
74	17	73.9	158	2 S74730	hypothetical prote
75	17	73.9	160	2 A53293	flm3-region hypoch
76	17	73.9	160	2 S76328	hypothetical prote
77	17	73.9	161	2 AC0966	probable PTS syste
78	17	73.9	174	2 S73301	hypothetical prote
79	17	73.9	174	2 T02276	hypothetical prote
80	17	73.9	174	2 T29491	hypothetical prote
81	17	73.9	180	2 G70028	conserved hypotet
82	17	73.9	180	2 T51724	phosphotransferase
83	17	73.9	182	2 T17625	hypothetical prote
84	17	73.9	182	2 S53822	fucoxanthin chloro
85	17	73.9	183	2 T38917	hypothetical prote
86	17	73.9	189	2 T51064	hypothetical prote
87	17	73.9	191	2 S76398	hypothetical prote
88	17	73.9	194	2 T00482	probable thioredox
89	17	73.9	201	2 AC3593	probable integral
90	17	73.9	204	2 B82410	conserved hypotet
91	17	73.9	205	2 S75300	hypothetical prote
92	17	73.9	206	2 E83515	conserved hypotet
93	17	73.9	207	2 AC0006	probable membrane
94	17	73.9	207	2 T46415	hypothetical prote
95	17	73.9	208	1 D71802	hypothetical prote
96	17	73.9	208	1 G64715	conserved hypotet
97	17	73.9	211	2 S53824	fucoxanthin chloro
98	17	73.9	212	2 B47698	hemagglutinin hag2
99	17	73.9	216	2 S53821	fucoxanthin chloro
100	17	73.9	217	2 C70629	probable mutf3 pro

ALIGNMENTS

RESULT 1

A24244
adipokinetin hormone - bollworm
N/Alternate names: Hez-AKH
C/Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C/Date: 31-Mar-1998 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C/Accession: A24244
R/Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
Biochem. Biophys. Res. Commun. 135, 622-628, 1986
A/Title: Isolation and primary structure of a peptide from the corpora cardiaca of Heliothis zea
A/Reference number: A24244; MUID:86186794; PMID:3964263
A/Accession: A24244
A/Molecule type: protein
A/Residues: 1-9 <JAF>
A/Cross-references: UNIPROT:P08901
C/Superfamily: adipokinetin hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 73.9%; Score 17; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| | |
DB 4 FTSSW 8

RESULT 2

T00172
hypothetical protein 38 - Staphylococcus aureus phage phi PVL
C/Species: Staphylococcus aureus phage phi PVL
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T00172
R/Kaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Y.
Biosci. Biotechnol. Biochem. 61, 1960-1962, 1997
A/Title: Panton-Valentine leukocidin genes in a phage-like particle isolated from mitomycin-resistant Staphylococcus aureus
A/Reference number: Z14119; MUID:98067870; PMID:9404084
A/Accession: T00172
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-53 <KAN>
A/Cross-references: UNIPROT:O80077; EMBL:AB009866; NID:d1204727; PIDN:BAA31912.1; PID:d1204727

Query Match 73.9%; Score 17; DB 2; Length 53;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| | |
DB 28 FTTAW 32

RESULT 3

D89989
hypothetical protein SAS063 [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: D89989
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: D89989
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-53 <KUR>

Query Match 73.9%; Score 17; DB 1; Length 65;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| | |

A/Cross-references: UNIPROT:Q99SQ2; GB:BA000018; PID:gl3701784; PIDN:BA043077.1; GSPDB:GN00022; CESP:F28F9
A/Experimental source: strain N315
C/Genetics:
A/Gene: SAS063

Query Match 73.9%; Score 17; DB 2; Length 53;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| | |
DB 28 FTTAW 32

RESULT 4

T29202
hypothetical protein F28F9.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T29202
R/Neelson, J.; Woldmann, P.
Submitted to the EMBL Data Library, September 1996
A/Description: The sequence of C. elegans cosmid F28F9.
A/Reference number: Z20587
A/Accession: T29202
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-63 <NEL>
A/Cross-references: UNIPROT:Q94194; EMBL:U70850; PIDN:AAB09124.1; GSPDB:GN00022; CESP:F28F9
A/Experimental source: strain Bristol N2; clone F28F9
C/Genetics:
A/Gene: CESP:F28F9.3
A/Map position: 4
A/Introns: 38/1

Query Match 73.9%; Score 17; DB 2; Length 63;
Best Local Similarity 40.0%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| | |
DB 30 FATAW 34

RESULT 5

A32613
adipokinetin hormone precursor - tobacco hornworm
C/Species: Manduca sexta (tobacco hornworm)
C/Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C/Accession: A32613
R/Bradfield, J.Y.; Keeley, L.L.
J. Biol. Chem. 264, 12791-12793, 1989.
A/Title: Adipokinetin hormone gene sequence from Manduca sexta.
A/Reference number: A32613; MUID:89327232; PMID:2753887
A/Accession: A32613
A/Molecule type: DNA
A/Residues: 1-65 <BRA>
A/Cross-references: UNIPROT:P08901; GB:J04972; NID:gl59478; PIDN:AAA29299.1; PID:gl59478
C/Genetics:
A/Introns: #status absent
C/Superfamily: adipokinetin hormone
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-28/Product: adipokinetin hormone #status predicted <MAT>
F/20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F/28/Modified site: amidated carboxyl end (Gly) (amide in mature form from following glycy-

Query Match 73.9%; Score 17; DB 1; Length 65;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| | |

Db 23 FTSSW 27

RESULT 6

T12860

hypothetical protein yopZ - Bacillus subtilis phage SPBc2

C:Species: Bacillus subtilis phage SPBc2

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: T12860; H69918

R:Lazarovic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.

submitted to the EMBL Data Library, August 1997

A:Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophage

A:Reference number: Z17593

A:Accession: T12860

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-67 <LAZ>

A:Cross-references: UNIPROT:O64109; EMBL:AF020713; NID:g3025478; PID:g3025574; PIDN:AAC1

R:Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertoni

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koester, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: H69918

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-67 <KUN>

A:Cross-references: GB:Z99114; GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB13989.1; PI

A:Experimental source: strain 168

C:Genetics:

A:Gene: yopZ

Query Match 73.9%; Score 17; DB 2; Length 67;

Best Local Similarity 40.0%; Pred. No. 1.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5

Db 49 FASSW 53

RESULT 7

A86942

hypothetical protein [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: A86942

R: Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: A86942

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-70 <STO>

A:Cross-references: UNIPROT:O69587; GB:AL450380; NID:g13092599; PIDN:CAC29773.1; GSPDB:C

C:Genetics:

A:Gene: ML0265

Query Match 73.9%; Score 17; DB 2; Length 70;

Best Local Similarity 40.0%; Pred. No. 1.6e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5

Db 14 FTTSW 18

RESULT 8

S15137

thioredoxin h2 - spinach (fragments)

C:Species: Spinacia oleracea (Spinach)

C>Date: 25-Feb-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: S15137

R:Marcus, F.; Chamberlain, S.H.; Chu, C.; Masiaz, F.R.; Shin, S.; Yee, B.C.; Buchanan,

A:Title: Plant thioredoxin h: an animal-like thioredoxin occurring in multiple cell comp

A:Reference number: S15137; MUID:91378382; PMID:1897989

A:Accession: S15137

A:Molecule type: protein

A:Residues: 1-72 <MAR>

A:Cross-references: UNIPROT:Q9S881

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

Query Match 73.9%; Score 17; DB 2; Length 72;

Best Local Similarity 40.0%; Pred. No. 1.6e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5

Db 6 FTASW 10

RESULT 9

S18581

pufQ protein - Rhodobacter sphaeroides

C:Species: Rhodobacter sphaeroides

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: S18581; S32854

R:Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.

Mol. Microbiol. 5, 2849-2861, 1991

A:Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon reg

A:Reference number: S18580; MUID:92140030; PMID:1779756

A:Accession: S18581

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-77 <HUN>

A:Cross-references: UNIPROT:P16069; EMBL:X68795; NID:g49170; PID:g49175

C:Genetics:

A:Gene: pufQ

C:Superfamily: pufQ protein

Query Match 73.9%; Score 17; DB 2; Length 77;

Best Local Similarity 40.0%; Pred. No. 1.7e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5

Db 60 FASAW 64

RESULT 10

T50756

pufQ protein [imported] - Rhodobacter sphaeroides

C:Species: Rhodobacter sphaeroides

C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004

C:Accession: T50756

R:Choudhary, M.; Kaplan, S.

Nucleic Acids Res. 28, 862-867, 2000

A:Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2

A:Reference number: Z25222; MUID:20115911; PMID:10648776

A;Accession: T50756
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-77 <CHO>

A;Cross-references: UNIPROT:P16069; EMBL:AF195122; PIDN:AAF24300.1

A;Experimental source: strain 2.4.1

C;Genetics:

A;Gene: pufQ

C;Superfamily: pufQ protein

Query Match 73.9%; Score 17; DB 2; Length 77;

Best Local Similarity 40.0%; Pred. No. 1.7e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5

| |

Db 60 FSAW 64

RESULT 11

E69268

hypothetical protein AF0149 - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: E69268

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: E69268

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-84 <KLE>

A;Cross-references: UNIPROT:O30088; GB:AE001096; GB:AE000782; NID:G2689419; PIDN:AA89108

Query Match

Best Local Similarity 73.9%; Score 17; DB 2; Length 84;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5

| |

Db 42 FAAW 46

RESULT 12

B46264

thioredoxin 2 - slime mold (Dictyostelium discoideum) (fragment)

C;Species: Dictyostelium discoideum

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Aug-2004

C;Accession: B46264

R;Wetterauer, B.; Jacquot, J.P.; Veron, M.

J. Biol. Chem. 267, 5895-5904, 1992

A;Title: Thioredoxins from Dictyostelium discoideum are a developmentally regulated mul

A;Reference number: A46264; MUID:92250653; PMID:1577820

A;Accession: B46264

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-88 <WET>

A;Cross-references: UNIPROT:P29446; GB:M91382; NID:G167930; PIDN:AAA33259.1; PID:G167931

C;Superfamily: Thioredoxin; thioredoxin homology

F;8-88/Domain: thioredoxin homology <THR>

Query Match 73.9%; Score 17; DB 2; Length 88;

Best Local Similarity 40.0%; Pred. No. 1.8e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5

| |

Db 26 FSAW 30

RESULT 13

F47624

IG heavy chain V-I region - African clawed frog (fragment)

C;Species: Xenopus laevis (African clawed frog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C;Accession: F47624

R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.

J. Exp. Med. 171, 1721-1737, 1990

A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation

A;Reference number: A47624; MUID:90237760; PMID:2110243

A;Accession: F47624

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-98 <HAI>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 73.9%; Score 17; DB 2; Length 98;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5

| |

Db 29 FSSTW 33

RESULT 14

S37444

Gene E2 protein - human papillomavirus type 5 (fragment)

C;Species: human papillomavirus type 5

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: S37444

R;Deau, A.C.

submitted to the EMBL Data Library, August 1993

A;Reference number: S37440

A;Accession: S37444

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-99 <DEA>

A;Cross-references: UNIPROT:Q81977; EMBL:X74648

C;Superfamily: papillomavirus E2 protein

Query Match

Best Local Similarity 73.9%; Score 17; DB 2; Length 99;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5

| |

Db 46 FSTTW 50

RESULT 15

S37447

Gene E2 protein - human papillomavirus type 5 (fragment)

C;Species: human papillomavirus type 5

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: S37447

R;Deau, A.C.

submitted to the EMBL Data Library, August 1993

A;Reference number: S37440

A;Accession: S37447

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-99 <DEA>

A;Cross-references: UNIPROT:Q81979; EMBL:X74651; NID:G404204; PIDN:CAA52715.1; PID:G4042

C;Superfamily: papillomavirus E2 protein

Query Match

Best Local Similarity 73.9%; Score 17; DB 2; Length 99;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|
46 FSTTW 50

Db

RESULT 16
S37441
gene E2 protein - human papillomavirus type 5 (fragment)
C;Species: human papillomavirus type 5
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37441
R;Deau, A.C.
submitted to the EMBL Data Library, August 1993
A;Reference number: S37440
A;Accession: S37441
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <DEA>
A;Cross-references: UNIPROT:Q81973; EMBL:X74645; NID:G404161; PIDN:CAA52709.1; PID:G4041
C;Superfamily: papillomavirus E2 protein

Query Match 73.9%; Score 17; DB 2; Length 99;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|
46 FSTTW 50

Db

RESULT 17
S37448
gene E2 protein - human papillomavirus type 5 (fragment)
C;Species: human papillomavirus type 5
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37448
R;Deau, A.C.
submitted to the EMBL Data Library, August 1993
A;Reference number: S37440
A;Accession: S37448
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <DEA>
A;Cross-references: UNIPROT:Q81981; EMBL:X74652
C;Superfamily: papillomavirus E2 protein

Query Match 73.9%; Score 17; DB 2; Length 99;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|
46 FSTTW 50

Db

RESULT 18
S37442
gene E2 protein - human papillomavirus type 5 (fragment)
C;Species: human papillomavirus type 5
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37442
R;Deau, A.C.
submitted to the EMBL Data Library, August 1993
A;Reference number: S37440
A;Accession: S37442
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <DEA>
A;Cross-references: UNIPROT:Q81975; EMBL:X74646
C;Superfamily: papillomavirus E2 protein

Query Match 73.9%; Score 17; DB 2; Length 99;

Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|
46 FSTTW 50

Db

RESULT 19
G71043
hypothetical protein PH1639 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: G71043
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: G71043
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-102 <KAW>
A;Cross-references: UNIPROT:O59305; GB:AP000006; NID:G2236133; PIDN:BAA30751.1; PID:G925
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1639

Query Match 73.9%; Score 17; DB 2; Length 102;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|
34 FASSW 38

Db

RESULT 20
B56956
GTP-binding protein-associated protein (clone c) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: B56956
R;Janoueix-Lerosey, I.; Jollivet, F.; Camonis, J.; Marche, P.N.; Goud, B.
J. Biol. Chem. 270, 14801-14808, 1995
A;Title: Two-hybrid system screen with the small GTP-binding protein Rab6. Identification
A;Reference number: A56956; MUID:95301579; PMID:7782346
A;Accession: B56956
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-102 <JAN>
A;Cross-references: UNIPROT:Q62145; GB:L40934; NID:G722666; PIDN:AAA78788.1; PID:G722667

Query Match 73.9%; Score 17; DB 2; Length 102;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
|
61 FASAW 65

Db

RESULT 21
A28086
thioredoxin - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Jun-1989 #sequence_revision 26-May-1994 #text_change 16-Aug-2004
C;Accession: A28086
R;Johnson, R.S.; Mathews, W.R.; Biemann, K.; Hopper, S.
J. Biol. Chem. 263, 9589-9597, 1988
A;Title: Amino acid sequence of thioredoxin isolated from rabbit bone marrow determined
A;Reference number: A28086; MUID:98257078; PMID:3164311

A;Accession: A28086
A;Molecule type: protein
A;Residues: 1-104 <JOH>
A;Cross-references: UNIPROT:P08628
C;Superfamily: Thioredoxin; thioredoxin homology
C;Keywords: redox-active disulfide
F;8-91/Domain: thioredoxin homology <THR>
F;31-34/Disulfide bonds: redox-active #status predicted

Query Match 73.9%; Score 17; DB 1; Length 104;
Best Local Similarity 40.0%; Pred. No. 2.le+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXX 5
Db 26 FSATW 30

RESULT 22
A30006
Thioredoxin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 31-Mar-1989 #sequence_revision 26-May-1994 #text_change 16-Aug-2004
C;Accession: A30006
R;Jones, S.W.; Luk, K.C.
J. Biol. Chem. 263, 9607-9611, 1988
A;Title: Isolation of a chicken thioredoxin cDNA clone: thioredoxin mRNA is differential
A;Reference number: A30006; MUID:88257080; PMID:2838473
A;Accession: A30006
A;Molecule type: mRNA
A;Residues: 1-105 <JON>
A;Cross-references: UNIPROT:P08629; GB:J03882; NID:G212765; PIDN:AAA49092.1; PID:G212766
C;Superfamily: Thioredoxin; thioredoxin homology
C;Keywords: redox-active disulfide
F;9-92/Domain: thioredoxin homology <THR>
F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 73.9%; Score 17; DB 1; Length 105;
Best Local Similarity 40.0%; Pred. No. 2.le+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXX 5
Db 27 FSATW 31

RESULT 23
JH0568
thioredoxin [validated] - human
N;Alternate names: APL-derived factor (ADF); eosinophil cytotoxicity-enhancing factor; b
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 26-May-1994 #text_change 16-Aug-2004
C;Accession: JH0568; S04106; S44375; A31993; PT0079; A60749; A38922; S53453; A60870
R;Tonissen, K.F.; Wells, J.R.E.
Gene 102, 221-228, 1991
A;Title: Isolation and characterization of human thioredoxin-encoding genes.
A;Reference number: JH0568; MUID:91340156; PMID:1874447
A;Accession: JH0568
A;Molecule type: DNA
A;Residues: 1-105 <TON>
A;Cross-references: UNIPROT:P10599; EMBL:X54539; NID:G37455; PIDN:CAA38410.1; PID:G82572
R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,
EMBO J. 8, 757-764, 1989
A;Title: APL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to thioredox
A;Reference number: S04106; MUID:89251607; PMID:2785919
A;Accession: S04106
A;Molecule type: mRNA
A;Residues: 1-105 <TAGI>
A;Cross-references: GB:X77584; NID:G453963; PIDN:CAA54687.1; PID:G453964
A;Note: this sequence has been revised in reference S44375
R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,
EMBO J. 13, 2244, 1994
A;Reference number: S44375; MUID:94244626; PMID:8187776

A;Contents: erratum
A;Accession: S44375
A;Molecule type: mRNA
A;Residues: 1-105 <TAG2>
A;Cross-references: EMBL:X77584; NID:G453963; PIDN:CAA54687.1; PID:G453964
R;Wollman, E.E.; d'Auriol, L.; Rimsky, L.; Shaw, A.; Jacquot, J.P.; Wingfield, P.; Grabe;
J. Biol. Chem. 263, 15506-15512, 1988
A;Title: Cloning and expression of a cDNA for human thioredoxin.
A;Reference number: A31993; MUID:89008454; PMID:3170595
A;Accession: A31993
A;Molecule type: mRNA
A;Residues: 1-38,'N',40-73,'T',75-105 <WOL>
A;Cross-references: GB:J04026; NID:G339648; PIDN:AAA74596.1; PID:G339649
R;Martin, H.; Dean, M.
Biochem. Biophys. Res. Commun. 175, 123-128, 1991
A;Title: Identification of a thioredoxin-related protein associated with plasma membrane
A;Reference number: PT0079; MUID:91151337; PMID:1998498
A;Accession: PT0079
A;Molecule type: protein
A;Residues: 2-13,'X',15 <MAR>
R;Silberstein, D.S.; Ali, M.H.; Baker, S.L.; David, J.R.
J. Immunol. 143, 979-983, 1989
A;Title: Human eosinophil cytotoxicity-enhancing factor. Purification, physical character
A;Reference number: A60749; MUID:89309777; PMID:2745979
A;Accession: A60749
A;Molecule type: protein
A;Residues: 2-12,'K',14-15,'XX',18-19,'X',21-22 <SIL>
A;Note: the abstract is inconsistent with figure 4 in having one undetermined residue aft
R;Rimsky, L.; Wakasugi, H.; Ferrara, P.; Robin, P.; Capdevielle, J.; Tursz, T.; Fradelizi
J. Immunol. 136, 3304-3310, 1986
A;Title: Purification to homogeneity and NH-2-terminal amino acid sequence of a novel int
A;Reference number: A38922; MUID:86169684; PMID:3485686
A;Accession: A38922
A;Molecule type: protein
A;Residues: 2-16 <WAK>
R;Dean, M.F.; Martin, H.; Sansom, P.A.
Biochem. J. 304, 861-867, 1994
A;Title: Characterization of a thioredoxin-related surface protein.
A;Reference number: S53453; MUID:95118305; PMID:7818492
A;Accession: S53453
A;Molecule type: protein
A;Residues: 1-21,38-57 <DEA>
R;Wakasugi, H.; Rimsky, L.; Mahe, Y.; Kamel, A.M.; Fradelizi, D.; Tursz, T.; Bertoglio, S
Proc. Natl. Acad. Sci. U.S.A. 84, 804-808, 1987
A;Title: Epstein-Barr virus-containing B-cell line produces an interleukin 1 that it use
A;Reference number: A60870; MUID:87118252; PMID:3027706
A;Contents: annotation
R;Weichsel, A.; Gasdaska, J.R.; Powis, G.; Montfort, W.R.
submitted to the Brookhaven Protein Data Bank, February 1996
A;Reference number: A65533; PDB:1ERT
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, reduced form, residues 1-1
R;Weichsel, A.; Gasdaska, J.R.; Powis, G.; Montfort, W.R.
submitted to the Brookhaven Protein Data Bank, February 1996
A;Reference number: A65534; PDB:1ERU
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, oxidized form, residues 1-1
R;Forman-Kay, J.D.; Clore, G.M.; Gronenborn, A.M.
submitted to the Brookhaven Protein Data Bank, December 1990
A;Reference number: A50924; PDB:4TRX
A;Contents: annotation; conformation by (1)H-NMR, residues 1-73,'T',75-105
R;Forman-Kay, J.D.; Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.
Biochemistry 30, 2685-2698, 1991
A;Title: High-resolution three-dimensional structure of reduced recombinant human thior
A;Reference number: A38953; MUID:91159399; PMID:2001356
A;Contents: annotation; conformation by (1)H- and (15)N-NMR
C;Comment: This small ubiquitous protein functions in many intracellular biological pathw
C;Genetics:
A;Gene: GDB:TXN
A;Cross-references: GDB:120475; OMIM:187700
A;Map position: 9q31-q31
A;Introns: 8/3; 43/3; 63/3; 85/3
C;Superfamily: Thioredoxin; thioredoxin homology
C;Keywords: redox-active disulfide

F;2-105/Product: thioredoxin #status experimental <MAT>
F;9-92/Domain: thioredoxin homology <THR>
F;32-35/Disulfide bonds: redox-active #status experimental

Query Match 73.9%; Score 17; DB 1; Length 105;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
|
DB 27 FSATW 31

RESULT 24

JS0667

C;Species: Macaca mulatta (rhesus macaque)
C;Date: 30-Jun-1992 #sequence_revision 26-May-1994 #text_change 16-Aug-2004
C;Accession: JS0667
R;An, G.; Wu, R.

Biochem. Biophys. Res. Commun. 183, 170-175, 1992
A;Title: Thioredoxin gene expression is transcriptionally up-regulated by retinol in monocytes
A;Reference number: JS0667; MUID:92181438; PMID:1543487
A;Accession: JS0667
A;Molecule type: mRNA
A;Residues: 1-105 <ANG>
A;Cross-references: UNIPROT:P29451; GB:M84643; NID:G342338; PIDN:AAA36921.1; PID:G342339
C;Superfamily: Thioredoxin; thioredoxin homology
C;Keywords: redox-active disulfide
F;9-92/Domain: thioredoxin homology <THR>
F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 73.9%; Score 17; DB 1; Length 105;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
|
DB 27 FSATW 31

RESULT 25

S04107

Thioredoxin - mouse
N;Alternate names: ATL-derived factor (ADF)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 16-Aug-2004
C;Accession: JC4068; S44376; S04107
R;Matsui, M.; Taniguchi, Y.; Hirota, K.; Taketo, M.; Yodoi, J.
Gene 152, 165-171, 1995
A;Title: Structure of the mouse thioredoxin-encoding gene and its processed pseudogene.
A;Reference number: JC4068; MUID:95137382; PMID:7835695
A;Accession: JC4068

A;Molecule type: DNA

A;Residues: 1-105 <MAT>

A;Cross-references: UNIPROT:P10639; DDBJ:D21855; NID:9517128
R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai, EMO J. 13, 2244, 1994

A;Reference number: S44375; MUID:94244626; PMID:8187776

A;Contents: erratum

A;Accession: S44376

A;Molecule type: mRNA

A;Residues: 1-105 <TAG1>

A;Cross-references: EMBL:X77585; NID:9453971; PIDN:CAA54688.1; PID:9453972

R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai, EMO J. 8, 757-764, 1989

A;Title: ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to thioredoxin
A;Reference number: S04106; MUID:89251607; PMID:2785919

A;Accession: S04107

A;Molecule type: mRNA

A;Residues: 1-93, 'N' 94-96, 'ALT', 100-104, 'S' <TAG2>

A;Cross-references: GB:X77585

C;Comment: This small ubiquitous protein functions in many intracellular biological path

C;Genetics:

A;Gene: MGI:Txn
A;Cross-references: MGI:36258

A;Map position: 4:24.6

A;Introns: 29/2: 44/1, 84/2

C;Superfamily: Thioredoxin; thioredoxin homology

C;Keywords: redox-active disulfide

F;9-92/Domain: thioredoxin homology <THR>

F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 73.9%; Score 17; DB 1; Length 105;
Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
|
DB 27 FSATW 31

RESULT 26

S04352

Thioredoxin - rat

N;Alternate names: thioredoxin-related surface protein SASP

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Mar-1990 #sequence_revision 26-May-1994 #text_change 16-Aug-2004

C;Accession: S04352; S66372

R;Tonissen, K.F.; Robins, A.J.; Wells, J.R.E.

Nucleic Acids Res. 17, 3973, 1989

A;Title: Nucleotide sequence of a cDNA encoding rat thioredoxin.

A;Reference number: S04352; MUID:89282399; PMID:2734107

A;Accession: S04352

A;Molecule type: mRNA

A;Residues: 1-105 <TON>

A;Cross-references: UNIPROT:P11232; EMBL:X14878; NID:957385; PIDN:CAA33019.1; PID:957386

R;Dean, M.F.; Martin, H.; Sansom, P.A.

Biochem. J. 304, 861-867, 1994

A;Title: Characterization of a thioredoxin-related surface protein.

A;Reference number: S53453; MUID:95118305; PMID:7818492

A;Accession: S66372

A;Molecule type: protein

A;Residues: 2-21 <DEA>

A;Note: 12-Lys, 15-Gly, 16-Leu, 17-Gln, and 18-Leu were also found

A;Note: described to be a surface-associated thioredoxin

C;Superfamily: Thioredoxin; thioredoxin homology

C;Keywords: redox-active disulfide

F;2-105/Product: thioredoxin #status experimental <MAT>

F;9-92/Domain: thioredoxin homology <THR>

F;32-35/Disulfide bonds: redox-active #status predicted

Query Match

Best Local Similarity 40.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
|
DB 27 FSATW 31

RESULT 27

T33843

hypothetical protein Y44E3A.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T33843

R;Woessner, J.; Graves, T.; Keppeler, D.

submitted to the EMBL Data Library, November 1998

A;Description: The sequence of C. elegans cosmid Y44E3A.

A;Reference number: Z21422

A;Accession: T33843

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-107 <WOB>

A;Cross-references: UNIPROT:Q97XY8; EMBL:AF106589; PIDN:AAC78230.1; GSPDB:GN00019; CESP:

A;Experimental source: strain Bristol N2; clone Y44E3A

C;Genetics:

A;Gene: CBSP:Y44E3A.3

A;Map position: 1

A;Introns: 31/2

C;Superfamily: thioredoxin; thioredoxin homology

Query Match 73.9%; Score 17; DB 2; Length 107;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

DB 27 FTASW 31

RESULT 28

AH2101

thioredoxin [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 16-Aug-2004

C;Accession: AH2101

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AH2101

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-108 <KUR>

A;Cross-references: UNIPROT:Q8YU9H; GB:BA000019; PIDN:BAB74066.1; PID:g17131459; GSPDB:G

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all2367

C;Superfamily: Thioredoxin; thioredoxin homology

Query Match 73.9%; Score 17; DB 2; Length 108;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

DB 28 FTATW 32

RESULT 29

PH0980

Ig heavy chain V region (clone 17s.13) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PH0980

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-778, 1992

A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH0980

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-112 <TIL>

A;Experimental source: B cell, strain [N2B x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 73.9%; Score 17; DB 2; Length 112;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

DB 29 FSSSW 33

RESULT 30

AF2549

hypothetical protein all7681 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120bet

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AF2549

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AF2549

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-112 <KUR>

A;Cross-references: UNIPROT:Q8ZS31; GB:AP003602; PIDN:BAB77324.1; PID:g17134766; GSPDB:GN

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all7681

A;Genome: plasmid

Query Match 73.9%; Score 17; DB 2; Length 112;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

DB 87 FASAW 91

RESULT 31

S57775

thioredoxin h, cytosolic [validated] - Chlamydomonas reinhardtii

C;Species: Chlamydomonas reinhardtii

C;Date: 27-Oct-1995 #sequence_revision 21-Jan-1997 #text_change 16-Aug-2004

C;Accession: S57775; S57799; S54868; S16090; S54870

R;Stein, M.; Jacquot, J.P.; Jeannette, E.; Decottignies, P.; Hodges, M.; Lancelin, J.M.;

Plant Mol. Biol. 28, 487-503, 1995

A;Title: Chlamydomonas reinhardtii thioredoxins: structure of the genes coding for the c

on and biochemical properties

A;Reference number: S57774; MUID:95359406; PMID:7632918

A;Accession: S57775

A;Molecule type: DNA

A;Residues: 1-113 <STE>

A;Cross-references: UNIPROT:P80028; EMBL:X80887; NID:g840742; PIDN:CAA56850.1; PID:g84074

A;Accession: S57799

A;Molecule type: protein

A;Residues: 2-15 <STW>

R;Stein, M.; Hodges, M.; Jeanette, E.; Lancelin, J.M.; Jacquot, J.P.

submitted to the EMBL Data Library, April 1994

A;Description: Chlamydomonas reinhardtii thioredoxins I : cDNA and amino acid deduced seq

A;Reference number: S54844

A;Accession: S54868

A;Molecule type: mRNA

A;Residues: 1-113 <STF>

A;Cross-references: EMBL:X78822; NID:g840740; PIDN:CAA55399.1; PID:g840741

R;Decottignies, P.; Schmitter, J.M.; Dutka, S.; Jacquot, J.P.; Miginiac-Maslou, M.

Eur. J. Biochem. 198, 505-512, 1991

A;Title: Characterization and primary structure of a second thioredoxin from the green a

A;Reference number: S16090; MUID:91249849; PMID:2040309

A;Accession: S16090

A;Molecule type: protein

A;Residues: 2-112 <MIG>

R;Mittard, V.; Blackledge, M.J.; Stein, M.; Jacquot, J.P.; Marion, D.; Lancelin, J.M.

submitted to the Brookhaven Protein Data Bank, May 1996

A;Reference number: A66748; PDB:1TOF

A;Contents: annotation; conformation by (1)H, (13)C, (15)N-NMR, residues 2-113

R;Mittard, V.; Morelle, N.; Brutscher, B.; Simorre, J.P.; Marion, D.; Stein, M.; Jacquot,

Eur. J. Biochem. 229, 473-485, 1995

A;Title: (1)H, (13)C, (15)N-NMR resonance assignments of oxidized thioredoxin h from the

R spectroscopy and computer-assisted backbone assignment.
 A;Reference number: A58618; MUID:95262711; PMID:7744070
 A;Contents: annotation; conformation by (1)H, (13)C, (15)N-NMR
 C;Genetics:

A;Introns: 27/3; 35/3; 69/3

C;Superfamily: Thioresdoxin; thioresdoxin homology

C;Keywords: redox-active disulfide

F;2-113/Product: thioresdoxin h #status experimental <MAT>

F;15-98/Domain: thioresdoxin homology <THR>

F;37-40/Disulfide bonds: redox-active #status experimental

Query Match 73.9%; Score 17; DB 1; Length 113;
 Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 32 FTATW 36

RESULT 32

JQ2242

N;Alternate names: Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 19-May-1994 #sequence_revision 26-May-1994 #text_change 16-Aug-2004

C;Accession: JQ2242; T45734; S29905

R;Rivera-Madrid, R.; Marinho, P.; Brugidou, C.; Chartier, Y.; Meyer, Y.

Plant Physiol. 102, 327-328, 1993

A;Title: Nucleotide sequence of a cDNA clone encoding an Arabidopsis thaliana thioresdoxin

A;Reference number: JQ2242; MUID:94151431; PMID:8108503

A;Accession: JQ2242

A;Molecule type: mRNA

A;Residues: 1-114<RTV>

A;Cross-references: UNIPROT:P29448; EMBL:Z14084; NID:gi16551; PIDN:CAA78462.1; PID:gi16552

R;Vitale, D.; Liguori, R.; Flores, M.; Argirou, A.; De Simone, V.; Mewes, H.W.; Lemcke,

submitted to the Protein Sequence Database, December 1999

A;Reference number: Z23012

A;Accession: T45734

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-114<VIT>

A;Cross-references: EMBL:AL132980

A;Experimental source: cultivar Columbia; BAC clone F24M12

C;Genetics:

A;Gene: F24M12.70

A;Map position: 3

A;Introns: 30/3; 71/3

C;Superfamily: Thioresdoxin; thioresdoxin homology

C;Keywords: redox-active disulfide

F;18-100/Domain: thioresdoxin homology <THR>

F;40-43/Disulfide bonds: redox-active #status predicted

Query Match 73.9%; Score 17; DB 1; Length 114;
 Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 35 FTATW 39

RESULT 33

G3HUJN

Ig heavy chain V-III region (Jon) - human (tentative sequence)

C;Species: Homo sapiens (man)

C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C;Accession: A02063

R;Capra, J.D.; Kehoe, J.M.

Proc. Natl. Acad. Sci. U.S.A. 71, 845-848, 1974

A;Title: Variable region sequences of five human immunoglobulin heavy chains of the V-HI

A;Reference number: A93794; MUID:74142702; PMID:4522793

A;Accession: A02063

A;Molecule type: protein

A;Residues: 1-115<CAP>

A;Cross-references: UNIPROT:P01780

C;Comment: This chain was isolated from an IgG3 myeloma protein.

C;Genetics:

A;Gene: GDB:IGHV@

A;Cross-references: GDB:128528; OMIM:147070

A;Map position: 14q32.33-14q32.33

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

F;22-96/Disulfide bonds: #status predicted

Query Match 73.9%; Score 17; DB 1; Length 115;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 29 FSTAW 33

RESULT 34

PL0238

Ig heavy chain V region (anti-DNA, 6NVH and 6QVH) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C;Accession: PL0238

R;Slomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A;Reference number: PL0231; MUID:9011618; PMID:2104919

A;Accession: PL0238

A;Molecule type: mRNA

A;Residues: 1-115<SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-30/Region: framework 1

F;15-98/Domain: immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;36-49/Region: framework 2

F;50-66/Region: complementarity-determining 2

F;67-98/Region: framework 3

F;99-107/Region: complementarity-determining 3

F;108-115/Region: framework 4

Query Match 73.9%; Score 17; DB 2; Length 115;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
 Db 29 FSSSW 33

RESULT 35

G72642

probable surface protein-1 APE0575 - Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C;Accession: G72642

R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: G72642

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-115<KAW>

A;Cross-references: UNIPROT:Q9YEK3; DDBJ:AP0000060; NID:95104188; PIDN:BAW79543.1; PID:d

A;Experimental source: strain K1

C;Genetics:

A;Gene: APE0575

Query Match 73.9%; Score 17; DB 2; Length 115;
 Best Local Similarity 40.0%; Pred. No. 2.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 |
 Db 2 FSAW 6

RESULT 36

T10739

thioredoxin - common buckwheat

C;Species: Fagopyrum esculentum (common buckwheat)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T10739

R;Ujino, K.

submitted to the EMBL Data Library, September 1996

A;Reference number: Z17109

A;Accession: T10739

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-116 <FUJ>

A;Cross-references: UNIPROT:Q96419; EMBL:D87984

A;Experimental source: cv. Kitayuki

C;Function:

A;Description: participates, by the reversible oxidation of an active center disulfide b

C;Superfamily: thioredoxin; thioredoxin homology

C;Keywords: redox-active disulfide

F;11-99/Domain: thioredoxin homology <TXN>

Query Match 73.9%; Score 17; DB 2; Length 116;

Best Local Similarity 40.0%; Pred. No. 2.3e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

|

Db 34 FTASW 38

RESULT 37

PL0237

Ig heavy chain V region (anti-DNA, 1A11VH) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C;Accession: PL0237

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0237

A;Molecule type: mRNA

A;Residues: 1-117 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-30/Region: framework 1

F;15-98/Domain: immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;36-49/Region: framework 2

F;50-66/Region: complementarity-determining 2

F;67-98/Region: framework 3

F;99-109/Region: complementarity-determining 3

F;110-117/Region: framework 4

Query Match 73.9%; Score 17; DB 2; Length 117;

Best Local Similarity 40.0%; Pred. No. 2.3e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

|

Db 29 FSSW 33

RESULT 38

PL0234

Ig heavy chain V region (anti-DNA, 3H9VH) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C;Accession: PL0234

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0234

A;Molecule type: mRNA

A;Residues: 1-117 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-30/Region: framework 1

F;15-98/Domain: immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;36-49/Region: framework 2

F;50-66/Region: complementarity-determining 2

F;67-98/Region: framework 3

F;99-109/Region: complementarity-determining 3

F;110-117/Region: framework 4

Query Match 73.9%; Score 17; DB 2; Length 117;

Best Local Similarity 40.0%; Pred. No. 2.3e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

|

Db 29 FSSW 33

RESULT 39

PL0235

Ig heavy chain V region (anti-DNA, 2F2VH and 4H8VH) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C;Accession: PL0235

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0235

A;Molecule type: mRNA

A;Residues: 1-117 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-30/Region: framework 1

F;15-98/Domain: immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;36-49/Region: framework 2

F;50-66/Region: complementarity-determining 2

F;67-98/Region: framework 3

F;99-109/Region: complementarity-determining 3

F;110-117/Region: framework 4

Query Match 73.9%; Score 17; DB 2; Length 117;

Best Local Similarity 40.0%; Pred. No. 2.3e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

|

Db 29 FSSW 33

RESULT 40

S34812

thioredoxin h2 - common tobacco

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Aug-2004

C;Accession: S34812

R;Brugidou, C.; Marty, I.; Chartier, Y.; Meyer, Y.
Mol. Gen. Genet. 238, 285-293, 1993
A;Title: The Nicotiana tabacum genome encodes two cytoplasmic thioredoxin genes which are
A;Reference number: S34812; MUID:93241165; PMID:8479434
A;Accession: S34812
A;Molecule type: DNA
A;Residues: 1-118 <BRU>
A;Cross-references: UNIPROT:Q07090; EMBL:Z11803; NID:G297518; PIDN:CAA77847.1; PID:G2975
C;Genetics:
A;Introns: 29/3; 70/3
C;Superfamily: Thioredoxin; thioredoxin homology
F;17-99/Domain: thioredoxin homology <THR>

Query Match 73.9%; Score 17; DB 1; Length 118;
Best Local Similarity 40.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 34 FTASW 38

Search completed: October 18, 2005, 15:31:03
Job time : 25.0588 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:30:23 ; Search time 107.294 Seconds
(without alignments)
31.079 Million cell updates/sec

Title: US-09-214-371-10

Perfect score: 23

Sequence: 1 FXXWXXX 8

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 1860064 seqs, 416830855 residues

Total number of hits satisfying chosen parameters: 1860064

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	17	73.9	8	18	US-10-818-036-24
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3	17	73.9	8	18	US-10-818-036-28
4	17	73.9	8	18	US-10-818-036-30
5	17	73.9	9	14	US-10-072-419-3
6	17	73.9	9	14	US-10-072-419-8
7	17	73.9	9	16	US-10-869-768-3
8	17	73.9	9	16	US-10-869-768-8
9	17	73.9	9	18	US-10-818-036-14
10	17	73.9	9	18	US-10-818-036-15
11	17	73.9	9	18	US-10-818-036-23
					Sequence 24, Appl
					Sequence 27, Appl
					Sequence 28, Appl
					Sequence 30, Appl
					Sequence 3, Appl
					Sequence 8, Appl
					Sequence 3, Appl
					Sequence 8, Appl
					Sequence 14, Appl
					Sequence 15, Appl
					Sequence 23, Appl

9	18	US-10-818-036-25	Sequence 25, Appl
9	18	US-10-818-036-26	Sequence 26, Appl
9	18	US-10-818-036-29	Sequence 29, Appl
10	11	US-09-842-776A-28	Sequence 28, Appl
10	18	US-10-996-316-139	Sequence 139, Appl
11	14	US-10-072-419-37	Sequence 37, Appl
11	16	US-10-869-768-37	Sequence 37, Appl
15	14	US-10-354-240-87	Sequence 87, Appl
15	14	US-10-354-240-88	Sequence 88, Appl
19	10	US-09-963-339-10	Sequence 10, Appl
19	14	US-10-145-586-59	Sequence 59, Appl
20	18	US-10-931-260-265	Sequence 265, Appl
24	18	US-10-931-260-264	Sequence 264, Appl
25	14	US-10-338-777-408	Sequence 408, Appl
27	9	US-09-864-761-46828	Sequence 46828, A
29	8	US-08-424-5508-428	Sequence 428, App
32	15	US-10-424-599-160512	Sequence 160512,
33	14	US-10-032-2018-157	Sequence 157, App
33	14	US-10-029-386-28347	Sequence 28347, A
35	15	US-10-307-817-584	Sequence 584, App
36	18	US-10-931-260-137	Sequence 137, App
37	14	US-10-193-795-10	Sequence 10, Appl
37	18	US-10-962-760-10	Sequence 10, Appl
37	18	US-10-818-036-1	Sequence 1, Appl
38	10	US-09-892-877-347	Sequence 347, App
38	10	US-09-948-783-287	Sequence 287, App
40	9	US-09-057-951-6	Sequence 6, Appl
40	9	US-09-864-761-46093	Sequence 46093, A
40	13	US-10-105-150-6	Sequence 6, Appl
40	18	US-10-818-036-10	Sequence 10, Appl
40	18	US-10-818-036-11	Sequence 11, Appl
40	18	US-10-818-036-13	Sequence 13, Appl
41	18	US-10-931-260-136	Sequence 136, App
43	10	US-09-732-436-20	Sequence 20, Appl
44	9	US-09-864-761-35268	Sequence 35268, A
45	10	US-09-809-391-475	Sequence 475, App
45	10	US-09-882-171-475	Sequence 475, App
45	15	US-10-164-861-475	Sequence 475, App
45	18	US-10-931-260-135	Sequence 135, App
46	9	US-09-864-761-35084	Sequence 35084, A
46	15	US-10-424-599-165545	Sequence 165545,
47	14	US-10-062-548-129	Sequence 129, App
47	16	US-10-363-829-381	Sequence 381, App
47	16	US-10-425-115-239397	Sequence 239397,
47	17	US-10-918-446-129	Sequence 129, App
47	19	US-11-002-755-129	Sequence 129, App
47	20	US-11-002-756-129	Sequence 129, App
49	15	US-10-424-599-190385	Sequence 190385,
49	16	US-10-425-115-334172	Sequence 334172,
50	16	US-10-437-963-162052	Sequence 162052,
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52	16	US-10-425-115-295762	Sequence 295762,
53	17	US-10-470-0488-97	Sequence 97, Appl
54	10	US-09-733-643-21	Sequence 21, Appl
54	16	US-10-437-963-104779	Sequence 104779,
55	15	US-10-424-599-274696	Sequence 274696,
55	16	US-10-425-115-307743	Sequence 307743,
56	14	US-10-146-574-6	Sequence 6, Appl
57	15	US-10-424-599-227004	Sequence 227004,
58	15	US-10-424-599-178883	Sequence 178883,
58	15	US-10-424-599-253041	Sequence 253041,
59	16	US-10-425-115-232429	Sequence 232429,
59	15	US-10-424-599-176362	Sequence 176362,
59	15	US-10-424-599-279702	Sequence 279702,
60	14	US-10-011-585A-485	Sequence 185, App
60	15	US-10-424-599-224438	Sequence 224438,
61	11	US-09-833-245-1075	Sequence 1075, Ap
61	15	US-10-424-599-195215	Sequence 195215,
62	16	US-10-425-115-354918	Sequence 354918,
63	14	US-10-106-698-4576	Sequence 4576, Ap
63	15	US-10-335-977-8336	Sequence 8336, Ap
65	16	US-10-437-963-155904	Sequence 155904,
65	16	US-10-425-115-241287	Sequence 241287,

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85 17 73.9 66 15 US-10-424-599-181984 Sequence 181984,
86 17 73.9 67 16 US-10-425-115-222248 Sequence 222248,
87 17 73.9 68 16 US-10-425-115-308662 Sequence 308662,
88 17 73.9 69 14 US-10-029-386-29425 Sequence 29425, A
89 17 73.9 69 15 US-10-412-699B-1967 Sequence 1967, Ap
90 17 73.9 69 18 US-10-450-763-41422 Sequence 41422, A
91 17 73.9 70 16 US-10-437-963-172557 Sequence 172557,
92 17 73.9 71 9 US-09-864-761-45867 Sequence 45867, A
93 17 73.9 71 16 US-10-425-115-204522 Sequence 204522,
94 17 73.9 71 16 US-10-425-115-268403 Sequence 268403,
95 17 73.9 72 16 US-10-425-115-286869 Sequence 286869,
96 17 73.9 73 16 US-10-425-115-236925 Sequence 236925,
97 17 73.9 74 16 US-10-425-115-200161 Sequence 200161,
98 17 73.9 75 9 US-09-867-550-510 Sequence 510, App
99 17 73.9 77 13 US-10-001-843-186 Sequence 186, App
100 17 73.9 77 16 US-10-437-963-150690 Sequence 150690,

ALIGNMENTS

RESULT 1
US-10-818-036-24
; Sequence 24, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
;
Query Match 73.9%; Score 17; DB 18; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 4 FTASW 8

RESULT 2
US-10-818-036-27
; Sequence 27, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
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Query Match 73.9%; Score 17; DB 18; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 4 FTASW 8

RESULT 3
US-10-818-036-28
; Sequence 28, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: AMIDATION
;
Query Match 73.9%; Score 17; DB 18; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 4 FTASW 8

RESULT 4
US-10-818-036-30
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; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
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Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 4 FTASW 8
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Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5
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Db 4 FTSSW 8

RESULT 5

US-10-072-419-3
; Sequence 3, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Apis mellifera
US-10-072-419-3

Query Match 73.9%; Score 17; DB 14; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5
|
Db 4 FTSSW 8

RESULT 6

US-10-072-419-8
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; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-072-419-8

Query Match 73.9%; Score 17; DB 14; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
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Qy 1 FXXW 5
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Db 4 FTSSW 8

RESULT 7

US-10-869-768-3
; Sequence 3, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768

; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
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; TYPE: PRT
; ORGANISM: Apis mellifera
US-10-869-768-3

Query Match 73.9%; Score 17; DB 16; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5
|
Db 4 FTSSW 8

RESULT 8

US-10-869-768-8
; Sequence 8, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Humans
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-869-768-8

Query Match 73.9%; Score 17; DB 16; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5
|
Db 4 FTSSW 8

RESULT 9

US-10-818-036-14
; Sequence 14, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-818-036-14

Query Match 73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 FXXW 5
Db 4 FTASW 8

RESULT 10
US-10-818-036-15
; Sequence 15, Application US/10818036
; Publication No. US2005022040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-818-036-15
Query Match 73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 4 FTASW 8

RESULT 11
US-10-818-036-23
; Sequence 23, Application US/10818036
; Publication No. US2005022040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
US-10-818-036-23
Query Match 73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 4 FTSSW 8
```

```
US-10-818-036-25
; Sequence 25, Application US/10818036
; Publication No. US2005022040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-818-036-25
Query Match 73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 4 FTASW 8
```

```
RESULT 13
US-10-818-036-26
; Sequence 26, Application US/10818036
; Publication No. US2005022040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
US-10-818-036-26
Query Match 73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 4 FTASW 8
```

```
RESULT 14
US-10-818-036-29
; Sequence 29, Application US/10818036
; Publication No. US2005022040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
US-10-818-036-29
Query Match 73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
Db 4 FTASW 8
```

```
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818.036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
; US-10-818-036-29

Query Match 73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXHW 5
Db 4 FTASW 8

RESULT 15
US-09-842-776A-28
; Sequence 28, Application US/09842776A
; Publication No. US2004002316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842.776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR1) of an
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease
; OTHER INFORMATION: epitope (alternative sequence)
; US-09-842-776A-28

Query Match 73.9%; Score 17; DB 11; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXHW 5
Db 4 FSTSW 8

RESULT 16
US-10-996-316-139
; Sequence 139, Application US/10996316
; Publication No. US20050129690A1
; GENERAL INFORMATION:
; APPLICANT: Alexion Pharmaceuticals, Inc.
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: McWhirter, John
; APPLICANT: Kretz-Rommel, Anke
```

```
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC
; FILE REFERENCE: LEUKEMIA CELLS AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/1087-43 CIP IV)
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US/10/996.316
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/894.672
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/736.188
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254.113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 10
; TYPE: PRT
; ORGANISM: murine
; US-10-996-316-139

Query Match 73.9%; Score 17; DB 18; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXHW 5
Db 4 FSAHW 8

RESULT 17
US-10-072-419-37
; Sequence 37, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072.419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanessa cardui
; US-10-072-419-37

Query Match 73.9%; Score 17; DB 14; Length 11;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXHW 5
Db 4 FTSSW 8

RESULT 18
US-10-869-768-37
; Sequence 37, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869.768
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072.419
; PRIOR FILING DATE: 2002-02-07
```

; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-869 768-17

Query Match 73.9%; Score 17; DB 16; Length 11;
Best Local Similarity 40.0%; Pred. No. 6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 4 FTSSW 8

RESULT 19
US-10-354-240-87
; Sequence 87, Application US/10354240
; Publication No. US20030185847A1
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwame, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-10301
; CURRENT APPLICATION NUMBER: US/10/354,240
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 09/142,524
; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4
US-10-354-240-87

Query Match 73.9%; Score 17; DB 14; Length 15;
Best Local Similarity 40.0%; Pred. No. 8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 9 FSTAW 13

RESULT 20
US-10-354-240-88
; Sequence 88, Application US/10354240
; Publication No. US20030185847A1
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwame, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-10301
; CURRENT APPLICATION NUMBER: US/10/354,240
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 09/142,524

; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5
US-10-354-240-88

Query Match 73.9%; Score 17; DB 14; Length 15;
Best Local Similarity 40.0%; Pred. No. 8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 4 FSTAW 8

RESULT 21
US-09-963-339-10
; Sequence 10, Application US/09963339
; Publication No. US20030049700A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN
; TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-090001
; CURRENT APPLICATION NUMBER: US/09/963,339
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/235,049
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-339-10

Query Match 73.9%; Score 17; DB 10; Length 19;
Best Local Similarity 40.0%; Pred. No. 9.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 4 FSTAW 8

RESULT 22
US-10-145-586-59
; Sequence 59, Application US/10145586
; Publication No. US20030138900A1
; GENERAL INFORMATION:
; APPLICANT: Alexandra Glucksmann, Maria
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: M. Galvin, Katherine
; APPLICANT: Weich, Nadine
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
; TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
; FILE REFERENCE: 10448-188001
; CURRENT APPLICATION NUMBER: US/10/145,586
; CURRENT FILING DATE: 2002-05-14
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 59
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-586-59

Query Match      73.9%; Score 17; DB 14; Length 19;
Best Local Similarity 40.0%; Pred. No. 9.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
Db      4 FSATW 8

RESULT 23
US-10-931-260-265
; Sequence 265, Application: US/10931260
; Publication No. US20050152927A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.;
; Bond, Julian F.;
; Garman, Richard D.;
; Kuo, Mei-Chang;
; Powers, Stephen P.;
; Exley, Mark A.;
; Chen, Xian;
; Shaked, Ze'ev
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; Japanese Cedar Pollen
; NUMBER OF SEQUENCES: 283
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State St
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/931,260
; FILING DATE: 30-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,203
; FILING DATE: 29-Jan-1999
; APPLICATION NUMBER: 08/467,023
; FILING DATE: 1995-JUN-06
; APPLICATION NUMBER: 08/350,225
; FILING DATE: 1994-DEC-06
; APPLICATION NUMBER: 08/226,248
; FILING DATE: 1994-APR-08
; APPLICATION NUMBER: PCT/US93/00139
; FILING DATE: 1993-JAN-15
; APPLICATION NUMBER: 07/938,990
; FILING DATE: 1992-SEP-01
; APPLICATION NUMBER: 07/730,452
; FILING DATE: 1991-JUL-15
; APPLICATION NUMBER: 07/729,134
; FILING DATE: 1991-JUL-12
; APPLICATION NUMBER: 07/975,179
; FILING DATE: 1992-NOV-12
; APPLICATION NUMBER: PCT/US92/05661
; FILING DATE: 1992-JUL-10
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras, Esq.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 265:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-10-931-260-265

Query Match      73.9%; Score 17; DB 18; Length 20;
Best Local Similarity 40.0%; Pred. No. 9.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
Db      12 FSTAW 16

RESULT 24
US-10-931-260-264
; Sequence 264, Application: US/10931260
; Publication No. US20050152927A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Irwin J.;
; Pollock, Joanne;
; Bond, Julian F.;
; Garman, Richard D.;
; Kuo, Mei-Chang;
; Powers, Stephen P.;
; Exley, Mark A.;
; Chen, Xian;
; Shaked, Ze'ev
; TITLE OF INVENTION: Allergenic Proteins And Peptides From
; Japanese Cedar Pollen
; NUMBER OF SEQUENCES: 283
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State St
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/931,260
; FILING DATE: 30-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,203
; FILING DATE: 29-Jan-1999
; APPLICATION NUMBER: 08/467,023
; FILING DATE: 1995-JUN-06
; APPLICATION NUMBER: 08/350,225
; FILING DATE: 1994-DEC-06
; APPLICATION NUMBER: 08/226,248
; FILING DATE: 1994-APR-08
; APPLICATION NUMBER: PCT/US93/00139
; FILING DATE: 1993-JAN-15
; APPLICATION NUMBER: 07/938,990
; FILING DATE: 1992-SEP-01
; APPLICATION NUMBER: 07/730,452
; FILING DATE: 1991-JUL-15
; APPLICATION NUMBER: 07/729,134
; FILING DATE: 1991-JUL-12
; APPLICATION NUMBER: 07/975,179
```

FILING DATE: 1992-NOV-12
 APPLICATION NUMBER: PCT/US92/05661
 FILING DATE: 1992-JUL-10
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragouras, Esq.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 264:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 264:
 US-10-931-260-264

Query Match 73.9%; Score 17; DB 18; Length 24;
 Best Local Similarity 40.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 DB 12 FSTW 16

RESULT 25

US-10-338-777-404
 Sequence 404, Application US/10338777
 Publication No. US20030188343A1
 GENERAL INFORMATION:

APPLICANT: Lynx Therapeutics, Inc.
 APPLICANT: United States Department of Agriculture
 APPLICANT: Bowen, Benjamin A
 APPLICANT: Haudenschild, Christian D
 APPLICANT: Huchler, Edward S

TITLE OF INVENTION: Identification of Genes Associated with Growth in Plants

FILE REFERENCE: 37-000510US
 CURRENT APPLICATION NUMBER: US/10/338,777
 CURRENT FILING DATE: 2003-01-07

NUMBER OF SEQ ID NOS: 405
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 404

LENGTH: 25
 TYPE: PRT
 ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: example conservative variation of residues 2-26 of SEQ ID NO:31

US-10-338-777-404

Query Match 73.9%; Score 17; DB 14; Length 25;
 Best Local Similarity 40.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 DB 20 FAASW 24

RESULT 26

US-09-864-761-46828
 Sequence 46828, Application US/09864761
 Patent No. US200408763A1
 GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aecomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 46828
 LENGTH: 27
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC007739.1
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.62
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.66
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.61
 US-09-864-761-46828

Query Match 73.9%; Score 17; DB 9; Length 27;
 Best Local Similarity 40.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 DB 4 FSATW 8

RESULT 27

US-08-424-550B-428
 Sequence 428, Application US/08424550B
 Publication No. US2002011947A1
 GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS
 APPLICANT: TAMI J. PILOT-MATIAS

APPLICANT: GEORGE J. DAWSON
 APPLICANT: GEORGE G. SCHLAUDER

APPLICANT: SURESH M. DESAI
 APPLICANT: THOMAS P. LEARY

APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 428:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-428

Query Match 73.9%; Score 17; DB 8; Length 29;
Best Local Similarity 40.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 12 PASAW 16

RESULT 28
US-10-424-599-160512
Sequence 160512, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 39-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 160512
LENGTH: 32
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_115960C.1.pap
US-10-424-599-160512

Query Match 73.9%; Score 17; DB 15; Length 32;
Best Local Similarity 40.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 18 FTASW 22

RESULT 29
US-10-032-201B-157
Sequence 157, Application US/10032201B
Publication No. US20030167524A1
GENERAL INFORMATION:
APPLICANT: Van Rooijen, Gijb
APPLICANT: Deckers, Harm
APPLICANT: Heifetz, Peter Bernard
APPLICANT: Briggs, Steven
APPLICANT: Dalmia, Bipin Kumar
APPLICANT: Del Val, Greg
APPLICANT: Zaplachinski, Steve
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
FILE REFERENCE: 38814 351B
COMPOSITIONS
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 157
LENGTH: 33
TYPE: PRT
ORGANISM: Sus scrofa
US-10-032-201B-157

Query Match 73.9%; Score 17; DB 14; Length 33;
Best Local Similarity 40.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 26 FSATW 30

RESULT 30
US-10-029-386-28347
Sequence 28347, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1
SEQ ID NO 28347
LENGTH: 33
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL133499.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.45
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.55
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.46
OTHER INFORMATION: SWISSPROT HIT: Q03368, EVALUE 8.60e+00
US-10-029-386-28347

Query Match 73.9%; Score 17; DB 14; Length 33;
Best Local Similarity 40.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 14 FSASW 18

RESULT 31

US-10-307-817-584

Sequence 584, Application US/10307817

Publication No. US20040058338A1

GENERAL INFORMATION:

APPLICANT: Agee et al.

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 21402-502C

CURRENT APPLICATION NUMBER: US/10/307,817

CURRENT FILING DATE: 2002-12-02

NUMBER OF SEQ ID NOS: 682

SOFTWARE: CutsseqList version 0.1

SEQ ID NO 584

LENGTH: 35

TYPE: PRT

ORGANISM: Mus musculus

US-10-307-817-584

Query Match 73.9%; Score 17; DB 15; Length 35;

Best Local Similarity 40.0%; Pred. No. 1.3e+04;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

Db 22 FSATW 26

RESULT 32

US-10-931-260-137

Sequence 137, Application US/10931260

Publication No. US20050152927A1

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;

Pollock, Joanne;

Bond, Julian F.;

Garman, Richard D.;

Kuo, Mei-Chang;

Powers, Stephen P.;

Exley, Mark A.;

Chen, Xian;

Shaked, Ze'ev

TITLE OF INVENTION: Allergenic Proteins And Peptides From Japanese Cedar Pollen

NUMBER OF SEQUENCES: 283

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lahive & Cockfield, LLP

STREET: 28 State St

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/931,260

FILING DATE: 30-Aug-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/240,203

FILING DATE: 29-Jan-1999

APPLICATION NUMBER: 08/467,023

FILING DATE: 1995-JUN-06

APPLICATION NUMBER: 08/350,225

FILING DATE: 1994-DEC-06

APPLICATION NUMBER: 08/226,248

FILING DATE: 1994-APR-08

APPLICATION NUMBER: PCT/US93/00139

FILING DATE: 1993-JAN-15

APPLICATION NUMBER: 07/938,990

FILING DATE: 1992-SEP-01

APPLICATION NUMBER: 07/730,452

FILING DATE: 1991-JUL-15

APPLICATION NUMBER: 07/729,134

FILING DATE: 1991-JUL-12

APPLICATION NUMBER: 07/975,179

FILING DATE: 1992-NOV-12

APPLICATION NUMBER: PCT/US92/05661

FILING DATE: 1992-JUL-10

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras, Esq.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 137:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 137:

US-10-931-260-137

Query Match 73.9%; Score 17; DB 18; Length 36;

Best Local Similarity 40.0%; Pred. No. 1.4e+04;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

Db 28 FSTAW 32

RESULT 33

US-10-193-795-10

Sequence 10, Application US/10193795

Publication No. US20030082202A1

GENERAL INFORMATION:

APPLICANT: Flohe, Leopold

NO. US20030082202A1ecke, Everson

Montemartini, Maria

Kalisz, Henryk

TITLE OF INVENTION: TRYPAEDOXIN, EXPRESSION PLASMID, PROCESS OF PRODUCTION, METHOD OF USE, TEST KIT, AND PHARMACEUTICAL COMPOSITION

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun

STREET: 233 South Wacker Drive/6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/193,795

FILING DATE: 12-Jul-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/330,914

FILING DATE: 11-Jun-1999

APPLICATION NUMBER: WO PCT/EP97/06983

FILING DATE: 12-DEC-1997

ATTORNEY/AGENT INFORMATION:


```
RESULT 37
US-09-948-783-287
; Sequence 287, Application US/09948783
; Publication No. US20030100051A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 97 Human secreted proteins
; FILE REFERENCE: P2028P2
; CURRENT APPLICATION NUMBER: US/09/948,783
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,846
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: 09/892,877
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/437,658
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/09847
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/085,093
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,094
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,105
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,180
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,927
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,906
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,924
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,928
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,920
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 465
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 287
; TYPE: PRT
; LENGTH: 38
; ORGANISM: Homo sapiens
US-09-948-783-287

Query Match 73.9% Score 17; DB 10; Length 38;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 19 FAAAW 23

RESULT 38
US-09-057-951-6
; Sequence 6, Application US/09057951
; Patent No. US20020025551A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

Query Match 73.9% Score 17; DB 10; Length 38;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 19 FAAAW 23

RESULT 39
US-09-864-761-46093
; Sequence 46093, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

Query Match 73.9% Score 17; DB 9; Length 40;
Best Local Similarity 40.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 6 FSAAW 10
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;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 46093
;; LENGTH: 40
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AF233390.1
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
US-09-864-761-46093

Query Match 73.9%; Score 17; DB 9; Length 40;
Best Local Similarity 40.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5
Db 23 FTSSW 27

RESULT 40

US-10-105-150-6
; Sequence 6, Application US/10105150
; Publication No. US20020119524A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED
; PROTEIN FAMILY AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/105,150
; FILING DATE: 25-Mar-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/057,951
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/046001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906

TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-105-150-6

Query Match 73.9%; Score 17; DB 13; Length 40;
Best Local Similarity 40.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5
Db 6 FSAW 10

Search completed: October 18, 2005, 15:50:34
Job time : 109.294 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:19:12 ; Search time 28.7059 Seconds
(without alignments)
20.804 Million cell updates/sec

Title: US-09-214-371-10

Perfect score: 23

Sequence: 1 FXXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued_patents_AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	73.9	13	3	US-09-085-072-7
2	17	73.9	15	4	US-09-142-524D-87
3	17	73.9	15	4	US-09-142-524D-88
4	17	73.9	29	4	US-08-469-260A-428
5	17	73.9	29	4	US-08-488-446-428
6	17	73.9	29	4	US-08-467-344A-428
7	17	73.9	29	4	US-08-424-550B-428
8	17	73.9	34	1	US-08-118-270-134
9	17	73.9	34	1	US-08-118-270-172
10	17	73.9	34	5	PCT-US93-08528-134
11	17	73.9	34	5	PCT-US93-08528-172
12	17	73.9	36	3	US-08-467-023-137
13	17	73.9	37	4	US-09-330-914A-10
14	17	73.9	41	3	US-08-467-023-136
15	17	73.9	45	3	US-08-467-023-135
16	17	73.9	45	4	US-09-149-476-475
17	17	73.9	47	4	US-09-369-247-129
18	17	73.9	49	1	US-08-118-270-209
19	17	73.9	49	5	PCT-US93-08528-209
20	17	73.9	54	4	US-09-434-840-73
21	17	73.9	54	4	US-09-733-643B-21
22	17	73.9	56	4	US-09-621-976-6592
23	17	73.9	60	4	US-09-270-767-35869
24	17	73.9	60	4	US-09-270-767-51086
25	17	73.9	61	3	US-09-134-001C-4258
26	17	73.9	62	4	US-09-252-991A-28658
27	17	73.9	62	4	US-09-621-976-5704
28	17	73.9	62	4	US-09-248-796A-26247
29	17	73.9	63	4	US-09-902-570-11838
30	17	73.9	69	4	US-09-621-976-6715
31	17	73.9	69	4	US-09-248-796A-24056
32	17	73.9	80	4	US-09-330-914A-4
33	17	73.9	80	4	US-09-270-767-37303
34	17	73.9	80	4	US-09-270-767-52520
35	17	73.9	80	4	US-09-248-796A-24759
36	17	73.9	82	4	US-09-248-796A-19864
37	17	73.9	84	2	US-08-353-476-78
38	17	73.9	84	3	US-08-679-493A-97
39	17	73.9	86	4	US-09-583-110-3199
40	17	73.9	89	4	US-09-621-976-6168
41	17	73.9	91	2	US-08-598-873-19
42	17	73.9	91	3	US-08-605-430-19
43	17	73.9	91	4	US-09-717-054-19
44	17	73.9	93	4	US-09-621-976-6449
45	17	73.9	93	4	US-09-248-796A-16647
46	17	73.9	95	4	US-09-949-016-9308
47	17	73.9	98	4	US-09-252-991A-22311
48	17	73.9	102	3	US-08-984-295-3
49	17	73.9	102	3	US-08-741-411-12
50	17	73.9	104	6	5210073-1
51	17	73.9	104	6	5210073-1
52	17	73.9	105	2	US-08-826-910-3
53	17	73.9	105	2	US-08-826-910-4
54	17	73.9	105	4	US-09-601-144-68
55	17	73.9	105	4	US-09-513-999C-8037
56	17	73.9	105	4	US-09-107-433-2856
57	17	73.9	109	4	US-09-902-540-13327
58	17	73.9	114	3	US-09-450-520A-9
59	17	73.9	114	3	US-09-450-520A-10
60	17	73.9	114	3	US-09-450-520A-11
61	17	73.9	114	4	US-09-897-425-41
62	17	73.9	116	3	US-09-065-059-9
63	17	73.9	116	3	US-08-545-809A-134
64	17	73.9	116	4	US-09-134-000C-6570
65	17	73.9	116	4	US-09-949-016-10735
66	17	73.9	117	1	US-07-634-278-105
67	17	73.9	117	1	US-08-477-728-105
68	17	73.9	117	1	US-08-474-040-105
69	17	73.9	117	1	US-08-487-200-105
70	17	73.9	117	3	US-08-484-537-105
71	17	73.9	120	3	US-09-065-059-1
72	17	73.9	121	3	US-09-107-532A-5275
73	17	73.9	122	3	US-09-540-014-2
74	17	73.9	122	4	US-09-538-864-25
75	17	73.9	122	4	US-10-091-841A-2
76	17	73.9	125	4	US-09-949-016-9663
77	17	73.9	127	3	US-09-540-014-4
78	17	73.9	127	4	US-09-252-991A-17639
79	17	73.9	127	4	US-09-252-991A-24186
80	17	73.9	127	4	US-10-091-841A-4
81	17	73.9	128	3	US-08-467-023-187
82	17	73.9	130	1	US-08-276-852-69
83	17	73.9	130	1	US-08-276-852-70
84	17	73.9	130	1	US-08-276-852-71
85	17	73.9	130	1	US-08-899-575-69
86	17	73.9	130	1	US-08-899-575-70
87	17	73.9	130	1	US-08-899-575-71
88	17	73.9	130	1	US-08-899-575-69
89	17	73.9	130	1	US-08-899-575-70
90	17	73.9	130	1	US-08-899-575-71
91	17	73.9	130	3	US-09-540-014-6
92	17	73.9	130	4	US-10-091-841A-6
93	17	73.9	130	5	PCT-US93-08743-69
94	17	73.9	130	5	PCT-US95-08743-70
95	17	73.9	130	5	PCT-US95-08743-71
96	17	73.9	131	4	US-09-248-796A-15325
97	17	73.9	132	4	US-09-386-658A-2
98	17	73.9	136	3	US-09-450-520A-4
99	17	73.9	136	3	US-09-450-520A-8
100	17	73.9	138	4	US-09-252-991A-26095

Sequence 26247, A
Sequence 11838, A
Sequence 6715, Ap
Sequence 21056, A
Sequence 4, Appli
Sequence 37103, A
Sequence 52520, A
Sequence 24759, A
Sequence 19864, A
Sequence 78, Appl
Sequence 97, Appl
Sequence 3199, Ap
Sequence 1668, Ap
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 6449, Ap
Sequence 16647, A
Sequence 9308, Ap
Sequence 22311, A
Sequence 3, Appli
Sequence 12, Appl
Patent No. 5210073
Patent No. 5210073
Sequence 3, Appli
Sequence 4, Appli
Sequence 68, Appli
Sequence 8037, Ap
Sequence 2856, Ap
Sequence 13327, A
Sequence 9, Appli
Sequence 10, Appl
Sequence 11, Appl
Sequence 41, Appl
Sequence 9, Appli
Sequence 134, App
Sequence 6570, App
Sequence 10735, A
Sequence 105, App
Sequence 105, App
Sequence 105, App
Sequence 105, App
Sequence 1, Appli
Sequence 5275, Ap
Sequence 2, Appli
Sequence 25, Appli
Sequence 2, Appli
Sequence 9663, Ap
Sequence 4, Appli
Sequence 17639, A
Sequence 24186, A
Sequence 4, Appli
Sequence 187, App
Sequence 69, Appl
Sequence 70, Appl
Sequence 71, Appl
Sequence 69, Appl
Sequence 70, Appl
Sequence 71, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 69, Appli
Sequence 70, Appl
Sequence 71, Appl
Sequence 15325, A
Sequence 2, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 26095, A

ALIGNMENTS

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RESULT 1
US-09-085-072-7
; Sequence 7, Application US/09085072
; Patent No. 6285150
; GENERAL INFORMATION:
; APPLICANT: L. Terstappen et al.
; TITLE OF INVENTION: PHAGE ANTIBODIES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,072
; FILING DATE: 26-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: 890-2 FWC/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acid
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-085-072-7

Query Match 73.9%; Score 17; DB 3; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 6 FASSW 10

RESULT 2
US-09-142-524D-87
; Sequence 87, Application US/09142524D
; Patent No. 6719976
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103
; CURRENT FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 87

Query Match 73.9%; Score 17; DB 3; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 6 FASSW 10

RESULT 3
US-09-142-524D-88
; Sequence 88, Application US/09142524D
; Patent No. 6719976
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103
; CURRENT APPLICATION NUMBER: US/09/142,524D
; CURRENT FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 88
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5
US-09-142-524D-88

Query Match 73.9%; Score 17; DB 4; Length 15;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 4 FSTAW 13

RESULT 4
US-08-469-260A-428
; Sequence 428, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
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; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4
US-09-142-524D-87

Query Match 73.9%; Score 17; DB 4; Length 15;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 9 FSTAW 13

RESULT 3
US-09-142-524D-88
; Sequence 88, Application US/09142524D
; Patent No. 6719976
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103
; CURRENT APPLICATION NUMBER: US/09/142,524D
; CURRENT FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 88
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5
US-09-142-524D-88

Query Match 73.9%; Score 17; DB 4; Length 15;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 4 FSTAW 8

RESULT 4
US-08-469-260A-428
; Sequence 428, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 428:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-260A-428

Query Match 73.9%; Score 17; DB 4; Length 29;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
Db 12 FASW 16

RESULT 5
US-08-446-428
; Sequence 428, Application US/08488446
; Patent No. 6558598
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 428:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-446-428

Query Match 73.9%; Score 17; DB 4; Length 29;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
|
Db 12 FASW 16

RESULT 6
US-08-467-344A-428
; Sequence 428, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 428:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 428:
US-08-467-344A-428

Query Match 73.9%; Score 17; DB 4; Length 29;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 12 FASW 16

RESULT 7

US-08-424-550B-428
Sequence 428, Application US/08424550B
Patent No. 6720166
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MIERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAIWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: POREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 428:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-428

Query Match 73.9%; Score 17; DB 4; Length 29;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 12 FASW 16

RESULT 8

US-08-118-270-134
Sequence 134, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-134

Query Match 73.9%; Score 17; DB 1; Length 34;
Best Local Similarity 40.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 16 FTSW 20

RESULT 9

US-08-118-270-172
Sequence 172, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-172

Query Match 73.9%; Score 17; DB 1; Length 34;
Best Local Similarity 40.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXHW 5
DB 16 FTTAW 20

RESULT 10
PCT-US93-08528-134
Sequence 134, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

TELEX: 248633
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-134

Query Match 73.9%; Score 17; DB 5; Length 34;
Best Local Similarity 40.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXHW 5
DB 16 FTTAW 20

RESULT 11
PCT-US93-08528-172
Sequence 172, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-172

Query Match 73.9%; Score 17; DB 5; Length 34;
Best Local Similarity 40.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXHW 5
DB 16 FTTAW 20

RESULT 12
US-08-467-023-137

Sequence 137, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-467-023-137

Query Match 73.9%; Score 17; DB 3; Length 36;
Best Local Similarity 40.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 28 FSTAW 32

RESULT 13
US-09-330-914A-10
Sequence 10, Application US/09330914A
Patent No. 6432671
GENERAL INFORMATION:
APPLICANT: Flohe, Leopold
No. 6432671cecke, Everson
Kalisz, Henryk
Montemartini, Marisa
TITLE OF INVENTION: TRYPAEDOXIN, EXPRESSION PLASMID, PROCESS OF
PRODUCTION, METHOD OF USE, TEST KIT, AND
PHARMACEUTICAL COMPOSITION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: Unites States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,914A
FILING DATE: 11-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP97/06983
FILING DATE: 12-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, James P.
REGISTRATION NUMBER: 28,491
REFERENCE/DOCKET NUMBER: 29473/35678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-330-914A-10

Query Match 73.9%; Score 17; DB 4; Length 37;
Best Local Similarity 40.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 11 FSASW 15

RESULT 14
US-08-467-023-136
Sequence 136, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-467-023-136

Query Match 73.9%; Score 17; DB 3; Length 41;
Best Local Similarity 40.0%; Pred. No. 4.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 33 FSTAW 37

RESULT 15
US-08-467-023-135
Sequence 135, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D.;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872

REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-467-023-135

Query Match 73.9%; Score 17; DB 3; Length 45;
Best Local Similarity 40.0%; Pred. No. 4.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 33 FSTAW 37

RESULT 16
US-09-149-476-475
Sequence 475, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500

1	EARLIER APPLICATION NUMBER: 60/056,894
2	EARLIER FILING DATE: 1997-08-22
3	EARLIER APPLICATION NUMBER: 60/056,911
4	EARLIER FILING DATE: 1997-08-22
5	EARLIER APPLICATION NUMBER: 60/056,636
6	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,874
8	EARLIER FILING DATE: 1997-08-22
9	EARLIER APPLICATION NUMBER: 60/056,910
10	EARLIER FILING DATE: 1997-08-22
11	EARLIER APPLICATION NUMBER: 60/056,864
12	EARLIER FILING DATE: 1997-08-22
13	EARLIER APPLICATION NUMBER: 60/056,631
14	EARLIER FILING DATE: 1997-08-22
15	EARLIER APPLICATION NUMBER: 60/056,845
16	EARLIER FILING DATE: 1997-08-22
17	EARLIER APPLICATION NUMBER: 60/056,892
18	EARLIER FILING DATE: 1997-08-22
19	EARLIER APPLICATION NUMBER: 60/057,761
20	EARLIER FILING DATE: 1997-08-22
21	EARLIER APPLICATION NUMBER: 60/047,595
22	EARLIER FILING DATE: 1997-05-23
23	EARLIER APPLICATION NUMBER: 60/047,599
24	EARLIER FILING DATE: 1997-05-23
25	EARLIER APPLICATION NUMBER: 60/047,588
26	EARLIER FILING DATE: 1997-05-23
27	EARLIER APPLICATION NUMBER: 60/047,585
28	EARLIER FILING DATE: 1997-05-23
29	EARLIER APPLICATION NUMBER: 60/047,586
30	EARLIER FILING DATE: 1997-05-23
31	EARLIER APPLICATION NUMBER: 60/047,590
32	EARLIER FILING DATE: 1997-05-23
33	EARLIER APPLICATION NUMBER: 60/047,594
34	EARLIER FILING DATE: 1997-05-23
35	EARLIER APPLICATION NUMBER: 60/047,589
36	EARLIER FILING DATE: 1997-05-23
37	EARLIER APPLICATION NUMBER: 60/047,593
38	EARLIER FILING DATE: 1997-05-23
39	EARLIER APPLICATION NUMBER: 60/047,614
40	EARLIER FILING DATE: 1997-05-23
41	EARLIER APPLICATION NUMBER: 60/043,578
42	EARLIER FILING DATE: 1997-04-11
43	EARLIER APPLICATION NUMBER: 60/043,576
44	EARLIER FILING DATE: 1997-04-11
45	EARLIER APPLICATION NUMBER: 60/047,501
46	EARLIER FILING DATE: 1997-05-23
47	EARLIER APPLICATION NUMBER: 60/043,670
48	EARLIER FILING DATE: 1997-04-11
49	EARLIER APPLICATION NUMBER: 60/056,632
50	EARLIER FILING DATE: 1997-08-22
51	EARLIER APPLICATION NUMBER: 60/056,664
52	EARLIER FILING DATE: 1997-08-22
53	EARLIER APPLICATION NUMBER: 60/056,876
54	EARLIER FILING DATE: 1997-08-22
55	EARLIER APPLICATION NUMBER: 60/056,881
56	EARLIER FILING DATE: 1997-08-22
57	EARLIER APPLICATION NUMBER: 60/056,909
58	EARLIER FILING DATE: 1997-08-22
59	EARLIER APPLICATION NUMBER: 60/056,875
60	EARLIER FILING DATE: 1997-08-22
61	EARLIER APPLICATION NUMBER: 60/056,862
62	EARLIER FILING DATE: 1997-08-22
63	EARLIER APPLICATION NUMBER: 60/056,887
64	EARLIER FILING DATE: 1997-08-22
65	EARLIER APPLICATION NUMBER: 60/056,908
66	EARLIER FILING DATE: 1997-08-22
67	EARLIER APPLICATION NUMBER: 60/048,964
68	EARLIER FILING DATE: 1997-06-06
69	EARLIER APPLICATION NUMBER: 60/057,650
70	EARLIER FILING DATE: 1997-09-05
71	EARLIER APPLICATION NUMBER: 60/056,884
72	EARLIER FILING DATE: 1997-08-22
73	EARLIER APPLICATION NUMBER: 60/057,669

; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 73.9%; Score 17; DB 4; Length 45;
Best Local Similarity 40.0%; Pred. No. 4.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 31 FSAW 35

RESULT 17

US-09-369-247-129
; Sequence 129, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 129
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-369-247-129

Query Match 73.9%; Score 17; DB 4; Length 47;
Best Local Similarity 40.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 39 FSSW 43

RESULT 18

US-08-118-270-209
; Sequence 209, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-118-270-209

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 209:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-209

Query Match 73.9%; Score 17; DB 1; Length 49;
Best Local Similarity 40.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 36 FTSW 40

RESULT 19

PCT-US93-08528-209
; Sequence 209, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 209:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

/ MOLECULE TYPE: peptide
PCT-US93-08528-209

Query Match 73.9%; Score 17; DB 5; Length 49;
Best Local Similarity 40.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 36 FTSAW 40

RESULT 20
US-09-434-840-73
; Sequence 73, Application US/09434840
; Patent No. 6620985
; GENERAL INFORMATION:
; APPLICANT: Glazebrook, Jane
; APPLICANT: Jirage, Dayadevi
; APPLICANT: Tootle, Tina L
; APPLICANT: Zhou, Nan
; APPLICANT: Fyfe, Bart
; TITLE OF INVENTION: PAP4 COMPOSITIONS AND METHODS THEREFOR
; FILE REFERENCE: 043503.0009
; CURRENT APPLICATION NUMBER: US/09/434,840
; EARLIER FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 09/190,733
; EARLIER FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 85
; SEQ ID NO 73
; TYPE: PRT
; ORGANISM: Thermomyces lanuginosus
US-09-434-840-73

Query Match 73.9%; Score 17; DB 4; Length 54;
Best Local Similarity 40.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 7 FTSSW 11

RESULT 21
US-09-733-643B-21
; Sequence 21, Application US/09733643B
; Patent No. 6734344
; GENERAL INFORMATION:
; APPLICANT: Laroche, Andre J.
; APPLICANT: Huang, Timothy Y
; APPLICANT: Lu, Zhen-Xiang
; APPLICANT: Frick, Michele M.
; APPLICANT: Huang, Hung Chang
; APPLICANT: Cheng, Kuo Joan
; TITLE OF INVENTION: Coniothyrium minitans beta-(1,3) exoglucanase gene
; FILE REFERENCE: cbegi
; FILE REFERENCE: 24014US1
; CURRENT APPLICATION NUMBER: US/09/733,643B
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/170,168
; PRIOR FILING DATE: 1999-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Exopg
US-09-733-643B-21

Query Match 73.9%; Score 17; DB 4; Length 54;
Best Local Similarity 40.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 23 FAAAW 27

RESULT 22
US-09-621-976-6592
; Sequence 6592, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6592
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6592

Query Match 73.9%; Score 17; DB 4; Length 56;
Best Local Similarity 40.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 8 FTSSW 12

RESULT 23
US-09-270-767-35869
; Sequence 35869, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35869
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35869

Query Match 73.9%; Score 17; DB 4; Length 60;
Best Local Similarity 40.0%; Pred. No. 5.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 13 FTSSW 17

RESULT 24
US-09-270-767-51086
; Sequence 51086, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn ver. 2.0

; SEQ ID NO 51086

; LENGTH: 60

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

; US-09-270-767-51086

Query Match 73.9%; Score 17; DB 4; Length 60;

Best Local Similarity 40.0%; Pred. No. 5.3e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 13 FTSSW 17

RESULT 25

US-09-134-001C-4258

; Sequence 4258, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 4258

; LENGTH: 61

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

; US-09-134-001C-4258

Query Match 73.9%; Score 17; DB 3; Length 61;

Best Local Similarity 40.0%; Pred. No. 5.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 14 FSTSW 18

RESULT 26

US-09-252-991A-28658

; Sequence 28658, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 28658

; LENGTH: 62

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

; US-09-252-991A-28658

Query Match

Best Local Similarity 73.9%; Score 17; DB 4; Length 62;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 58 FAASW 62

RESULT 27

US-09-621-976-5704

; Sequence 5704, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTS and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 5704

; LENGTH: 62

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: -43..-1

; US-09-621-976-5704

Query Match

Best Local Similarity 73.9%; Score 17; DB 4; Length 62;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 35 FTAAM 39

RESULT 28

US-09-248-796A-26247

; Sequence 26247, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 26247

; LENGTH: 62

; TYPE: PRT

; ORGANISM: Candida albicans

; US-09-248-796A-26247

Query Match

Best Local Similarity 73.9%; Score 17; DB 4; Length 62;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 27 FSTSW 31

RESULT 29
US-09-902-540-11838
; Sequence 11838, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Columan, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: MYXOCOCCUS XANTHUS Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11838
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11838

Query Match 73.9%; Score 17; DB 4; Length 63;
Best Local Similarity 40.0%; Pred. No. 5.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 27 FATAM 31

RESULT 30
US-09-621-976-6715
; Sequence 6715, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6715
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6715

Query Match 73.9%; Score 17; DB 4; Length 69;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 62 FATW 66

RESULT 31
US-09-248-796A-24056
; Sequence 24056, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24056
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24056

Query Match 73.9%; Score 17; DB 4; Length 69;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 62 FTTAW 66

RESULT 32
US-09-330-914A-4
; Sequence 4, Application US/09330914A
; Patent No. 6432671
; GENERAL INFORMATION:
; APPLICANT: Flohe, Leopold
; APPLICANT: Kalisz, Henryk
; APPLICANT: Montemartini, Marisa
; TITLE OF INVENTION: TRYPAEDOXIN, EXPRESSION PLASMID, PROCESS OF
; PRODUCTION, METHOD OF USE, TEST KIT, AND
; PHARMACEUTICAL COMPOSITION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: Unites States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,914A
; FILING DATE: 11-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/06983
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, James P.
; REGISTRATION NUMBER: 28,491
; REFERENCE/DOCKET NUMBER: 29473/35678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-330-914A-4

Query Match 73.9%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 8 FSASW 12

RESULT 33

US-09-270-767-37303
; Sequence 37303, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 37303

; LENGTH: 80

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-37303

Query Match 73.9%; Score 17; DB 4; Length 80;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 41 FTASW 45

RESULT 34

US-09-270-767-52520

; Sequence 52520, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 52520

; LENGTH: 80

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-52520

Query Match 73.9%; Score 17; DB 4; Length 80;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 41 FTASW 45

RESULT 35

US-09-248-796A-24759

; Sequence 24759, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 24759

; LENGTH: 80

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-24759

Query Match 73.9%; Score 17; DB 4; Length 80;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 72 FTTAW 76

RESULT 36

US-09-248-796A-19864

; Sequence 19864, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 19864

; LENGTH: 82

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-19864

Query Match 73.9%; Score 17; DB 4; Length 82;

Best Local Similarity 40.0%; Pred. No. 6.6e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
| |
Db 74 FTTAW 78

RESULT 37

US-08-353-476-78

; Sequence 78, Application US/08353476

; Patent No. 5871902

; GENERAL INFORMATION:

; APPLICANT: Weininger, Susan

; APPLICANT: Weininger, Arthur M

; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A

; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

; NUMBER OF SEQUENCES: 117

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik & Saliwanchik

; STREET: 2421 N.W. 41st St., Suite A-1

; CITY: Gainesville

; STATE: Florida

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/353,476
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bencon, Gerard H
/ REGISTRATION NUMBER: 35,746
/ REFERENCE/DOCKET NUMBER: GP-100
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (904) 375-8100
/ TELEFAX: (904) 372-5800
/ INFORMATION FOR SEQ ID NO: 78:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 84 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: internal
/ US-08-353-476-78

Query Match 73.9%; Score 17; DB 2; Length 84;
Best Local Similarity 40.0%; Pred. No. 6.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 31 FSTW 35

RESULT 38
US-08-679-493A-97
/ Sequence 97, Application US/08679493A
/ Patent No. 6303295
/ GENERAL INFORMATION:
/ APPLICANT: Taylor, Ethan W.
/ TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
/ FILE REFERENCE: 55-95
/ CURRENT APPLICATION NUMBER: US/08/679,493A
/ CURRENT FILING DATE: 1996-07-12
/ PRIOR APPLICATION NUMBER: 60/001203
/ PRIOR FILING DATE: 1995-07-14
/ PRIOR APPLICATION NUMBER: 60/003,112
/ PRIOR FILING DATE: 1995-09-01
/ NUMBER OF SEQ ID NOS: 216
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 97
/ LENGTH: 84
/ TYPE: PRT
/ ORGANISM: bovine papillomavirus type 8
/ US-08-679-493A-97

Query Match 73.9%; Score 17; DB 3; Length 84;
Best Local Similarity 40.0%; Pred. No. 6.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 31 FSTW 35

RESULT 39
US-09-583-110-3199
/ Sequence 3199, Application US/09583110
/ Patent No. 6699703
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al.
/ TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
/ TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
```

```
/ FILE REFERENCE: PATH00-07A
/ CURRENT APPLICATION NUMBER: US/09/583,110
/ CURRENT FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/107,433
/ PRIOR FILING DATE: 1998-06-30
/ PRIOR APPLICATION NUMBER: US 60/085,131
/ PRIOR FILING DATE: 1998-05-12
/ PRIOR APPLICATION NUMBER: US 60/051,553
/ PRIOR FILING DATE: 1997-07-02
/ NUMBER OF SEQ ID NOS: 5322
/ SEQ ID NO 3199
/ LENGTH: 86
/ TYPE: PRT
/ ORGANISM: Streptococcus pneumoniae
/ US-09-583-110-3199

Query Match 73.9%; Score 17; DB 4; Length 86;
Best Local Similarity 40.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 4 FSAW 8

RESULT 40
US-09-621-976-6168
/ Sequence 6168, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S. Y.
/ APPLICANT: Giordano, J. Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 6168
/ LENGTH: 89
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-621-976-6168

Query Match 73.9%; Score 17; DB 4; Length 89;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
DB 58 FSAW 62

Search completed: October 18, 2005, 15:32:10
Job time : 30.7059 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:14:39 ; Search time 111.529 Seconds
(without alignments)
27.742 Million cell updates/sec

Title: US-09-214-371-10

Perfect score: 23

Sequence: 1 FXXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	73.9	9	7	ADC07129 Honeybee
2	17	73.9	9	7	ADC07134 Painted 1
3	17	73.9	10	3	AB10010 H. pylori
4	17	73.9	10	4	AB86090 H. pylori
5	17	73.9	10	4	AB86058 H. pylori
6	17	73.9	11	7	ADC07163 Painted 1
7	17	73.9	13	4	AAE05735 Complemen
8	17	73.9	13	6	ABG75574 CDR3 pept
9	17	73.9	14	4	AA098088 Human pep
10	17	73.9	15	2	AA097874 Japan ced
11	17	73.9	15	2	AA097875 Japan ced
12	17	73.9	15	2	AA057758 Residues
13	17	73.9	19	5	AAE23038 Human thi
14	17	73.9	20	2	AAW42165 T-cell ep
15	17	73.9	20	4	AA062999 Complemen
16	17	73.9	25	7	ADE25429 Plant gro
17	17	73.9	27	4	AA018617 Peptide #
18	17	73.9	27	4	AA031077 Peptide #
19	17	73.9	27	4	ABG52487 Human liv
20	17	73.9	27	5	ABG40522 Human pep
21	17	73.9	29	3	AA093101 Hepatitis
22	17	73.9	32	4	AA071365 Human gen
23	17	73.9	33	5	ABP60808 Sus scrof
24	17	73.9	33	8	ABO54713 Human gen
25	17	73.9	34	2	AA050631 G-Protein

26	17	73.9	34	2	AA050593	AA050593 G-protein
27	17	73.9	34	2	AA02823	AA02823 G-protein
28	17	73.9	34	2	AA02785	AA02785 G-protein
29	17	73.9	35	4	AA08042	AA08042 Human pol
30	17	73.9	36	2	AA03693	AA03693 Japanese
31	17	73.9	37	4	AA08979	AA08979 Human pol
32	17	73.9	38	3	AA076339	AA076339 Fragment
33	17	73.9	38	3	AA010451	AA010451 Arabidops
34	17	73.9	38	7	ADE11915	ADE11915 Human sec
35	17	73.9	40	2	AA041113	AA041113 TNFR/NGFR
36	17	73.9	40	3	AA051555	AA051555 Arabidops
37	17	73.9	40	4	AA037764	AA037764 Peptide #
38	17	73.9	40	4	AA064755	AA064755 Human sec
39	17	73.9	40	4	AA006835	AA006835 Human pol
40	17	73.9	40	4	AA064830	AA064830 Human bra
41	17	73.9	40	4	ABG59226	ABG59226 Human liv
42	17	73.9	40	5	ABG46611	ABG46611 Human pep
43	17	73.9	41	2	AA053692	AA053692 Japanese
44	17	73.9	41	4	AA007778	AA007778 Human pol
45	17	73.9	44	4	AA015556	AA015556 Peptide #
46	17	73.9	44	4	AB034562	AB034562 Peptide #
47	17	73.9	44	4	AA028045	AA028045 Peptide #
48	17	73.9	44	4	AB029389	AB029389 Peptide #
49	17	73.9	44	4	AB019970	AB019970 Protein #
50	17	73.9	44	4	AA067745	AA067745 Human bon
51	17	73.9	44	4	AA012937	AA012937 Human pol
52	17	73.9	44	4	AA055349	AA055349 Human bra
53	17	73.9	44	4	ABG49383	ABG49383 Human liv
54	17	73.9	45	2	AA053691	AA053691 Japanese
55	17	73.9	45	5	ABG95335	ABG95335 Human nov
56	17	73.9	45	6	AB034529	AB034529 Region of
57	17	73.9	45	7	ADI23190	ADI23190 Novel hum
58	17	73.9	45	8	ADH74192	ADH74192 Human sec
59	17	73.9	46	4	AA027852	AA027852 Peptide #
60	17	73.9	46	4	AB029210	AB029210 Peptide #
61	17	73.9	46	4	AB019786	AB019786 Protein #
62	17	73.9	46	4	AA067559	AA067559 Human bon
63	17	73.9	46	4	AA055165	AA055165 Human bra
64	17	73.9	46	4	AA031130	AA031130 Peptide #
65	17	73.9	47	2	AA030880	AA030880 Human sec
66	17	73.9	47	5	ABP51359	ABP51359 Human MDD
67	17	73.9	49	2	AA050668	AA050668 G-protein
68	17	73.9	49	2	AA02860	AA02860 G-protein
69	17	73.9	50	5	ABP05131	ABP05131 Human ORF
70	17	73.9	51	4	AA058484	AA058484 Propionib
71	17	73.9	51	6	ABM55003	ABM55003 Propionib
72	17	73.9	52	3	AB045468	AB045468 Human sec
73	17	73.9	52	4	AAU56768	AAU56768 Propionib
74	17	73.9	52	6	ABM53287	ABM53287 Propionib
75	17	73.9	53	3	AA016526	AA016526 Bacteriop
76	17	73.9	53	4	AA008445	AA008445 Human pol
77	17	73.9	53	6	ABJ18951	ABJ18951 Pathogen
78	17	73.9	53	6	ABM71514	ABM71514 Staphyloc
79	17	73.9	54	3	AA056440	AA056440 Helicobac
80	17	73.9	54	7	ADH62390	ADH62390 Thermomyc
81	17	73.9	55	4	AAE01321	AAE01321 Human gen
82	17	73.9	55	6	ADA98194	ADA98194 Human sec
83	17	73.9	55	6	ADA44043	ADA44043 Human sec
84	17	73.9	55	7	ADC20359	ADC20359 Human sec
85	17	73.9	55	7	ADF10696	ADF10696 Human sec
86	17	73.9	56	3	AA027801	AA027801 Human sec
87	17	73.9	56	3	AAG41143	AAG41143 Zea mays
88	17	73.9	56	4	AAE05519	AAE05519 Human TNF
89	17	73.9	56	4	AAU64706	AAU64706 Propionib
90	17	73.9	56	5	ABP11292	ABP11292 Human ORF
91	17	73.9	56	6	ABM61225	ABM61225 Propionib
92	17	73.9	58	4	AA011806	AA011806 Human pol
93	17	73.9	58	4	AAU46944	AAU46944 Propionib
94	17	73.9	58	6	ABM43463	ABM43463 Propionib
95	17	73.9	59	4	AA090403	AA090403 Human imm
96	17	73.9	60	4	AAU64940	AAU64940 Propionib
97	17	73.9	60	5	AB079236	AB079236 Human pro
98	17	73.9	60	6	ABM61459	ABM61459 Propionib

99 17 73.9 61 4 AA04154 Human Gen
100 17 73.9 61 4 AAU45906 Propionib

ALIGNMENTS

```

RESULT 1
ADC07129
ID ADC07129 standard; peptide; 9 AA.
XX
AC ADC07129;
XX
DT 18-DEC-2003 (first entry)
XX
DE Honeybee AKH peptide.
XX
KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;
KW obesity; type II diabetes; cholelithiasis; hypertension;
KW coronary heart disease; atherosclerosis; glycogenosis; arthritis; cancer;
KW renal failure; liver; chronic pain; sleep apnea; stroke;
KW urinary incontinence; honeybee.
XX
OS Synthetic.
OS Apis mellifera.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "Pyroglutamic acid"
FT Misc-difference 9
FT /note= "Preferably C-terminal amide"
FT
XX WO2003066080-A1.
XX
PN 14-AUG-2003.
XX
PD 07-FEB-2003; 2003WO-US0003800.
XX
PF 07-FEB-2002; 2002US-00072419.
XX
PR (BLMB-) BLM GROUP.
XX
PA Schacter BZ, Schacter LP;
XX
PI WPI; 2003-712542/67.
XX
DR Pharmaceutical composition useful for promoting weight loss, comprises an
XX insect adipokinetic hormone, having a pyroglutamate residue at its amino
XX terminus.
XX
PS Claim 29; Page 20; 82pp; English.
XX
CC The invention relates to a novel method of promoting lipid mobilisation
CC in a human which comprises administering an insect adipokinetic hormone
CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,
CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,
CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The
CC method of the invention may be useful for treating obesity, type II
CC diabetes, cholelithiasis, hypertension, coronary heart disease, renal
CC atherosclerosis, types I to VI glycogenosis, arthritis, cancer, renal
CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary
CC incontinence. The current sequence is that of the honeybee AKH peptide of
CC the invention.
XX
SQ Sequence 9 AA;

```

Query Match 73.9%; Score 17; DB 7; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 FXXW 5
DB 4 FTSSW 8

RESULT 2
ADC07134
ID ADC07134 standard; peptide; 9 AA.
XX
AC ADC07134;
XX
DT 18-DEC-2003 (first entry)
XX
DE Painted lady AKH peptide.
XX
KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;
KW obesity; type II diabetes; cholelithiasis; hypertension;
KW coronary heart disease; atherosclerosis; glycogenosis; arthritis; cancer;
KW renal failure; liver; chronic pain; sleep apnea; stroke;
KW urinary incontinence; painted lady.
XX
OS Synthetic.
OS Vanessa cardui.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "Pyroglutamic acid"
FT Misc-difference 9
FT /note= "Preferably C-terminal amide"
FT
XX WO2003066080-A1.
XX
PN 14-AUG-2003.
XX
PD 07-FEB-2003; 2003WO-US0003800.
XX
PF 07-FEB-2002; 2002US-00072419.
XX
PR (BLMB-) BLM GROUP.
XX
PA Schacter BZ, Schacter LP;
XX
PI WPI; 2003-712542/67.
XX
DR Pharmaceutical composition useful for promoting weight loss, comprises an
XX insect adipokinetic hormone, having a pyroglutamate residue at its amino
XX terminus.
XX
PS Claim 29; Page 20; 82pp; English.
XX
CC The invention relates to a novel method of promoting lipid mobilisation
CC in a human which comprises administering an insect adipokinetic hormone
CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,
CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,
CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The
CC method of the invention may be useful for treating obesity, type II
CC diabetes, cholelithiasis, hypertension, coronary heart disease, renal
CC atherosclerosis, types I to VI glycogenosis, arthritis, cancer, renal
CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary
CC incontinence. The current sequence is that of the painted lady AKH
CC peptide of the invention.
XX
SQ Sequence 9 AA;

```

Query Match 73.9%; Score 17; DB 7; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5

Db 4 FTSSW 8

RESULT 3
AAB10010
ID AAB10010 standard; protein; 10 AA.

XX AC AAB10010;
XX 01-NOV-2000 (first entry)

XX DE H. pylori beta-urease-binding antibody heavy chain CDR1 protein #2.
XX DE Acid-resistant microorganism; detection; faecal; intestine; infection;
XX KW monoclonal antibody; heavy chain; complementarity determining region;
XX KW CDR; beta-urease.

XX OS Unidentified.

XX PN WO200026671-A1.

XX PD 11-MAY-2000.

XX PF 29-OCT-1999; 99WO-EP008212.

XX PR 29-OCT-1998; 98EP-00120517.

XX PR 06-NOV-1998; 98EP-00120687.

XX PA (CONN-) CONNEX GMBH.

XX PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
XX PI Ringels A;

XX DR WPI: 2000-365747/31.
XX DR N-PSDB; AAA40166.

XX PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter
XX PT pylori, comprises reacting a fecal sample with two binding reagents for
XX PT antigens that survive intestinal passage.

XX PS Claim 26; Page 22; 84pp; German.

XX CC This invention describes a novel method for the detection of a mammalian
XX CC infection by an acid-resistant microorganism (A) by treating a faecal
XX CC sample with at least two different monoclonal antibodies (Mab) (or their
XX CC fragments or derivatives) or aptamers (collectively (I)) and detecting
XX CC formation of a complex (C) between (I) and the corresponding antigen of
XX CC (A). The first and second (I) bind to epitopes of different antigens
XX CC (Ag). These epitopes are present, after passage through the intestines,
XX CC in at least some mammals, and have either: (i) their native structure; or
XX CC (ii) a structure against which an antibody is produced by an animal
XX CC infected or immunized with (A), or its extract, lysate, derived protein
XX CC or fragment, or with a synthetic peptide. Practically all mammals display
XX CC at least one of the specified epitopes. The method is used to detect
XX CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
XX CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M.
XX CC tuberculosis, C. jejuni and C. pylori. (I) may also be used
XX CC therapeutically. The method is direct and non-invasive, and provides an
XX CC inexpensive and easily standardizable diagnosis, despite possible
XX CC degradation of antigens during passage through the intestines. This
XX CC sequence represents a fragment of a H. pylori beta-urease-binding
XX CC antibody heavy chain complementarity determining region CDR1 which is
XX CC used to illustrate the method of the invention

XX SQ Sequence 10 AA;

Query Match 73.9%; Score 17; DB 3; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 FXXW 5
Db 4 FTSSW 8

RESULT 4
AAB86090

ID AAB86090 standard; peptide; 10 AA.

XX AC AAB86090;

XX 17-JUL-2001 (first entry)

XX DE H. pylori beta-urease derived antibody light chain CDR1 #1.

XX DE Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
XX KW acid-resistant microorganism; complementarity determining region; CDR;
XX KW feces; heavy chain; light chain.

XX OS Unidentified.

XX PN WO200127612-A2.

XX PD 19-APR-2001.

XX PF 12-OCT-2000; 2000WO-EP010057.

XX PR 12-OCT-1999; 99EP-00120351.

XX PR 16-MAR-2000; 2000EP-00105592.

XX PR 31-MAR-2000; 2000EP-00107028.

XX PR 10-MAY-2000; 2000EP-00110110.

XX PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

XX PI Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;
XX PI WPI: 2001-282086/29.

XX DR N-PSDB; AAF88117.

XX PT Detecting infections by acid-resistant microorganisms, particularly for
XX PT diagnosing Helicobacter pylori, comprises immunochromatographic detection
XX PT of antigen in feces.

XX PS Claim 27; Page 27; 90pp; German.

XX CC This invention describes a novel method for detecting infection by an
XX CC acid-resistant microorganism (A), in a mammal, using
XX CC immunochromatography. The method is used to diagnose infection by an acid
XX CC -resistant microorganism (A), in a mammal, such as Helicobacter,
XX CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
XX CC H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,
XX CC inexpensive and non-invasive, and may indicate the stage of infection. A
XX CC test strip used in the method may include a filter to eliminate particles
XX CC present in the sample and only a single receptor provides a reasonably
XX CC secure diagnosis, with specificity and selectivity improved by detecting
XX CC several epitopes (of catalase) or different antigens (catalase and beta-
XX CC urease). The method can be automated. This sequence represents a
XX CC complementarity determining region (CDR) from an antibody raised against
XX CC the H. pylori catalase or beta-urease antigen which is used to illustrate
XX CC the method of the invention

XX SQ Sequence 10 AA;

Query Match 73.9%; Score 17; DB 4; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 FXXW 5
Db 4 FTSSW 8

RESULT 5
AAB86058

ID AAB86058 standard; peptide; 10 AA.

XX

AC AAB86058;
 XX
 DT 17-JUL-2001 (first entry)
 XX
 DE H. pylori beta-urease derived antibody light chain CDR1 #1.
 XX
 KW Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;
 KW infection; acid-resistant microorganism; fecal; antibody; diagnosis;
 KW antibacterial; complementarity determining region.
 XX
 OS Unidentified.
 XX
 PN WO200127613-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 12-OCT-2000; 2000WO-EP010058.
 XX
 PR 12-OCT-1999; 99EP-00120351.
 PR 16-MAR-2000; 2000EP-00105592.
 PR 31-MAR-2000; 2000EP-00107028.
 PR 10-MAY-2000; 2000EP-00110110.
 XX
 PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & B.
 XX
 PI Reiter C, Cullmann G, Heppner P, Ringels A, Mueller H, Haindl B;
 XX
 XX WPI: 2001-282087/29.
 DR N-PSDB; AAF88060.
 DR
 XX
 PT Detecting infections by acid-resistant microorganisms, particularly for
 PT diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
 PT sample.
 XX
 PS Claim 23; Page 17; 89pp; German.
 XX
 CC This invention describes a novel method for detecting, in a mammal,
 CC infection by an acid-resistant microorganism (A) which comprises reacting
 CC a fecal sample with: (i) a receptor (R) such that a complex is formed
 CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part
 CC complex is formed with Ag, and the formation of a complex detected. R are
 CC specific for an Ag which, after passage through the intestines, at least
 CC in some mammals, retains a native (or corresponding) structure against
 CC which the mammal produces antibodies (when immunized or infected with
 CC (A), or its extracts, lysates or derived proteins (or fragments) or
 CC synthetic peptides). The products of the invention have antibacterial
 CC activity. The method is used to diagnose infection by Helicobacter,
 CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
 CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the
 CC progress of treatment. Receptors, particularly antibodies, directed
 CC against Ag can be used therapeutically for treatment of infections. The
 CC method requires only one R to provide a reasonably secure diagnosis.
 CC (although use of two R improves sensitivity), so is relatively
 CC inexpensive and more easily standardized. Also it is direct, non-
 CC invasive, suitable for automation and may indicate the stage of an
 CC infection. This sequence represents a complementarity determining region
 CC (CDR) from an antibody generated against a Helicobacter pylori antigen
 CC (catalase or beta-urease) which is used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 10 AA;
 Query Match 73.9%; Score 17; DB 4; Length 10;
 Best Local Similarity 40.0%; Pred. No. 3.4e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 DB 4 FSTSW 8
 RESULT 6
 AAB86058
 ADC07163

ID ADC07163 standard; peptide; 11 AA.
 XX
 AC ADC07163;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Painted lady AKH peptide 2.
 XX
 KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;
 KW antidiabetic; hypotensive; cardiant; antiarthritic; cyostatic;
 KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;
 KW obesity; type II diabetes; cholelithiasis; hypertension;
 KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;
 KW renal failure; liver; chronic pain; sleep apnea; stroke;
 KW urinary incontinence; painted lady.
 XX
 OS Synthetic.
 OS Vanessa cardui.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "Pyroglutamic acid"
 FT Misc-difference 11
 FT /note= "Preferably C-terminal amide"
 FT
 XX WO2003066080-A1.
 PN
 XX 14-AUG-2003.
 PD
 XX 07-FEB-2003; 2003WO-US003800.
 XX
 PR 07-FEB-2002; 2002US-00072419.
 XX
 PA (BLMB-) BLM GROUP.
 XX
 PI Schacter BZ, Schacter LP;
 XX
 XX WPI: 2003-712542/57.
 XX
 PT Pharmaceutical composition useful for promoting weight loss, comprises an
 PT insect adipokinetic hormone, having a pyroglutamate residue at its amino
 PT terminus.
 XX
 PS Claim 29; Page 20; 82pp; English.
 XX
 CC The invention relates to a novel method of promoting lipid mobilisation
 CC in a human which comprises administering an insect adipokinetic hormone
 CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,
 CC hypotensive, cardiant, antiarthritic, cyostatic, nephrotropic,
 CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The
 CC method of the invention may be useful for treating obesity, type II
 CC diabetes, cholelithiasis, hypertension, coronary heart disease,
 CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal
 CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary
 CC incontinence. The current sequence is that of the painted lady AKH
 CC peptide 2 of the invention.
 XX
 SQ Sequence 11 AA;
 Query Match 73.9%; Score 17; DB 7; Length 11;
 Best Local Similarity 40.0%; Pred. No. 3.6e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 DB 4 FTSSW 8
 RESULT 7
 AAE05735
 ID AAE05735 standard; peptide; 13 AA.
 XX

AC AAE05735;
 DT 24-SEP-2001 (first entry)
 XX Complementarity-determining region 3 (CDR3) of MoPhabs #7.
 DE CDR3; complementarity-determining region 3; monoclonal phage antibody;
 KW MoPhabs; antigen.
 KW Synthetic.
 XX US6265150-B1.
 XX 24-JUL-2001.
 XX 26-MAY-1998; 98US-00085072.
 XX 07-JUN-1995; 95US-00483633.
 PR 18-SEP-1997; 97US-00932892.
 XX (BECT) BECTON DICKINSON & CO.
 PA (CRUC-) CRUCCELL HOLLAND BV.
 XX Terstappen LW, Logtenberg T;
 PI WPI; 2001-463929/50.
 XX Obtaining a phage particle, useful for obtaining human antibodies against
 PT known and novel surface antigens, by incubating a phage library with
 PT target cells to allow binding of the antibody fragment to the antigen.
 XX Example 6; Col 6; 6pp; English.
 XX The invention relates to a method of obtaining a phage particle which has
 CC an antibody fragment directed against an antigen associated with the
 CC surface of target cells in a heterogeneous cell population. The method
 CC involves incubating a library of phage particles with the target cells to
 CC allow binding of the antibody fragment expressed on the surface of the
 CC phage particles to the antigen associated with the target cells. The
 CC method is useful for obtaining human antibodies against known and novel
 CC surface antigens in their native configuration, expressed on
 CC phenotypically defined subpopulations of cells. The present sequence is
 CC complementarity-determining region 3 (CDR3) of monoclonal phage
 CC antibodies (MoPhabs) used in the exemplification of the invention
 XX
 SQ Sequence 13 AA;
 Query Match 73.9%; Score 17; DB 4; Length 13;
 Best Local Similarity 40.0%; Pred. No. 4.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXX 5
 Db 6 FASSW 10
 RESULT 8
 ABG75574
 ID ABG75574 standard; peptide; 13 AA.
 XX
 AC ABG75574;
 XX 22-APR-2003 (first entry)
 DT CDR3 peptide sequence, #7, used in phage antibody construction.
 DE Phage; antibody; antigen; target cell; phage particle;
 XX cell-type specific phage antibody library; phage antibody; Phab;
 KW monoclonal phage antibody; MoPhab; blood cell; foetal bone marrow cell;
 KW complementarity determining region 3; CDR3; human.
 XX
 XX Homo sapiens.
 OS Synthetic.

XX US2002132228-A1.
 XX 19-SEP-2002.
 XX 24-MAY-2001; 2001US-00865048.
 XX 07-JUN-1995; 95US-00483633.
 PR 18-SEP-1997; 97US-00932892.
 PR 26-MAY-1998; 98US-00085072.
 XX (TERS/) TERSTAPPEN L W M M.
 PA (LOGT/) LOGTENBERG T.
 XX Terstappen LWM, Logtenberg T;
 PI WPI; 2003-174076/17.
 XX Obtaining phage having antibody specific for cell surface antigen of
 PT target cells in heterogeneous cell population, by incubating phage
 PT antibody library with target cells, and separating phage particles bound
 PT target cells.
 XX Example 6; Page 4; 5pp; English.
 XX The invention discloses a method for obtaining a phage comprising an
 CC antibody, or its fragment, directed against antigens associated with a
 CC target cells surface in a heterogeneous cell population. The method
 CC comprises providing a library of antibodies, or their fragments,
 CC expressed on the surface of phage particles, incubating the phage
 CC antibody library with the target cells, separating the target cells and
 CC phage particles associated with them from the phage particles not
 CC associated with the target cells and then recovering the phage particles.
 CC Also disclosed is a cell-type specific phage antibody library and an
 CC antibody, or antibody fragment, obtained using the method. The method is
 CC useful for obtaining a selection of phage antibodies (Phabs) and
 CC monoclonal phage antibodies (MoPhabs). The method is also useful for
 CC detecting known and novel structures on various populations of blood and
 CC foetal bone marrow cells. The sequence presented is an example of the
 CC partly randomised human complementarity determining region 3 (CDR3) used
 CC in the construction of the antibodies
 XX
 SQ Sequence 13 AA;
 Query Match 73.9%; Score 17; DB 6; Length 13;
 Best Local Similarity 40.0%; Pred. No. 4.2e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 FXXXX 5
 Db 6 FASSW 10
 RESULT 9
 AAM98088
 ID AAM98088 standard; peptide; 14 AA.
 XX
 AC AAM98088;
 XX 24-JAN-2002 (first entry)
 DT Human peptide #1363 encoded by a SNP oligonucleotide.
 DE Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 XX neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
 KW anyloid protein; angiopoietin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 XX Homo sapiens.

Query Match 73.9%; Score 17; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 |
 Db 4 FSTW 8

RESULT 12
 AAW57758
 ID AAW57758 standard; peptide; 15 AA.
 XX AC
 XX AAW57758;
 XX AC
 DT 17-SEP-1998 (first entry)
 XX Residues 16-30 of Cry j 2.
 DE Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;
 KW HLA class II molecule.
 KW Cryptomeria japonica.
 XX OS
 XX WO9820902-A1.
 XX PN
 XX 22-MAY-1998.
 XX PD
 XX 12-NOV-1997; 97WO-JP04129.
 XX PF
 XX 13-NOV-1996; 96JP-00302053.
 XX PR
 XX (MEIP) MEIJI MILK PROD CO LTD.
 XX PA
 XX Sone T, Kume A, Dairiki K, Kino K;
 XX WPI; 1998-297617/26.
 XX DR
 XX Peptides derived from Japanese cedar pollen antigens are
 PT immunotherapeutic agents - useful for allergy treatment and typing HLA
 PT class II molecules in allergy sufferers.
 XX PS
 XX Claim 12; Page 29; 50pp; Japanese.
 XX CC
 XX This sequence represents residues 16-30 of the Cry j 2 protein, and is a
 CC peptide of the invention. The peptides are derived from Japanese cedar
 CC pollen antigens, and are used as immunotherapeutic agents in the
 CC treatment of allergy. The peptides can be used for identification and
 CC typing of the particular HLA class II molecules in an allergy sufferer,
 CC and also for peptide immunotherapy of an allergy. Using these peptides
 CC the immunotherapy can be targeted more specifically to the requirements
 CC of the individual patient, allowing more effective treatment of an
 CC allergy, including those patients for whom treatment with a conventional
 CC immunotherapeutic agent is ineffective
 XX SQ
 SQ Sequence 15 AA;

Query Match 73.9%; Score 17; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 |
 Db 9 FSTW 13

RESULT 13
 AAE23038
 ID AAE23038 standard; peptide; 19 AA.
 XX AC
 XX AAE23038;
 XX AC

DT 21-AUG-2002 (first entry)
 XX Human thioredoxin, 47916 peptide.
 DE
 XX Human; thioredoxin; 22108; 47916; haematopoietic disorder; leukaemia;
 KW cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;
 KW cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;
 KW brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;
 KW cytostatic; carcinoma; cardiant; neuroprotective; antiinflammatory;
 KW gene therapy; nootropic.
 XX OS
 XX Homo sapiens.
 XX PN
 XX WO200226803-A2.
 XX PD
 XX 04-APR-2002.
 XX PF
 XX 25-SEP-2001; 2001WO-US029967.
 XX PR
 XX 25-SEP-2000; 2000US-0235049P.
 XX PA
 XX (MILL-) MILLENIUM PHARM INC.
 XX PI
 XX Bandaru R, Kapeller-Libermann R;
 XX WPI; 2002-416475/44.
 XX DR
 XX New human thioredoxin nucleic acid and polypeptide molecules, designated
 PT 22108 and 47916, useful for diagnosing, preventing or treating cancer
 PT (e.g. carcinoma), cardiovascular diseases (e.g. heart failure) or brain
 PT disorders.
 XX PS
 XX Disclosure; Page 11; 124pp; English.
 XX CC
 XX The invention relates to human thioredoxin nucleic acid and polypeptide
 CC molecules, designated 22108 and 47916. The compound that modulates the
 CC activity or expression of 22108 and 47916 nucleic acid is useful for
 CC treating or preventing a disorder characterised by aberrant activity of
 CC 22108 and 47916-expressing cell, specifically for reducing or inhibiting
 CC the aberrant activity of the 22108 and 47916-expressing cancer cell. The
 CC 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,
 CC preventing or treating cancer in a subject (e.g. carcinoma, sarcoma,
 CC metastatic or haematopoietic disorders (e.g. leukaemia), or cancers of the
 CC lung, breast, thyroid, head neck, prostate or genito-urinary tract),
 CC cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart
 CC failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's
 CC diseases). The thioredoxin DNA is also useful in gene therapy. The
 CC present sequence is human thioredoxin, 47916 peptide
 XX SQ
 SQ Sequence 19 AA;

Query Match 73.9%; Score 17; DB 5; Length 19;
 Best Local Similarity 40.0%; Pred. No. 5.6e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 |
 Db 4 FSATW 8

RESULT 14
 AAW42165
 ID AAW42165 standard; peptide; 20 AA.
 XX AC
 XX AAW42165;
 XX DT
 XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 16-JUN-1998 (first entry)
 XX T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.
 DE Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;
 KW

KW diagnosis; allergy; spring tree pollen disease; pollinosis.
 XX
 OS Chamaecypariss obtusa.
 PN WO9747648-A1.
 XX
 PD 18-DEC-1997.
 XX
 PF 12-JUN-1997; 97WO-JP002031.
 XX
 PR 14-JUN-1996; 96JP-00153527.
 XX
 PA (MEIP) MEIJI MILK PROD CO LTD.
 XX
 PI Kino K, Dairiri K;
 XX
 XX WPI; 1998-052242/05.
 XX
 XX T-cell epitope peptide portion of Japanese cypress pollen antigens Chao1
 PT and Chao2 - used for diagnosis and treatment of spring tree pollen
 PT disease.
 XX
 PS Claim 2; Page 36; 71pp; Japanese.
 XX
 CC The present sequence represents a T-cell epitope peptide from Japanese
 CC cypress pollen antigen Chao2. The present invention describes peptides
 CC which correspond to the T-cell epitope sites on Japanese cypress pollen
 CC antigens Chao1 and Chao2. The peptides can be used as a reagent for the
 CC diagnosis of allergy to Japanese cypress pollen, and as an antigen in the
 CC treatment and prevention of spring tree pollen disease in which the
 CC pollinosis involves reactivity to Japanese cypress pollen. (Updated on 25
 CC -MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 20 AA;
 Query Match 73.9%; Score 17; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 5.8e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 | | |
 Db 8 FATTW 12
 RESULT 15
 AAG62999 standard; peptide; 20 AA.
 ID AAG62999
 XX
 AC AAG62999;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Complementarity determining region 3 (CDR3) of VH chain of clone G101.
 XX
 KW Antibody; light chain; VH; amyloid protein; blood brain barrier;
 KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
 KW transferrin receptor; neurological disease; Alzheimer's disease;
 KW prion disease; AIDS-related dementia; epilepsy; brain injury.
 XX
 OS Homo sapiens.
 XX
 XX WO20014300-A2.
 PN
 XX 21-JUN-2001.
 PD
 XX 27-NOV-2000; 2000WO-GB004501.
 PF
 XX 13-DEC-1999; 99US-0170599P.
 PR
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA
 XX Webster C, Osbourn J, Ward G, Miller K;
 PT

XX
 DR WPI; 2001-398131/42.
 XX
 PT Mixture or panel of antibodies for selecting specific binding members
 PT that cross the blood brain barrier, for use in delivering different
 PT molecules and treating neurological diseases.
 XX
 PS Claim 1; Page 76; 109pp; English.
 XX
 CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
 CC of VL and VH chains of antibodies of the invention. The specification
 CC describes a mixture or panel of 5 different specific binding members,
 CC each comprising an antibody VH and/or VL variable domain and capable,
 CC when displayed on the surface of filamentous bacteriophage particles or
 CC in the case of a specific binding member comprising the D5 VH and/or VL
 CC variable domain when bound to human serum amyloid protein, to pass
 CC through a mammalian blood brain barrier (BBB). The panel is useful for
 CC the selection of specific binding members with a desired property such as
 CC ability to cross BBB, ability to bind endothelial cells or other brain
 CC cell antigen, ability to bind areas of inflammation in the brain or BBB
 CC breakdown or ability to bind intracellular adhesion molecules and to bind
 CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
 CC and treatment of human or animal body, including neurological diseases,
 CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
 CC epilepsy and traumatic brain injury and any diseases involving
 CC inflammation occurring within the brain or central nervous system
 XX
 SQ Sequence 20 AA;
 Query Match 73.9%; Score 17; DB 4; Length 20;
 Best Local Similarity 40.0%; Pred. No. 5.8e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 | | |
 Db 4 FSSSW 8
 RESULT 16
 ADE25429 standard; peptide; 25 AA.
 ID ADE25429
 XX
 AC ADE25429;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Plant growth associated peptide #1.
 XX
 KW plant growth; plant growth trait modulation; Brassicaceae; Arabidopsis;
 KW Brassica; Zea; Oryza; Triticum; Hordeum; Lolium; Sorghum; Glycine;
 KW Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon;
 KW Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Populus; Pinus;
 KW Quercus.
 XX
 OS Magnoliophyta.
 XX
 PN US2003188343-A1.
 XX
 PD 02-OCT-2003.
 XX
 PF 07-JAN-2003; 2003US-00338777.
 XX
 PR 09-JAN-2002; 2002US-0347288P.
 XX
 PA (LYNX-) LYNX THERAPEUTICS INC.
 XX
 PI Bowen BA, Haudenschild CD, Buckler ES;
 XX
 XX WPI; 2003-803305/75.
 DR
 XX New isolated or recombinant polypeptide for use in modulating a plant
 PT growth trait in a flowering plant e.g. in Arabidopsis, Brassica, Zea, or
 PT Oryza.

CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagazer syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: the sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 27 AA;
 Query Match 73.9%; Score 17; DB 5; Length 27;
 Best Local Similarity 40.0%; Pred. No. 7.4e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXX 5
 Db 4 FSATW 8
 RESULT 21
 AAB09301
 ID AAB09301 standard; protein; 29 AA.
 XX
 AC AAB09301;
 DT 06-AUG-2003 (revised)
 DT 30-AUG-2000 (first entry)
 XX
 DE Hepatitis GB virus protein sequence SEQ ID NO:428.
 XX
 KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
 KW detection; characterisation; hepatitis.
 XX
 OS Hepatitis GB virus.
 XX
 PN US6051374-A.
 XX
 PD 18-APR-2000.
 XX
 PF 07-JUN-1995; 95US-00488445.
 XX
 PR 14-FEB-1994; 94US-00196030.
 PR 13-MAY-1994; 94US-00242654.
 PR 29-JUL-1994; 94US-00283314.
 PR 23-NOV-1994; 94US-00344185.
 PR 23-NOV-1994; 94US-00344190.
 PR 30-JAN-1995; 95US-00377557.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
 PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
 XX
 DR WPI; 2000-338307/29.
 XX
 PT Detecting target hepatitis GB virus nucleic acid in a test sample
 PT suspected of containing HGBV comprises reacting the test sample the HGBV
 PT polynucleotide probe and detecting the complex that contains target HGBV.
 XX
 PS Example 18; Col 491-492; 369pp; English.
 XX
 CC The present invention describe a method for detecting target hepatitis GB
 CC virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of
 CC containing HGBV. The method involves reacting (T) with a HGBV
 CC polynucleotide probe (I) containing 15 contiguous nucleotides, and which
 CC selectively hybridises to the HGBV genome or its full complement, and
 CC detecting the complex that contains THN, indicating the presence of
 CC target HGBV. The method is used for detecting target HGBV nucleic acid in
 CC the test sample suspected of containing HGBV and for characterisation of
 CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
 CC -E hepatitis causing agents collectively termed as hepatitis GB virus.
 CC AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and

CC protein sequences used in the exemplification of the present invention.
 CC (Updated on 06-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 29 AA;
 Query Match 73.9%; Score 17; DB 3; Length 29;
 Best Local Similarity 40.0%; Pred. No. 7.8e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXX 5
 Db 12 PASAW 16
 RESULT 22
 AAG71365
 ID AAG71365 standard; peptide; 32 AA.
 XX
 AC AAG71365;
 DT 30-JUL-2001 (first entry)
 XX
 DE Human gene 10-encoded secreted protein fragment, SEQ ID NO:216.
 XX
 KW Human; secreted protein; proliferative disorder; cancer; chromosome 1;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angioinfectious disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder; tumour;
 KW endocrine disorder; infection; wound healing; vulnery; cell culture;
 KW chemotaxis; food additive; binding partner identification.
 XX
 OS Homo sapiens.
 XX
 PN WO200132674-A1.
 XX
 PD 10-MAY-2001.
 XX
 PF 25-OCT-2000; 2000WO-US029360.
 XX
 PR 29-OCT-1999; 99US-0162211P.
 PR 30-JUN-2000; 2000US-0215138P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Komatsoulis GA, Young PE, Moore PA;
 PI WPI; 2001-291051/30.
 DR
 XX
 PT New nucleic acid molecule encoding a human secreted protein, useful for
 PT preventing, treating or ameliorating medical conditions such as
 PT rheumatoid arthritis, Alzheimer's disease and microbial infections.
 XX
 PS Disclosure; Page 27; 581pp; English.
 XX
 CC AAH31349-AAH31428 represent cDNAs corresponding to 26 human secreted
 CC protein genes, and AAG71243-AAG71319 represent the proteins they encode.
 CC AAG71320-AAG71403 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 52 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin

CC disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention
 XX
 SQ Sequence 32 AA;

Query Match 73.9%; Score 17; DB 4; Length 32;
 Best Local Similarity 40.0%; Pred. No. 8.5e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 Db 15 FAATW 19

RESULT 23
 ABP60808
 ID ABP60808 standard; protein; 33 AA.
 AC ABP60808;
 DT 06-SEP-2002 (first entry)
 XX
 DE Sus scrofa thiodoxin SEQ ID NO:157.
 KW Multimeric protein; redox protein; thiodoxin; thiodoxin reductase;
 KW oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
 KW vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;
 KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KW gastro oesophageal reflux disease.
 XX
 OS Sus scrofa.

XX
 XX WO200250289-A1.
 XX
 XX 27-JUN-2002.
 XX
 XX 19-DEC-2001; 2001WO-US050240.
 XX
 XX 19-DEC-2000; 2000US-00742900.
 XX 05-JUL-2001; 2001US-0302885P.
 XX 04-DEC-2001; 2001US-00006038.
 XX
 XX (SENB-) SENBIOSYS GENETICS INC.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 XX Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
 XX Del Val G, Zaplachinski S, Moloney M;
 XX WPI; 2002-508806/54.
 XX

PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 PS Claim 81; Page 248; 362pp; English.
 XX The present invention describes a method (M1) for producing an oil body

CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 33 AA;

Query Match 73.9%; Score 17; DB 5; Length 33;
 Best Local Similarity 40.0%; Pred. No. 8.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
 Db 26 FSATW 30

RESULT 24
 ABO54713
 ID ABO54713 standard; protein; 33 AA.
 AC ABO54713;
 XX
 XX 29-JUL-2004 (first entry)
 DT Human genome derived single exon protein #947.
 XX
 DE Human; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 KW
 XX Homo sapiens.

OS
 XX US2003194704-A1.
 PN
 XX 16-OCT-2003.
 XX
 XX 03-APR-2002; 2002US-00029386.
 XX
 XX 03-APR-2002; 2002US-00029386.
 XX
 XX (PENN/) PENN S G.
 XX (RANK/) RANK D R.
 XX (HANZ/) HANZEL D K.
 XX
 XX Penn SG, Rank DR, Hanzel DK;
 XX
 XX WPI; 2004-119264/12.
 XX

XX New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 XX

PS Claim 45; SEQ ID NO 28347; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule

expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterizing alternative splicing events, in detecting and characterizing gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030194704

XX Sequence 33 AA;

Query Match 73.9%; Score 17; DB 8; Length 33;
Best Local Similarity 40.0%; Pred. No. 8.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 FXXXX 5
Db 14 FSASW 18

RESULT 25

AAR50631
ID AAR50631 standard; peptide; 34 AA.

XX AAR50631;

XX 08-MAY-1996 (first entry)

XX G-protein coupled receptor TM3 consensus polypeptide #77.

XX G-protein coupled receptor; ligand binding assay; transmembrane domain; psychotropic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin; muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine; rhodopsin; opsin; odorant; cytomegalovirus; serotonergic.

XX Synthetic.

XX WO9405695-A1.

XX 17-MAR-1994.

XX 09-SEP-1993; 93WO-US008528.

XX 10-SEP-1992; 92US-00943236.

XX (UUNY) UNIV NEW YORK STATE.

XX Murphy RB, Schuster DI;

XX WPI; 1994-101120/12.

XX Polypeptides of G-coupled receptor proteins (GPRs) - useful for binding

PT GPR ligands or modulating GPR binding.

PS Claim 9; Page 28; 160pp; English.

XX Polypeptides AAR48768-81 and AAR50569-R50718 are based on the consensus transmembrane domain III sequence from G-protein coupled receptor (GPR) proteins, and can be used in G-protein coupled receptor ligand binding assays. The assay can be used to identify fragments pref. transmembrane fragments, from GPR proteins (see AAR48686-R48758 for examples) which retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotropic disorder such as schizophrenia

XX Sequence 34 AA;

Query Match 73.9%; Score 17; DB 2; Length 34;
Best Local Similarity 40.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 FXXXX 5
Db 16 FTTAW 20

RESULT 26

AAR50593
ID AAR50593 standard; peptide; 34 AA.

XX AAR50593;

XX 03-MAY-1996 (first entry)

XX G-protein coupled receptor TM3 consensus polypeptide #39.

XX G-protein coupled receptor; ligand binding assay; transmembrane domain; psychotropic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin; muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine; rhodopsin; opsin; odorant; cytomegalovirus; serotonergic.

XX Synthetic.

XX WO9405695-A1.

XX 17-MAR-1994.

XX 09-SEP-1993; 93WO-US008528.

XX 10-SEP-1992; 92US-00943236.

XX (UUNY) UNIV NEW YORK STATE.

XX Murphy RB, Schuster DI;

XX WPI; 1994-101120/12.

XX Polypeptides of G-coupled receptor proteins (GPRs) - useful for binding GPR ligands or modulating GPR binding.

PS Claim 9; Page 27; 160pp; English.

XX Polypeptides AAR48768-81 and AAR50569-R50718 are based on the consensus transmembrane domain III sequence from G-protein coupled receptor (GPR) proteins, and can be used in G-protein coupled receptor ligand binding assays. The assay can be used to identify fragments pref. transmembrane fragments, from GPR proteins (see AAR48686-R48758 for examples) which retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotropic disorder

```

CC  such as schizophrenia
XX
SQ  Sequence 34 AA;

Query Match      73.9%; Score 17; DB 2; Length 34;
Best Local Similarity 40.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1 FXXW 5
Db  16 FTSW 20

RESULT 27
AAW02823
ID  AAW02823 standard; peptide; 34 AA.
XX
AC  AAW02823;
XX
DT  25-MAR-2003 (revised)
DT  20-SEP-1996 (first entry)
XX
DE  G-protein coupled receptor TM3 consensus polypeptide #78.
XX
KW  G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW  schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
KW  muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
KW  odorant; cytomagalovirus; serotonergic.
XX
OS  Synthetic.
XX
PN  US5508384-A.
XX
PD  16-APR-1996.
XX
PF  09-SEP-1993; 93US-00118270.
XX
PR  10-SEP-1992; 92US-00943236.
XX
PA  (UUNY ) UNIV NEW YORK STATE.
XX
PI  Schuster DI, Murphy RB;
XX
DR  WPI; 1996-208785/21.
XX
OS  Synthetic.
XX
PN  US5508384-A.
XX
PD  16-APR-1996.
XX
PF  09-SEP-1993; 93US-00118270.
XX
PR  10-SEP-1992; 92US-00943236.
XX
PA  (UUNY ) UNIV NEW YORK STATE.
XX
PI  Schuster DI, Murphy RB;
XX
DR  WPI; 1996-208785/21.
XX
PT  New dopamine receptor peptide - useful as antipsychotic agent, e.g. for
PT  treating schizophrenia.
XX
PS  Disclosure; Col 227-228; 184pp; English.
XX
CC  Polypeptides AAW02747-W02910 are based on the consensus transmembrane
CC  domain III sequence from G-protein coupled receptor (GPR) proteins and
CC  can be used in GPR ligand binding assays. The assays can be used to
CC  identify fragments, pref. transmembrane fragments, from GPR proteins (see
CC  AAW02657-W02635) which retain biological activity such as binding a GPR
CC  ligand or modulating a GPR ligand binding to a GPR (see W02747-AAW02999
CC  for examples of polypeptide fragments). The polypeptide fragments can be
CC  used in compns. for treating subjects suffering from a pathology related
CC  to a GPR abnormality e.g. schizophrenia. (Updated on 25-MAR-2003 to
CC  correct PF field.)
XX
SQ  Sequence 34 AA;

Query Match      73.9%; Score 17; DB 2; Length 34;
Best Local Similarity 40.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1 FXXW 5
Db  16 FTSW 20

RESULT 29
AAW08042
ID  AAW08042 standard; protein; 35 AA.
XX
AC  AAW08042;
XX
DT  06-NOV-2001 (first entry)
XX
DE  Human polypeptide SEQ ID NO 21934.
XX
KW  Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW  vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW  tissue growth factor; immunomodulatory; cancer; leukaemia;
KW  nervous system disorders; arthritis; inflammation.
XX

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```

OS Homo sapiens.
PN WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US004927.
XX
XX 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
DR N-PSDB; AAI87973.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 20; SEQ ID NO 21934; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 35 AA;
  Query Match 73.9%; Score 17; DB 4; Length 35;
  Best Local Similarity 40.0%; Pred. No. 9.1e+03;
  Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 3 FAATW 7

RESULT 30
AAI79941
ID AAI79941 standard; protein; 36 AA.
XX
XX AAI79941;
XX
XX 25-MAR-2003 (revised)
DT 01-FEB-1995 (first entry)
XX
XX Japanese cedar pollen allergen Cry j II fragment.
XX
XX Cedar pollinosis; diagnostic.
XX
XX Cryptomeria japonica.
XX
XX WO9411512-A2.
XX
XX 26-MAY-1994.
XX
XX 12-NOV-1993; 93WO-US011000.
XX
XX 12-NOV-1992; 92US-00975179.
XX
XX (IMMU-) IMMULOGIC PHARM CORP.
XX

PI Kuo M, Yeung S, Brauer A, Pollock J;
XX WPI; 1994-183513/22.
XX
XX Allergenic Cry j II protein and fragments from Japanese cedar pollen -
PT used to diagnose, treat and prevent Japanese cedar pollinosis.
XX
XX Disclosure; Page 47; 89pp; English.
XX
XX The sequence is of a Japanese cedar pollen allergen Cry j II fragment.
CC The protein and fragments can be used for diagnosis and treatment of
CC Japanese cedar pollinosis and to identify similar sequences in other
CC plants. See also AAR53690-6. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 36 AA;
  Query Match 73.9%; Score 17; DB 2; Length 36;
  Best Local Similarity 40.0%; Pred. No. 9.3e+03;
  Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 28 FSTAW 32

RESULT 31
AAO08979
ID AAO08979 standard; protein; 37 AA.
XX
XX AAO08979;
XX
XX 06-NOV-2001 (first entry)
DT Human polypeptide SEQ ID NO 22871.
DE
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US004927.
XX
XX 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
DR N-PSDB; AAI88910.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 20; SEQ ID NO 22871; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or

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CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: the sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
 XX
 SQ Sequence 37 AA;
 Query Match 73.9%; Score 17; DB 4; Length 37;
 Best Local Similarity 40.0%; Pred. No. 9.5e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 | | |
 Db 6 FAATW 10
 | | |
 XX
 RESULT 32
 AAY76339
 ID AAY76339 standard; protein; 38 AA.
 XX
 AC AAY76339;
 XX
 DT 23-MAR-2000 (first entry)
 XX
 DE Fragment of human secreted protein encoded by gene 38.
 XX
 KW Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO958660-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 06-MAY-1999; 99WO-US009847.
 XX
 PR 12-MAY-1998; 98US-0085093P.
 PR 12-MAY-1998; 98US-0085094P.
 PR 12-MAY-1998; 98US-0085105P.
 PR 12-MAY-1998; 98US-0085180P.
 PR 18-MAY-1998; 98US-0085906P.
 PR 18-MAY-1998; 98US-0085920P.
 PR 18-MAY-1998; 98US-0085921P.
 PR 18-MAY-1998; 98US-0085922P.
 PR 18-MAY-1998; 98US-0085923P.
 PR 18-MAY-1998; 98US-0085924P.
 PR 18-MAY-1998; 98US-0085925P.
 PR 18-MAY-1998; 98US-0085927P.
 PR 18-MAY-1998; 98US-0085928P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
 PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Latleur DW;
 PI Endress GA, Ebner R;
 XX
 DR WPI; 2000-062296/05.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders.
 XX
 PS Disclosure; Page 450; 475pp; English.
 XX
 CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
 CC AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human
 CC genes. This sequence represents a fragment of one of the human secreted

CC proteins. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions, e.g.
 CC by protein or gene therapy. Also pathological conditions can be diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new genes. Specific uses are
 CC described for each of the 97 genes, based on which tissues they are most
 CC highly expressed in, and include developing products for the diagnosis or
 CC treatment of cancer, tumours, developmental abnormalities and foetal
 CC deficiencies, blood disorders, diseases of the immune system, autoimmune
 CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
 CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
 CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
 CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
 CC also useful for identifying their binding partners. The sequences shown
 CC in AAY76224 to AAY76424 represent fragments of the secreted proteins
 XX
 SQ Sequence 38 AA;
 Query Match 73.9%; Score 17; DB 3; Length 38;
 Best Local Similarity 40.0%; Pred. No. 9.7e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FXXXW 5
 | | |
 Db 19 FFAAW 23
 | | |
 XX
 RESULT 33
 AAG10451
 ID AAG10451 standard; protein; 38 AA.
 XX
 AC AAG10451;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 8778.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-00301439.
 XX
 PR 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.
 PR 16-APR-1999; 99US-0129845P.
 PR 19-APR-1999; 99US-0130077P.
 PR 21-APR-1999; 99US-0130449P.
 PR 23-APR-1999; 99US-0130510P.
 PR 23-APR-1999; 99US-0130891P.
 PR 28-APR-1999; 99US-0131449P.
 PR 30-APR-1999; 99US-0132048P.
 PR 30-APR-1999; 99US-0132407P.
 PR 04-MAY-1999; 99US-0132484P.
 PR 05-MAY-1999; 99US-0132485P.
 PR 06-MAY-1999; 99US-0132486P.
 PR 06-MAY-1999; 99US-0132487P.
 PR 07-MAY-1999; 99US-0132863P.
 PR 11-MAY-1999; 99US-0134256P.
 PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135333P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136302P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139889P.
PR 23-JUN-1999; 99US-0140333P.
PR 24-JUN-1999; 99US-0140334P.
PR 24-JUN-1999; 99US-0140354P.
PR 28-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140931P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142330P.
PR 08-JUL-1999; 99US-0142803P.
PR 08-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144332P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 21-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 23-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 13-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.

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PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161392P.
PR 28-OCT-1999; 99US-0161393P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 73.9%; Score 17; DB 3; Length 38;
Best Local Similarity 40.0%; Pred. No. 9.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 23 FTTSW 27

RESULT 34
ID ADE11915 standard; protein; 38 AA.
XX AC ADE11915;
XX XX
DT 29-JAN-2004 (first entry)
XX XX
DE Human secreted polypeptide #169.
XX XX
KW Secreted protein; cancer; liver disorder; hepatitis; neural disorder;
KW Alzheimer's disease; human.
XX XX
OS Synthetic.
OS Homo sapiens.
XX XX
PN US2003100051-A1.
XX XX
PD 29-MAY-2003.
XX XX
PF 10-SEP-2001; 2001US-00948783.
XX XX
PR 12-MAY-1998; 98US-0085093P.
PR 12-MAY-1998; 98US-0085094P.
PR 12-MAY-1998; 98US-0085105P.
PR 12-MAY-1998; 98US-0085180P.
PR 18-MAY-1998; 98US-0085906P.
PR 18-MAY-1998; 98US-0085920P.
PR 18-MAY-1998; 98US-0085921P.
PR 18-MAY-1998; 98US-0085922P.
PR 18-MAY-1998; 98US-0085923P.
PR 18-MAY-1998; 98US-0085924P.
PR 18-MAY-1998; 98US-0085925P.
PR 18-MAY-1998; 98US-0085927P.
PR 06-MAY-1999; 99MO-US0059847.
PR 10-NOV-1999; 99US-00437658.
PR 11-SEP-2000; 2000US-0231846P.
PR 28-JUN-2001; 2001US-00892877.
XX XX
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (NIJU/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIV/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPPET D R.
PA (LAFLE/) LAFLEUR D W.

```

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PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
XX XX
PI Ruben SM, Florence KA, Ni J, Rosen CA, Carter KC, Moore PA;
PI Olsen HS, Shi Y, Young PE, Wei Y, Brewer LA, Soppet DR, Lafleur DW;
PI Endress GA, Ebner R, Birse CE;
XX XX
DR WPI; 2003-801210/75.
XX XX
PT New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g. cancer,
PT liver disorders or neural disorders.
XX XX
PS Claim 11; SEQ ID NO 287; 453pp; English.
XX XX
CC The invention relates to human secreted polypeptides and the
CC polynucleotides encoding them. The sequences are useful for preparing
CC medicaments for preventing, treating or ameliorating medical conditions
CC e.g., cancer, liver disorders such as hepatitis or neural disorders such
CC as Alzheimer's disease. This sequence represents a human secreted
CC polypeptide of the invention.
XX XX
SQ Sequence 38 AA;

Query Match 73.9%; Score 17; DB 7; Length 38;
Best Local Similarity 40.0%; Pred. No. 9.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 19 FFAAW 23

RESULT 35
AAV41113
ID AAY41113 standard; peptide; 40 AA.
XX XX
AC AAY41113;
XX XX
DT 17-JAN-2000 (first entry)
XX XX
DE TNFR/NGFR cysteine-rich domain of T129 polypeptide.
XX XX
KW Tumor necrosis factor receptor; TNF; T129 protein; TANGO 129; human;
KW cellular process; immunological disorder; abnormal lymphoid development;
KW thymic development; T-cell mediated immune response; humoral B cell;
KW skeletal muscle disorder; drug screening.
XX XX
OS Homo sapiens.
XX XX
PN WO952924-A1.
XX XX
PD 21-OCT-1999.
XX XX
PF 08-APR-1999; 99WO-US007832.
XX XX
PR 09-APR-1998; 98US-00057951.
XX XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX XX
PI Holtzman D;
XX XX
DR WPI; 1999-620368/53.
XX XX
PT New isolated tumor necrosis factor receptor member used to develop
PT products for treating, e.g. immunological disorders or disorders of the
PT skeletal muscle.
XX XX
PS Example 3; Fig 2; 118pp; English.
XX XX
CC The invention provides an isolated human tumor necrosis factor (TNF)
CC receptor member, T129 (also referred as TANGO 129). The T129 polypeptide

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CC can be expressed by standard recombinant methodology. The T219
 CC polypeptides are useful as modulating agents in regulating a variety of
 CC cellular processes. Agents or modulators which have a stimulatory or
 CC inhibitory effect on T129 activity (e.g. T129 gene expression) as
 CC identified by a screening assay can be administered to individuals to
 CC treat (prophylactically or therapeutically) disorders, e.g. an
 CC immunological disorder associated with aberrant T129 activity, disorders
 CC associated with abnormal lymphoid and/or thymic development, T-cell
 CC mediated immune response, T-cell dependent help for B cells, and abnormal
 CC humoral B cell activity, and possibly disorders of the skeletal muscle.
 CC The products can also be used for detection, diagnosis, drug screening
 CC and production of transgenic animals. The present sequence represents a
 CC TNFR/NGFR cysteine-rich domain of T129 polypeptide
 XX
 SQ

Sequence 40 AA;

Query Match 73.9%; Score 17; DB 2; Length 40;
 Best Local Similarity 40.0%; Pred. No. 1e+04; 3; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXKW 5
 Db 6 FSAAW 10

RESULT 36

AAG51555
 ID AAG51555 standard; protein; 40 AA.

AC AAG51555;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 65445.

KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-01231180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126244P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.

XX 23-APR-1999; 99US-0130510P.

XX 28-APR-1999; 99US-0130891P.

XX 30-APR-1999; 99US-0131449P.

XX 04-MAY-1999; 99US-0132048P.

XX 05-MAY-1999; 99US-0132484P.

PR 14-MAY-1999; 99US-0134370P.
 PR 18-MAY-1999; 99US-0134768P.
 PR 19-MAY-1999; 99US-0134941P.
 PR 20-MAY-1999; 99US-0135124P.
 PR 21-MAY-1999; 99US-0135533P.
 PR 24-MAY-1999; 99US-0135629P.
 PR 25-MAY-1999; 99US-0136021P.
 PR 27-MAY-1999; 99US-0136392P.
 PR 28-MAY-1999; 99US-0136782P.
 PR 01-JUN-1999; 99US-0137222P.
 PR 03-JUN-1999; 99US-0137528P.
 PR 04-JUN-1999; 99US-0137502P.
 PR 07-JUN-1999; 99US-0137724P.
 PR 08-JUN-1999; 99US-0138094P.
 PR 10-JUN-1999; 99US-0138540P.
 PR 10-JUN-1999; 99US-0138847P.
 PR 14-JUN-1999; 99US-0139119P.
 PR 16-JUN-1999; 99US-0139452P.
 PR 16-JUN-1999; 99US-0139453P.
 PR 17-JUN-1999; 99US-0139452P.
 PR 18-JUN-1999; 99US-0139454P.
 PR 18-JUN-1999; 99US-0139455P.
 PR 18-JUN-1999; 99US-0139456P.
 PR 18-JUN-1999; 99US-0139457P.
 PR 18-JUN-1999; 99US-0139458P.
 PR 18-JUN-1999; 99US-0139459P.
 PR 18-JUN-1999; 99US-0139460P.
 PR 18-JUN-1999; 99US-0139461P.
 PR 18-JUN-1999; 99US-0139462P.
 PR 18-JUN-1999; 99US-0139463P.
 PR 18-JUN-1999; 99US-0139750P.
 PR 18-JUN-1999; 99US-0139763P.
 PR 21-JUN-1999; 99US-0139817P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 73.9%; Score 17; DB 3; Length 40;
Best Local Similarity 40.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 33 FSSAW 37

RESULT 37
AAM37764
ID AAM37764 standard; protein; 40 AA.
XX
AC AAM37764;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #11801 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
(MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-48897/53.
XX
Human genome-derived single exon nucleic acid probes useful for analyzing
gene expression in human placenta.
XX
Claim 27; SEQ ID NO 38033; 654pp; English.
XX
The present invention relates to single exon nucleic acid probes (SENP:
see AAI31315-AAI57546). The present sequence is a peptide encoded by one
such probe. The probes are useful for producing a microarray for
predicting, measuring and displaying gene expression in samples derived
from human placenta. The probes are useful for antenatal diagnosis of
human genetic disorders
XX
SQ Sequence 40 AA;

Query Match 73.9%; Score 17; DB 4; Length 40;
Best Local Similarity 40.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
|
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Db      23 FTSSW 27
RESULT 38
AAB64755
ID AAB64755 standard; protein; 40 AA.
XX
AC AAB64755;
XX
DT 23-MAR-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 36 SEQ ID NO:149.
XX
KW Human; secreted protein; diagnosis; cytostatic; antirheumatic;
KW antiarthritic; dermatological; cardiant; antiinflammatory; anti-ulcer;
KW gastrointestinal; solid tumour; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; myocardial angiogenesis; Crohn's disease; ulcer.
XX
OS Homo sapiens.
XX
PN WO200077237-A1.
XX
PD 21-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US014928.
XX
PR 11-JUN-1999; 99US-0138633P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM, Komatsoulis GA;
XX
DR WPI; 2001-071280/08.
XX
PT Nucleic acids encoding 49 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating diseases such as tumors,
PT rheumatoid arthritis, psoriasis and diabetic retinopathy.
XX
PS Disclosure; Page 510; 520pp; English.
XX
CC The polynucleotide sequences given in AAF33037 to AAF33085 encode the
CC human secreted proteins given in AAB64666 to AAB64714. AAB64715 to
CC AAB64771 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Examples of activities include:
CC cytostatic; antirheumatic; antiarthritic; dermatological; cardiant;
CC antiinflammatory; gastrointestinal; and anti-ulcer. The polynucleotides
CC and polypeptides can be used in the prevention, treatment and diagnosis
CC of diseases associated with inappropriate polypeptide expression.
CC Disorders that may be treated or prevented include solid tumours,
CC rheumatoid arthritis, psoriasis, diabetic retinopathy, myocardial
CC angiogenesis, Crohn's disease and ulcers. The polynucleotides and their
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate
CC the presence of similar nucleic acid sequences in samples, and therefore
CC which patients may be in need of restorative therapy. The polypeptides
CC may also be used as antigens in the production of antibodies against the
CC polypeptide and in assays to identify modulators (agonists and
CC antagonists) of polypeptide expression and activity. The anti-polypeptide
CC antibodies and antagonists may also be used to down regulate expression
CC and activity. AAF33028 to AAF33036 and AAB64665 represent sequences used
CC in the exemplification of the present invention
XX
SQ Sequence 40 AA;

Query Match 73.9%; Score 17; DB 4; Length 40;
Best Local Similarity 40.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXX 5
| |
Db 20 FATTW 24

RESULT 40
AAB64830
ID AAB64830 standard; protein; 40 AA.
XX
AC AAB64830;
XX
DT 05-NOV-2001 (first entry)
XX

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```

Db      8 FAATW 12
RESULT 39
AAO06835
ID AAO06835 standard; protein; 40 AA.
XX
AC AAO06835;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 20727.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US004927.
XX
PR 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI86766.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
PS Claim 20; SEQ ID NO 20727; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO33910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 40 AA;

Query Match 73.9%; Score 17; DB 4; Length 40;
Best Local Similarity 40.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXX 5
| |
Db 20 FATTW 24

RESULT 40
AAB64830
ID AAB64830 standard; protein; 40 AA.
XX
AC AAB64830;
XX
DT 05-NOV-2001 (first entry)
XX

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XX Human brain expressed single exon probe encoded protein SEQ ID NO: 36935.
DE Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
KW Homo sapiens.
OS WO200157275-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000667.
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX Example 4; SEQ ID NO 36935; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX Sequence 40 AA;
SQ

Query Match 73.9%; Score 17; DB 4; Length 40;
Best Local Similarity 40.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 23 FTSSW 27

Search completed: October 18, 2005, 15:26:10
Job time : 116.529 secs

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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:22:12 ; Search time 351.059 Seconds
(without alignments)
26.617 Million cell updates/sec

Title: US-09-214-371-10
Perfect score: 23
Sequence: 1 FXXWXXX 8

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 6959266 seqs, 116806243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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15: /cgn2_6/ptodata/1/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
29.725 Million cell updates/sec

Title: US-09-214-371-10

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Total number of hits satisfying chosen parameters: 1237731

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Tue Oct 18 16:44:44 2005

us-09-214-371-10.max.rapn

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:55:09 ; Search time 49.8824 Seconds
(without alignments)
29.915 Million cell updates/sec

Title: US-09-214-371-10
Perfect score: 23
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Searched: 850841 seqs, 186528192 residues

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Post-processing: Minimum Match 0%
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7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID
No.	Score	Match	Length	ID	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:41:40 ; Search time 312.471 Seconds
(without alignments)
29.904 Million cell updates/sec

Title: US-09-214-371-10
Perfect score: 23
Sequence: 1 FXXWXXX 8

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 1237731

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

Pending Patents AA Main:*

- 1: /cgn2_6/ptodata/1/paa/PCTUS COMB.pep:*
- 2: /cgn2_6/ptodata/1/paa/US06 COMB.pep:*
- 3: /cgn2_6/ptodata/1/paa/US07 COMB.pep:*
- 4: /cgn2_6/ptodata/1/paa/US080 COMB.pep:*
- 5: /cgn2_6/ptodata/1/paa/US081 COMB.pep:*
- 6: /cgn2_6/ptodata/1/paa/US082 COMB.pep:*
- 7: /cgn2_6/ptodata/1/paa/US083 COMB.pep:*
- 8: /cgn2_6/ptodata/1/paa/US084 COMB.pep:*
- 9: /cgn2_6/ptodata/1/paa/US085 COMB.pep:*
- 10: /cgn2_6/ptodata/1/paa/US086 COMB.pep:*
- 11: /cgn2_6/ptodata/1/paa/US087 COMB.pep:*
- 12: /cgn2_6/ptodata/1/paa/US088 COMB.pep:*
- 13: /cgn2_6/ptodata/1/paa/US089 COMB.pep:*
- 14: /cgn2_6/ptodata/1/paa/US090 COMB.pep:*
- 15: /cgn2_6/ptodata/1/paa/US091 COMB.pep:*
- 16: /cgn2_6/ptodata/1/paa/US092 COMB.pep:*
- 17: /cgn2_6/ptodata/1/paa/US093 COMB.pep:*
- 18: /cgn2_6/ptodata/1/paa/US094 COMB.pep:*
- 19: /cgn2_6/ptodata/1/paa/US095 COMB.pep:*
- 20: /cgn2_6/ptodata/1/paa/US096 COMB.pep:*
- 21: /cgn2_6/ptodata/1/paa/US097A COMB.pep:*
- 22: /cgn2_6/ptodata/1/paa/US097B COMB.pep:*
- 23: /cgn2_6/ptodata/1/paa/US098 COMB.pep:*
- 24: /cgn2_6/ptodata/1/paa/US099 COMB.pep:*
- 25: /cgn2_6/ptodata/1/paa/US099A COMB.pep:*
- 26: /cgn2_6/ptodata/1/paa/US099B COMB.pep:*
- 27: /cgn2_6/ptodata/1/paa/US100 COMB.pep:*
- 28: /cgn2_6/ptodata/1/paa/US101 COMB.pep:*
- 29: /cgn2_6/ptodata/1/paa/US102 COMB.pep:*
- 30: /cgn2_6/ptodata/1/paa/US103 COMB.pep:*
- 31: /cgn2_6/ptodata/1/paa/US104 COMB.pep:*
- 32: /cgn2_6/ptodata/1/paa/US105 COMB.pep:*
- 33: /cgn2_6/ptodata/1/paa/US106 COMB.pep:*
- 34: /cgn2_6/ptodata/1/paa/US107 COMB.pep:*
- 35: /cgn2_6/ptodata/1/paa/US108 COMB.pep:*
- 36: /cgn2_6/ptodata/1/paa/US109 COMB.pep:*
- 37: /cgn2_6/ptodata/1/paa/US110 COMB.pep:*
- 38: /cgn2_6/ptodata/1/paa/US60 COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 19, 2005, 15:33:09 ; Search time 50.8235 Seconds
(without alignments)
31.758 Million cell updates/sec

Title: US-09-214-371-10
Perfect score: 23
Sequence: 1 FXXXXXX 8

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 897115 seqs, 201758920 residues

Total number of hits satisfying chosen parameters: 172224

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Pending Patents AA New:*

1:	/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
2:	/cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3:	/cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4:	/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5:	/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6:	/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7:	/cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep.*
8:	/cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	ID	Description
No.	Score	Match Length	DB

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 19, 2005, 15:41:40 ; Search time 351.529 Seconds
(without alignments)
29.904 Million cell updates/sec

Title: US-09-214-371-11
Perfect score: 24
Sequence: 1 XPXXXXXX 9

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 1237731

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Pending Patents AA Main:*

1:	/cgn2_6/ptodata/1/paa/PCTUS COMB.pep.*
2:	/cgn2_6/ptodata/1/paa/US06 COMB.pep.*
3:	/cgn2_6/ptodata/1/paa/US07 COMB.pep.*
4:	/cgn2_6/ptodata/1/paa/US08 COMB.pep.*
5:	/cgn2_6/ptodata/1/paa/US081 COMB.pep.*
6:	/cgn2_6/ptodata/1/paa/US082 COMB.pep.*
7:	/cgn2_6/ptodata/1/paa/US083 COMB.pep.*
8:	/cgn2_6/ptodata/1/paa/US084 COMB.pep.*
9:	/cgn2_6/ptodata/1/paa/US085 COMB.pep.*
10:	/cgn2_6/ptodata/1/paa/US086 COMB.pep.*
11:	/cgn2_6/ptodata/1/paa/US087 COMB.pep.*
12:	/cgn2_6/ptodata/1/paa/US088 COMB.pep.*
13:	/cgn2_6/ptodata/1/paa/US089 COMB.pep.*
14:	/cgn2_6/ptodata/1/paa/US090 COMB.pep.*
15:	/cgn2_6/ptodata/1/paa/US091 COMB.pep.*
16:	/cgn2_6/ptodata/1/paa/US092 COMB.pep.*
17:	/cgn2_6/ptodata/1/paa/US093 COMB.pep.*
18:	/cgn2_6/ptodata/1/paa/US094 COMB.pep.*
19:	/cgn2_6/ptodata/1/paa/US095 COMB.pep.*
20:	/cgn2_6/ptodata/1/paa/US096 COMB.pep.*
21:	/cgn2_6/ptodata/1/paa/US097A COMB.pep.*
22:	/cgn2_6/ptodata/1/paa/US097B COMB.pep.*
23:	/cgn2_6/ptodata/1/paa/US098 COMB.pep.*
24:	/cgn2_6/ptodata/1/paa/US099A COMB.pep.*
25:	/cgn2_6/ptodata/1/paa/US099B COMB.pep.*
26:	/cgn2_6/ptodata/1/paa/US100 COMB.pep.*
27:	/cgn2_6/ptodata/1/paa/US101 COMB.pep.*
28:	/cgn2_6/ptodata/1/paa/US102 COMB.pep.*
29:	/cgn2_6/ptodata/1/paa/US103 COMB.pep.*
30:	/cgn2_6/ptodata/1/paa/US104 COMB.pep.*
31:	/cgn2_6/ptodata/1/paa/US105 COMB.pep.*
32:	/cgn2_6/ptodata/1/paa/US106 COMB.pep.*
33:	/cgn2_6/ptodata/1/paa/US107 COMB.pep.*
34:	/cgn2_6/ptodata/1/paa/US108 COMB.pep.*
35:	/cgn2_6/ptodata/1/paa/US109 COMB.pep.*
36:	/cgn2_6/ptodata/1/paa/US110 COMB.pep.*
37:	/cgn2_6/ptodata/1/paa/US60 COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:33:09 ; Search time 57.1765 Seconds
(without alignments)
31.758 Million cell updates/sec

Title: US-09-214-371-11
Perfect score: 24
Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 897115 seqs, 201758920 residues

Total number of hits satisfying chosen parameters: 172224

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Pending Patents AA New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	DB ID	Description
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:22:12 ; Search time 394.941 Seconds
(without alignments)
26.617 Million cell updates/sec

Title: US-09-214-371-11
Perfect score: 24
Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending Patents AA Main:
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/1/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/1/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/1/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/1/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep.*
25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
28: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
29: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
30: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*
31: /cgn2_6/ptodata/1/paa/US105_COMB.pep.*
32: /cgn2_6/ptodata/1/paa/US106_COMB.pep.*
33: /cgn2_6/ptodata/1/paa/US107_COMB.pep.*
34: /cgn2_6/ptodata/1/paa/US108_COMB.pep.*
35: /cgn2_6/ptodata/1/paa/US109_COMB.pep.*
36: /cgn2_6/ptodata/1/paa/US110_COMB.pep.*
37: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:26:23 ; Search time 58.2353 Seconds
(without alignments)
28.827 Million cell updates/sec

Title: US-09-214-371-11
Perfect score: 24
Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 850841 seqs, 186528192 residues

Total number of hits satisfying chosen parameters: 850841

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending Patents AA New.*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:50:44 ; Search time 353.647 Seconds
(without alignments)
29.725 Million cell updates/sec

Title: US-09-214-371-11
Perfect score: 24
Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 1237731

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

Pending Patents AA Main:*

- 1: /cgn2_6/ptodata/1/paa/PCTUS COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06 COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07 COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08 COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US081 COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US082 COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US083 COMB.pep.*
- 8: /cgn2_6/ptodata/1/paa/US084 COMB.pep.*
- 9: /cgn2_6/ptodata/1/paa/US085 COMB.pep.*
- 10: /cgn2_6/ptodata/1/paa/US086 COMB.pep.*
- 11: /cgn2_6/ptodata/1/paa/US087 COMB.pep.*
- 12: /cgn2_6/ptodata/1/paa/US088 COMB.pep.*
- 13: /cgn2_6/ptodata/1/paa/US089 COMB.pep.*
- 14: /cgn2_6/ptodata/1/paa/US090 COMB.pep.*
- 15: /cgn2_6/ptodata/1/paa/US091 COMB.pep.*
- 16: /cgn2_6/ptodata/1/paa/US092 COMB.pep.*
- 17: /cgn2_6/ptodata/1/paa/US093 COMB.pep.*
- 18: /cgn2_6/ptodata/1/paa/US094 COMB.pep.*
- 19: /cgn2_6/ptodata/1/paa/US095 COMB.pep.*
- 20: /cgn2_6/ptodata/1/paa/US096 COMB.pep.*
- 21: /cgn2_6/ptodata/1/paa/US097A COMB.pep.*
- 22: /cgn2_6/ptodata/1/paa/US097B COMB.pep.*
- 23: /cgn2_6/ptodata/1/paa/US098 COMB.pep.*
- 24: /cgn2_6/ptodata/1/paa/US099A COMB.pep.*
- 25: /cgn2_6/ptodata/1/paa/US099B COMB.pep.*
- 26: /cgn2_6/ptodata/1/paa/US100 COMB.pep.*
- 27: /cgn2_6/ptodata/1/paa/US101 COMB.pep.*
- 28: /cgn2_6/ptodata/1/paa/US102 COMB.pep.*
- 29: /cgn2_6/ptodata/1/paa/US103 COMB.pep.*
- 30: /cgn2_6/ptodata/1/paa/US104 COMB.pep.*
- 31: /cgn2_6/ptodata/1/paa/US105 COMB.pep.*
- 32: /cgn2_6/ptodata/1/paa/US106 COMB.pep.*
- 33: /cgn2_6/ptodata/1/paa/US107 COMB.pep.*
- 34: /cgn2_6/ptodata/1/paa/US108 COMB.pep.*
- 35: /cgn2_6/ptodata/1/paa/US109 COMB.pep.*
- 36: /cgn2_6/ptodata/1/paa/US110 COMB.pep.*
- 37: /cgn2_6/ptodata/1/paa/US60 COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:55:09 ; Search time 56.1176 Seconds
(without alignments)
29.915 Million cell updates/sec

Title: US-09-214-371-11
Perfect score: 24
Sequence: 1 XFXXXXXXX 9

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 850841 seqs, 186528192 residues

Total number of hits satisfying chosen parameters: 171822

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Pending Patents AA New:
1: /cgn2_6/ptodata/2/paa/PCT NEW COMB.pcp.*
2: /cgn2_6/ptodata/2/paa/US06 NEW COMB.pcp.*
3: /cgn2_6/ptodata/2/paa/US07 NEW COMB.pcp.*
4: /cgn2_6/ptodata/2/paa/US08 NEW COMB.pcp.*
5: /cgn2_6/ptodata/2/paa/US09 NEW COMB.pcp.*
6: /cgn2_6/ptodata/2/paa/US10 NEW COMB.pcp.*
7: /cgn2_6/ptodata/2/paa/US11 NEW COMB.pcp.*
8: /cgn2_6/ptodata/2/paa/US60 NEW COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	70.8	9	7	US-11-223-021-6720 Sequence 6720, Ap
2	17	70.8	9	7	US-11-223-045-6023 Sequence 6023, Ap
3	17	70.8	14	5	US-09-749-280D-9233 Sequence 9233, Ap
4	16	66.7	6	6	US-10-945-751-97 Sequence 97, Appl
5	16	66.7	7	7	US-11-129-741-699 Sequence 699, Appl
6	16	66.7	8	6	US-10-945-751-71 Sequence 71, Appl
7	16	66.7	8	6	US-10-776-521B-215 Sequence 215, Appl
8	16	66.7	8	6	US-10-820-067A-239 Sequence 239, Appl
9	16	66.7	8	6	US-10-820-067A-243 Sequence 243, Appl
10	16	66.7	8	6	US-10-820-067A-725 Sequence 725, Appl
11	16	66.7	9	1	PCT-US04-27792A-35 Sequence 35, Appl
12	16	66.7	9	1	PCT-US04-33241-18 Sequence 18, Appl
13	16	66.7	9	6	US-10-817-970-2854 Sequence 2854, Ap
14	16	66.7	9	6	US-10-817-970-3154 Sequence 3154, Ap
15	16	66.7	9	6	US-10-817-970-14185 Sequence 14185, A
16	16	66.7	9	6	US-10-817-970-14186 Sequence 14186, A
17	16	66.7	9	6	US-10-817-970-14188 Sequence 14188, A
18	16	66.7	9	6	US-10-817-970-14189 Sequence 14189, A
19	16	66.7	9	6	US-10-817-970-14419 Sequence 14419, A
20	16	66.7	9	6	US-10-010-748A-797 Sequence 797, Appl
21	16	66.7	9	6	US-10-010-748A-817 Sequence 817, Appl
22	16	66.7	9	7	US-11-010-748A-797 Sequence 797, Appl
23	16	66.7	9	7	US-11-010-748A-817 Sequence 817, Appl
24	16	66.7	9	7	US-11-027-670-768 Sequence 768, Appl
25	16	66.7	9	7	US-11-027-670-815 Sequence 815, Appl

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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:26:23 ; Search time 51.7647 Seconds
(without alignments)
28.827 Million cell updates/sec

Title: US-09-214-371-10
Perfect score: 23
Sequence: 1 FXXWXXX 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 850841 seqs, 186528192 residues

Total number of hits satisfying chosen parameters: 850841

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US05_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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